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/tissue type="Human Placenta"  
/lab host="DH10B Tona"  
/clone lib="NIH MGC 147"  
/note="Organ: placenta; Vector: pBluescriptR; Site 1:  
all-XhoI; Site 2: BamH; Oligo-dr primed using primer  
5'-TTTTTTTTTTTTTNN-3', size-selected for average  
insert size 2.3 kb and normalized to ROT 5. This is a  
primary library enriched for full-length clones and  
constructed using the Cap-trapper method (Carninci, in  
preparation). Library constructed by M. Brownstein, in  
(NIH/NHGRI, National Institutes of Health). Note: This is  
a NIH MGC library."  
BASE COUNT 147 a 246 c 245 g 124 t 9 others  
ORIGIN
```

Alignment Scores:

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Pred. No.: 1.35e-59 Length: 771  
Score: 892.50 Matches: 170  
Percent Similarity: 88.00% Conservative: 6  
Best Local Similarity: 85.00% Mismatches: 19  
Query Match: 60.51% Indels: 5  
DB: 14 Gaps: 2
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US-10-047-021-86_COPY_28_303 (1-276) x CB959649 (1-771)

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Qy 1 GlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGly 20  
Db |||||  
147 CAGGACTCCCCCGCCACAGATCTAGTCCACCCACAGGACCAGCTGTTCCAGGGCCCTGGC 206  
  
Qy 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTyrLeuLeu 40  
Db |||||  
207 CCTGCCAGGATGAGTGCAGACCTCAGGCCAGCCACCTCCACCATCCGCTGGTTGCTG 266  
  
Qy 41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60  
Db |||||  
267 AATGGGACGCCCTGAGATGGTGGCCGCCACACCCACACCTCCCTGCTGATGGGACC 326  
  
Qy 61 LeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80  
Db |||||  
327 CTTCGTGCTGTACAGCCCTGCGGGGACATGCCCCACGATGGCCAGGCCCTGTCCACA 386  
  
Qy 81 AspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100  
Db |||||  
387 GACCTGGGTGTCTACACATGTGAGGCCAGCAACCGCTTGGCAGCGCAGTCAGCAGAGGC 446  
  
Qy 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal 120  
Db |||||  
447 GCTCGGCTGTCTGTGGCTGTCTCGGGAGGATTTCCAGATCCAGCCTCGGGACATGGTG 506  
  
Qy 121 AlaValValGlyGluGlnPheThrLeuGluCysGlyProProTyrGlyHisProGluPro 140  
Db |||||  
507 GCTGTGGTGGGTGAGCAGCTTACTCTGGAATGTGGCCGCCCTGGGGCCACCAGAGCCC 566  
  
Qy 141 ThrValSerTyrTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThr--- 159  
Db |||||  
567 ACAGTCTCATGTGGAAGATGGGAAACCCCTGGCCCTCCAGCCCGGAAGGCACACAGTG 626  
  
Qy 160 ValSerGlyGlySerLeuLeuMetAla-----ArgAlaGluLysSerAspGlu 175  
Db |||||  
627 GTCCGGGGGGGTCCCTNCTGATGGCAANGAGCAGAGAGATGGACGAGAGGGGACCCT 686  
  
Qy 176 ***ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArg 195  
Db |||||  
687 ANNCATGTGTGGTGGGCCANNCCACACGGCGCAGGACCATAGGGGAGAAAGCCCGC 746
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Job time : 1681.59 secs

AUTHORS TITLE JOURNAL COMMENT

NIH-MGC <http://mgc.mci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM12364 row: o column: 16
High quality sequence stop: 535.

FEATURES

source

1..1230
Location/Qualifiers
1. 1230
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/clone="IMAGE:5590503"
/lab_host="DH10B"
/clone_lib="NIH_MGC_125"
/note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
Site 1: EcoRV (destroyed); Site 2: NotI; RNA source pool
of three ovaries, from females ranging in age from 38 to
49 yo. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 2.1 kb, insert size range 1-3.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 036."

BASE COUNT 257 a 429 c 326 g 217 t 1 others
ORIGIN

Alignment Scores:

Pred. No.: 1.06e-59 Length: 1230
Score: 897.00 Matches: 195
Percent Similarity: 64.31% Conservative: 14
Best Local Similarity: 60.00% Mismatches: 37
Query Match: 60.81% Indels: 79
DB: 12 Gaps: 10

US-10-047-021-86_COPY_28_303 (1-276) x BM906521 (1-1230)

Qy 1 GlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPheInclnGlyProGly 20
Db 116 CAGGACTCCCGCCCGCAGATCTAGTCCACCCCGGACCCAGCAGCTGTCCAGGGCCCTGGC 175
Qy 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTrpLeuLeu 40
Db 176 CTTGCCAGGATGAGTGTCCAGCCTCAGCCAGCCACCTCCACCATCCGCTGGTGTGTG 235
Qy 41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60
Db 236 AATGGGACGCCCTGAGCATGTGCTCCCGGAGACATGCCACAGCCAGCAGCTCTGCTGATGGACC 295
Qy 61 LeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80
Db 296 CTTCTGCTGTACTAGCCCTCCCGGGGACATGCTCCACAGTGGCGGACGCCCTGTCCACA 355
Qy 81 AspLeuGlyValThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100
Db 356 GACCTGGGTGTACATGTGAGGCCAGCAACCGGCTTGGCCAGCGCAGTCCAGCAGAGCC 415
Qy 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal 120
Db 416 GCTGGCTGTCTGTGCTGTCTCTCCGGGAGGATTTCCAGATCCAGCTCGGGACATGTGTG 475
Qy 121 AlaValValGlyGlnPheThrLeuGluCysGlyProProTrpGlyHisProGlnPro 140
Db 476 GCTGTGGTGGTGAGCAGTTTACTCTGGAATGTGGCGCGCCCTGGGGCCACCCAGAGCCC 535
Qy 141 ThrValSerTrpTrpLeuAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrVal 160

Db 536 ACAGTCTCATGTGGAAGATGGAAACCCCTGGCCCTCCAGCCCGGAAGGCACAGTG 595
Qy 161 ---SerGlyGlySerLeuLeuMetAla-----ArgAlaGlu 171
Db 596 TGCCGGGGGGGTCCCTGGTTGATGGCCATATGCCACAGCTTTCTGGGCTAAAGGCATTA 655
Qy 172 Lys-----
Db 656 AAATGTTGTGTCGCGCCCGCTAAACCCCAAGGACCCCTTGGACAGGCACAGACAC 715
Qy 173 -----SerAspGlu***ThrTyrMetCysVal----- 181
Db 716 TACAGGCGCCCTTTCTCGGTAATGACCCCGCTACATACTCATGACACCCCATTCGTCTC 775
Qy 182 ---AlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIle----- 198
Db 776 CCCCCTTCTTCTGCGCGCGGTGCGCCACCTTACTTTCTCGCGCTCGACACACGCGCCAC 835
Qy 199 -----GlnGluProGlnAsp-----TyrThr 205
Db 836 CTGGGACTTTTGACCGGACCGCGCAGACTAAGATCCGACAGAGCTATCTCTACACC 895
Qy 206 GluProValGluLeuLeuAlaValArgIleGlnLeuGluAsnValThrLeuLeuAsnPro 225
Db 896 GCCCCAGCA-----TCAGATGCGCGGAGCTCGAAGCGTTCCTCCGCTCCACCGT 946
Qy 226 AspPro-----AlaGluGly 230
Db 947 TACCGCGCCCTCTCTTGTATGTACCGAGGAGAAATTTGCGCGCATCGGGCGGAAGA 1006
Qy 231 ProLysProArg-ProAlaValTrpLeu***TrpLysValSerGlyPro***ArgLeuPr 250
Db 1007 CCGGAA---AGAGCCCGCC-----TGGCGAACCGGACGACATATAAAGCGCC 1051
Qy 250 oAsnLeuThrArg 254
Db 1052 AGATCTATGAAGA 1064
RESULT 15
CB959649
LOCUS
DEFINITION
AGENCOURT 13893577 NIH MGC 147 Homo sapiens cDNA clone
IMAGE:30344820 5', mRNA sequence.
ACCESSION
CB959649
VERSION
CB959649.1 GI:30215765
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 771)
AUTHORS
NIH-MGC <http://mgc.mci.nih.gov/>.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: NDAM381 row: 1 column: 13
High quality sequence stop: 628.
Location/Qualifiers
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/db_xref="taxon:9606"
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 Qy 151 LeuAlaLeuGlnProGlyArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAla 170
 Db 183 CTGGCCCTCCAGCCCGGAGGACACACATGTGTCGGGGGGTCCCTGCTGATGGCAAGACA 242
 Qy 171 GluYsSerAspGlu***ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGlu 190
 Db 243 GAGAAGAGTACGAGGAGGACCTACATGTGTGTGGCCACCAACAGCGCAGGACATAGGGAG 302
 Qy 191 SerArgAlaAlaArgValSerIleGlnProGlnAspTyrThrGluProValGluLeu 210
 Db 303 AGCCGCGCAGCCCGGTTTCCATCAGAGAGCCCGAGGACTACAGGAGCCCTGTGGAGCTT 362
 Qy 211 LeuAlaValArgIleGlnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGly 230
 Db 363 CTGGCTGTGCATTCAGCTGGAAATGTGACATGCTGAACCCGGATCTTCGAGAGGC 422
 Qy 231 ProYsProArgProAlaValTrpLeu***TrpYsValSerGlyPro***ArgLeuPr 250
 Db 423 CCCAAGCCTAGACCGCGGTGTGGCTCAGCTGGAAGGTCACTGGGCCCTGTGCGCTGCC 482
 Qy 250 AsnLeuThrArgProCysSerGlyProArgLeuProArgGluAlaArgGluLeuArgG1 270
 Db 483 CAATCTTACCGGGCTTGTTCAGGACCCAGACTGCCCGGGAAGCAGGAGCTTCGCGG 542
 Qy 270 YGlnArg 272
 Db 543 CGAGAGG 549

CB961002 797 bp mRNA linear EST 29-APR-2003
 AGENCOURT 1376127 NIH_MGC_147 Homo sapiens cDNA clone
 IMAGE:30343790 5', mRNA sequence.
 CB961002
 VERSION CB961002.1 GI:30217119
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-re@mail.nih.gov
 Tissue Procurement: Dr. Stefan Hansson
 cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
 and advice from Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: NDAM379 row: a column: 15
 High quality sequence stop: 475.
 Location/Qualifiers
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 /db_xref="taxon:9606"
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 /lab_host="DH10B Tona"
 /clone_lib="NIH_MGC_147"
 /note="Organ: placenta; Vector: pBluescriptR; Site 1:
 ali-XhoI; Site 2: BamH; Oligo-dT primed using primer
 5'-TTTTTTTTTTTNN-3', size-selected for average
 insert size 2.3 kb and normalized to 10^5. This is a
 primary library enriched for full-length clones and
 constructed using the Cap-trapper method (Carninci, in

preparation). Library constructed by M. Brownstein
 (NHGRI/NHGRI, National Institutes of Health). Note: This is
 a NIH_MGC library."

BASE COUNT 161 a 243 c 260 g 133 t
 ORIGIN

Alignment Scores:
 Pred. No.: 1.36e-61 Length: 797
 Score: 918.50 Matches: 190
 Percent Similarity: 91.47% Conservatism: 3
 Best Local Similarity: 90.05% Mismatches: 10
 Query Match: 62.27% Indels: 8
 DB: 14 Gaps: 2

US-10-047-021-86_COPY_28_303 (1-276) x CB961002 (1-797)

Qy 61 LeuLeuLeuLeuGln-ProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerTh 80
 Db 92 CTCCTGTCTCATCATGGCCCTTGCCTGGGAGACATGCCACGATGCCAGGCCCTGTCCAC 151
 Qy 80 rAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgG1 100
 Db 152 AGACCTGGGTGTTCACATGTGAGCCAGCAACCGCTTGGCAGCGAGTACAGAGG 211
 Qy 100 YAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVa 120
 Db 212 CGCTCGGCTGTCTGTGGCTGTCTCGGGAGGATTTCCAGATCCAGCTCGGGACATGGT 271
 Qy 120 lAlaValValGlyGlnIlePheThrLeuGluCysGlyProProTrpGlyHisProGluPr 140
 Db 272 GGCTGTGGTGGTGAGCAGTTTACTCTGGAATGTGGGCCCTCGGGGCCACCCAGAGCC 331
 Qy 140 oThrValSerTrpTrpYsAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrVa 160
 Db 332 CACAGTCTCATGTGTGGAAGATGGGAACCCCTCGCCCTCCAGCCCGGAAGGACACAGT 391
 Qy 160 lSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu***ThrTyrMetCy 180
 Db 392 GTCCGGGGGTCTCTGTGATGGCAGAGAGAGAGTGCAGAGGACCTACATGTG 451
 Qy 180 sValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnG1 200
 Db 452 TGTGGCCACCAACAGCCAGGACACAGCGAGAGCCGCGAGCGCGGTTCATCCAGGA 511
 Qy 200 uProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGlnLeuGlu-AenV 220
 Db 512 GCCCCAGGACTACAGGAGCTGTGGAGCTTCTGGCTGTGGCAATTCAGCTGGAAAAATG 571
 Qy 220 alThr-LeuLeuAsn-ProAspProAlaGluGlyProYsProArgProAlaValTrpLe 239
 Db 572 TGACACCTGTGTAACCCCGGATCTCTGAGAGGGCCCCCAACCTAGACCGGGGTGTGGCT 631
 Qy 239 u***TrpYsValSerGlyPro***ArgLeu-ProAsnLeuThrArgProCysSerG 258
 Db 632 CAACTGGAAAGTCACTGTGGCCCTCTGCTGCCCTGCCCCCATCTTACAGCGGCTTTGGTT 691
 Qy 258 ly-----ProArgLeuProArg 263
 Db 692 CACGAGCCCAAAAATACTGCCCGG 714

RESULT 14
 CB961002
 LOCUS
 DEFINITION AGENCOURT 6620212 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5590503
 5', mRNA sequence.
 ACCESSION BM906521
 VERSION BM906521.1 GI:19356900
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1230)

found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: NDAM360 row: n column: 04
 High quality sequence stop: 535.
 Location/Qualifiers

FEATURES

source

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1..803
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/tissue_type="pre-eclatmpic placenta"
/lab_host="DH10B TonA"
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note="Organ: placenta; Vector: pBluescriptR; Site 1:
all-XhoI; Site 2: BamH; Library is oligo-dT primed and
directionally cloned using primer
5'-TTTTTTTTTTTTTTTT-3', size-selected for average insert
size 2.3 kb and normalized to ROT 5. This is a primary
library enriched for full-length clones and constructed
using the Cap-trapper method (Carninci, in preparation).
Library constructed by M. Brownstein (NIMH/NHGRI,
National Institutes of Health). Note: this is a NIH_MGC
Library."
BASE COUNT      156 a      262 c      247 g      138 t
ORIGIN
Alignment Scores:
Pred. No.:      4,248-68      Length:      803
Score:          1002.50      Matches:      194
Percent Similarity: 94.84%      Conservative: 8
Best Local Similarity: 91.08%      Mismatches: 7
Query Match:    67.97%      Indels:      4
DB:             14          Gaps:      1

US-10-047-021-86_COPY_28_303 (1-276) x CB997292 (1-803)
QY 1 GlnAspSerProProGlnLeuValHisProGlnAspGlnLeuPheGlnGlyProGly 20
DB 119 CAGGACTCCCCCGCCAGATCTTAGTCACCCCGAGGACCAGCTGTTTCAGGGCCCTGGC 178
QY 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProToThrIleArgTrpLeuLeu 40
DB 179 CCTGCCAGGATGAGCTGCGAGCCTCAGCCAGCCACCTCCACCACCTCCGCTGTTGCTG 238
QY 41 AenGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60
DB 239 AATGGGACGCCCCCTGAGCATGTGTCGCCAGACCCACACACACACCTCCTCCCTGATGGGACC 298
QY 61 LeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80
DB 299 CTTCTGCTGTACAGCCCCCTGCCCGGGGACATGCCACGATGGCCAGGCCCTGTCCACA 358
QY 81 AspLeuGlyValTyThrCysGluAlaSerAenArgLeuGlyThrAlaValSerArgGly 100
DB 359 GACCTGGGTGTCTACACATGTGAGGCCAGCAACCGCTTGGCAGCGCAGTCAGCAGAGGC 418
QY 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal 120
DB 419 GCTCGGCTGTCTGTGGCTGTCTCCGGGAGGATTTCCAGATCCAGCCTCGGGACATGTGT 478
QY 121 AlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpTrpGlyHisProGluPro 140
DB 479 GCTGTGTGGGTGACAGCTTACTCTGGANGTGGGCCGCCCTGGGGCCACCCAGAGGCC 538
QY 141 ThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrVal 160
DB 539 ACAGTCTCATGTGGAAGATGGGAAACCCCTGGCCCTCCAGCCCGGAAAGCACACAGTG 598
QY 161 SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu***ThyTrpMetCys 180
DB 599 TCCGGGGGGTCCCTCTGATGCAGACAAAGCAAGATGACGAAGGGAACCTACCTGTGT 658
QY 181 ValAlaThrAenSerAlaGlyHis-ArgGluSerArgAlaAla-ArgValSer-IleGln 199

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659 GTGGCCACCCACAGCGCAGGACATAGGAGGAGCGCGCAACCCCGGTTTCCCATCCAG 718
QY 200 ---GluProGlnAspTyThrGluProValGlu 209
DB 719 GGAGCCCTAGGAATACCCCGAAGCCTGTGAA 751

RESULT 12
LOCUS      BM914311
DEFINITION AGNCOURT_6615385 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5479976
5', mRNA sequence.
ACCESSION  BM914311
VERSION     BM914311.1 GI:19364690
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1087)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished
COMMENT      Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone Distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LCM2002 row: b column: 09
            High quality sequence stop: 535.
            Location/Qualifiers
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            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:5479976"
            /lab_host="DH10B (phage-resistant)"
            /note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
            EcoRI; cDNA made by oligo-dT priming. Directionally cloned
            into EcoRI/XhoI sites using the following 5' adaptor:
            GGACAGAG(G). Library constructed by Ling Hong in the
            laboratory of Gerald M. Rubin (University of California,
            Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
            Superscript II RT (Life Technologies). Note: this is a
            NIH_MGC Library."
BASE COUNT      268 a      307 c      352 g      159 t      1 others
ORIGIN
Alignment Scores:
Pred. No.:      1,5e-61      Length:      1087
Score:          920.00      Matches:      176
Percent Similarity: 96.17%      Conservative: 0
Best Local Similarity: 96.17%      Mismatches: 6
Query Match:    62.37%      Indels:      1
DB:             12          Gaps:      0

US-10-047-021-86_COPY_28_303 (1-276) x BM914311 (1-1087)
QY 91 AsnArgLeuGlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGlu 110
DB 3 AACCGCTTGGCAGCGCAGTCAGCAGAGCGCTCGGCTGTCTGTGGCTGTCTCCGGGAG 62
QY 111 AspPheGlnIleGlnProArgAspMetValAlaValGlyGluGlnPheThrLeuGlu 130
DB 63 GATTTCAGATCCAGCCTCGGACATGTGGCTGTGGTGGGTGAGCAGCTTACTCTGAA 122
QY 131 CysGlyProProTrpTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLysPro 150

```

```

Qy 199 nGluProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGlnLeuGlu 218
Db 670 GGAGCCCCAGGACTACACGGAGCCTGTGGAGCTTCTGGCTGTGCCGAATCAGTGGAC 727

RESULT 10
BQ890126 941 bp mRNA linear EST 16-AUG-2002
LOCUS AGNCOURT 7902449 Lupski dorsal root ganglion Homo sapiens cDNA
clone IMAGE:6186214 5', mRNA sequence.
ACCESSION BQ890126
VERSION BQ890126.1 GI:22282140
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 941)
REFERENCE NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13578 row: d column: 23
High quality sequence start: 6
High quality sequence stop: 612.
Location/Qualifiers
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/lab_host="DH10B"
/dev_stage="adult, 36 yr"
/clone_lib="Lupski dorsal root ganglion"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
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Directionally cloned using the following adaptors:
5'-TCGACCCAGCGTCCG-3' and
5'-GACTAGTTCTAGATCGGAGCGCGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.7 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies."
BASE COUNT 182 a 300 c 309 g 149 t 1 others
ORIGIN

Alignment Scores:
Pred. No.: 7.2e-69 Length: 941
Score: 1013.50 Matches: 214
Percent Similarity: 80.07% Conservative: 3
Best Local Similarity: 78.97% Mismatches: 31
Query Match: 68.71% Indels: 24
DB: 13 Gaps: 7

US-10-047-021-86_COPY_28_303 (1-276) x BQ890126 (1-941)

Qy 1 GlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGly 20
Db 134 CAGGACTCCCGCCCCAGATCTAGTCCACCCCGGAGCCAGCTGTTCAGGGCCCTGCG 193

Qy 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTrpLeu 40
Db 194 CCGCCAGGATGAGCTGCAAGCCTCAGGCCAGCCACCTCCACCATCGCTGTGTGCTG 253

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Qy 41 AsnGlyGlnProLeuSerMetValProProAspProHisLeuLeuProAspGlyThr 60
Db 254 AATGGGAGCCCTGAGCATGGTCCCCCAGACCCACACACCTCTCTGCTGATGGGACC 313

Qy 61 LeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80
Db 314 CTTCTGCTGTACAGCCCTCTGCCCGGGAGCATGCCACGATGGCCAGGCCCTGTCCACA 373

Qy 81 AspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100
Db 374 GACCTGGGTGTACACATGTGAGCCAGCAACCGCTTGGCAGCGCATGAGCAGAGGC 433

Qy 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal 120
Db 434 GCTCGGCTGTCTGGCTGTCTCCGGAGGATTTCCAGATCCAGCTCCGGGACATGGTG 493

Qy 121 AlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluPro 140
Db 494 GCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGCGCGCTGGGGCCACCCAGAGGCC 553

Qy 141 ThrValSerTrpTyrAspGlyLysProLeuAlaLeuGlnProGlyArgHis--ThrV 160
Db 554 ACAGTCTCATGTGTGAAGATGGGAAACCCCTGGCCCTCCAGCCCGGAAGGACACAGTGG 613

Qy 160 alSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu***ThrTyrMetC 180
Db 614 TCCGGGGGGTCCCTCTGCTGATGTCAGAGCAGAGAGAGTGACAGAGGACCTACATGT 673

Qy 180 YsValAlaThrAsnSerAlaGlyHisArg---GluSerArgAlaAlaArgValSerIleG 199
Db 674 GTGTGGCCACCAACAGCGCAGGACATAAGAGGAGAGCGCGCCACCCCGGNTTCCCATC 733

Qy 199 In---GluProGlnAspTyrThrGluProValGluLeuAlaVal-----ArgIleG 216
Db 734 CAGGAGCCCCCAGGACTACACGGAAGCCTGGGGAGCCTTCCGGG-CTGGGCGCAATTC 792

Qy 216 InLeuGluAsnVal---ThrLeuLeuAsnPro---AspPro--AlaGluGlyProLysPr 233
Db 793 AGCTTGGAAATTTGTGTGACCCCTGTGAAACCCCGGGGATCTCTTGACAAAGGGGCC--CC 849

Qy 233 oArgPro-----AlaValTrpLeu***Tr 241
Db 850 AAGCGCTAAAAAAGCGGGGGTGGGGGCTCCACCTCGAAAGGGGCAATGGGCCCTTG 909

Qy 241 pLysValSerGlyPro***ArgLeu 249
Db 910 GTTGGCGCCCGGCCCAATTCCTTTA 934

RESULT 11
LOCUS AGNCOURT 13623935 NIH_MGC_148 Homo sapiens cDNA clone
IMAGE:30336795 5', mRNA sequence.
ACCESSION CB997292
VERSION CB997292.1 GI:30291812
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 803)
REFERENCE NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Dr. Stefan
Email: cgapbs-remail.nih.gov
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be

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Db 238 GGGGAGCCCTCAGCATGCCACCCAGACCTACATTACCTTTTGGCGATGGGACCTC 297
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Qy 81 AspLeuGlyValThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100
Db 358 ATCTGGGTGTACACATGTGAGGCCAGCAACCGCTGGGCACAGCATGAGCGGGGT 417
Qy 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgMetVal 120
Db 418 GCTAGGCTCTGTGGCTCTCTCCAGGAGGACTTCCAGATCCAACTCCGGACAGTG 477
Qy 121 AlaValValGluGlnPheThrLeuGluCysGlyProProThrGlyHisProGluPro 140
Db 478 GCGGTGGTGGGAGAGCTTGGTCTTGTAGTGTGCTCTCCCTGGGGCTACCCAAACCC 537
Qy 141 ThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrVal 160
Db 538 TGGTCTCATGTGTGAAAGACCGGAAACCCCTGTCTCCAGCCAGGGAGGCGCAAGTA 597
Qy 161 SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu**ThrTrpMetCys 180
Db 598 TCTGGGATTCCTGATGTGTCAAGAGCAGAGAGAAATGACTCGGGAGCTATATGTGT 657
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Qy 201 ProGlnAspTyThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluAlaVal 220
Db 718 TCCAGGACCAAGAACATCTAGAGCTTCTGGCTGTTCGATTCAGCTGGAATGTG 777
Qy 221 ThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAlaValTrpLeu** 240
Db 778 ACCCTGCTAAACCCGAACTGTAAAGGTCCCAAGCTGGGCCATCGTGTGGCTCAGC 837
Qy 241 TrpLysValSerGlyPro***ArgLeuProAsnLeuThrArgProCysSerGlyProAr 260
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VERSION B1762862.1 GI:15754428
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 729)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/,
NATIONAL INSTITUTES OF HEALTH, MAMMALIAN GENE COLLECTION (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11471 row: g column: 21
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High quality sequence stop: 723.
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sample anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH MGC Library."
BASE COUNT 137 a 240 c 229 g 123 t
ORIGIN
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Alignment Scores:
Pred. No.: 3.05e-70 Length: 729
Score: 1029.50 Matches: 202
Percent Similarity: 94.14% Conservatives: 7
Best Local Similarity: 90.99% Mismatches: 8
Query Match: 69.80% Indels: 5
DB: 12 Gaps: 1
US-10-047-021-86_COPY_28_303 (1-276) x B1762862 (1-729)
Qy 1 GlnAspSerProProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGly 20
Db 73 CAGGACTCCCGTCCGAGATCTAGTCCACCCAGACAGCTGTT---CCAGGCCCTGGC 129
Qy 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTrpLeuLeu 40
Db 130 CTTGCCAGATGAGTGCACAGCTTCAGGCAGACCCCTCCACCATCCGCTGGTGTCTG 189
Qy 41 AsnGlyGln-ProLeuSerMetValProProAspProHisHisLeuLeuProAspGly 60
Db 190 AATGGCAGCCCCATGAGCATGGTGCCGCCAGACCCACACCATCTCTGCTGATGGGAC 249
Qy 60 rLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerTh 80
Db 250 CTTTCTGTGTACAGCCCTTGCCCGGGACATGTCACCATGTCAGGCCCTGTCCAC 309
Qy 80 rAsp-LeuGlyValTyThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArg 100
Db 310 AGACCATGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCACCGAGTCCAGAG 369
Qy 100 lValaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetV 120
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Qy 120 alAlaValValGlyGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluP 140
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Qy 160 alSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu**ThrTyT--Me 179
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Qy 179 tCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleG 199
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 Carninci, P. and Hayashizaki, Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636

2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE 20499374
 PUBMED 11042159

3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
 MEDLINE 20530913
 PUBMED 11076861

4 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojohori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schrim, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., But, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marzocchi, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.P., Suzuki, H., Toyooka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y.
 TITLE Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409 (6821), 685-690 (2001)
 MEDLINE 21085660
 PUBMED 11217851

5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
 TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 JOURNAL Nature 420, 563-573 (2002)
 MEDLINE 12185178
 PUBMED 12185178

6 (bases 1 to 3865)
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Iehii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akhiba, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
 TITLE Direct Submission

JOURNAL

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-research@riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
 COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.go.jp/
 URL: http://fantom.gsc.riken.go.jp/.

FEATURES

source

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CDS

BASE COUNT 826 a 1188 c 1038 g 813 t
 ORIGIN

Alignment Scores:
 Pred. No.: 6,23e-72 Length: 3865
 Score: 1062.50 Matches: 204
 Percent Similarity: 83.52% Conservative: 24
 Best Local Similarity: 74.73% Mismatches: 43
 Query Match: 72.03% Indels: 2
 DB: 11 Gaps: 1

US-10-047-021-86_COPY_28_303 (1-276) x AK087355 (1-3865)

Qy 2 AspSerProGlnIleLeuValHisProGlnaspGlnLeuPheGlnGlyProGlyPro 21
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 Db 118 GATTCTCCACCCAGATCTTAGTTTACCCCCAGACACAGTACTTACAGGGCTTGGCCCA 177
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Qy 22 AlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTrpLeuAsn 41
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 Db 178 GCCAAGTAGAGTGCAGATCATCGGCCCAACACCTCCATCCATCGCTGCTGTAAT 237
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Qy 42 GlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThrLeu 61
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Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y.,
Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T.,
Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K.,
Yoshino,M., Muramatsu,M. and Hayashizaki,Y.

TITLE
JOURNAL

Submitted (10-JUN-2000) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
URL: <http://genome.gsc.riken.go.jp/>, Tel:81-45-503-9222,
Fax:81-45-503-9216)

COMMENT

On Dec 10, 2002 this sequence version replaced gi:12836108.
Please visit our web site (<http://genome.gsc.riken.go.jp/>) for
further details.

CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues. First strand cDNA was primed with a primer
[5'-GAGAGAGAGCGCGCACTCGAGTTTCTTTTCTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse transcriptase
and subsequently enriched for full-length by cap-trapper. Second
strand cDNA was prepared with the primer adapter of sequences [5',
GAGAGAGAGAGGATCCAGAGCTCAATTAATTAACCCCCCCC 3']. cDNA was
cleaved with XhoI and SstI. Cloning sites, 5' end: SstI; 3' end:
XhoI. Host: SOLR.

FEATURES

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CDS

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BASE COUNT 802 a 1115 c 1011 g 761 t

Alignment Scores:

Pred. No.: 5,9e-72 Length: 3689
Score: 1062.50 Matches: 204
Percent Similarity: 83.52% Conservative: 24

Best Local Similarity: 74.73% Mismatches: 43
Query Match: 72.03% Indels: 2
DB: 11 Gaps: 1

US-10-047-021-86_COPY_28_303 (1-276) x AK004723 (1-3689)

QY 2 AspSerProGlnInLeuValHisProGlnAspGlnLeuPheGlnGlyProGlyPro 21
DB 121 GATTCTCCACCCAGATCCTAGTTTACCCCCAGGACCACTTCTCAGGGCTCTGGCCCA 180
QY 22 AlargMetSerCysArgAlaSerGlyClnProProProThrIleAtrTripleLeuAen 41
DB 181 GCCAAGATGAGGTGCAGATCATCCGGCCCAACCCCTCCACTATCCGCTGGTGTGTAAT 240
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DB 241 GGGCAGCCCCCTCAGCATGGCCACCCAGCACTTACCTATACCTTTTCCCGGATGGGACCTTC 300
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QY 81 AspLeuGlyValTyrThrCysGluAlaSerAenArgLeuGlyThrAlaValSerArgGly 100
DB 361 ATCTCTGGGTGCTACATGTGAGGCCCAACCGGCTGGGCACAGCAGTGTAGCCGGGT 420
QY 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal 120
DB 421 GCTAGGCTGTCTGTGGCTGTCTCCAGGAGACTTCCAGATCCAACTCCGGGACACAGTG 480
QY 121 AlaValValGlyGlnGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluPro 140
DB 481 GCCGTGGTGGGAGAGAGCTTGGTTCTTGAGTGTGTCTCTCCCTGGGGCTACCCAAACCC 540
QY 141 ThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrVal 160
DB 541 TCGGTCTCATGGTGGAAAGACGGGAAACCCCTGGTCTCTCCAGCCAGGAGGCGCAGTA 600
QY 161 SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu---ThrTyrMetCys 180
DB 601 TCTGGGATTCCTCGATGGTGTCAAGAGCAGAGAGAAATGACTCGGGACCTATATATGT 660
QY 181 ValAlaThrAenSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu 200
DB 661 ATGCCCAACCAACATGTGGCAACGGGAGAGCCGAGCAGCAGGGTCTCTATCCAGGA 720
QY 201 ProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluAenVal 220
DB 721 TCCAGGAGCACCAAGGAACATCTAGAGCTTCTGGCTGTTCGCAATTCAGCTGGAAATGTG 780
QY 221 ThrLeuLeuAenProAspProAlaGluGlyProLysProArgProAlaValTripleLeu*** 240
DB 781 ACCCTGTCTAAACCCCAACCTGTAAAGGTGCCAAGCCTGGGCCCATCGCTGTGGTCTAGC 840
QY 241 TrpLysValSerGlyPro***-ArgLeuProAenLeuThrArgProCysSerGlyProArg 260
DB 841 TGGAGGTGAGCGGCCCTCTGTGCACCTGTCTAGTCATACACAGCTCTCTTTCAGGACTCAG 900
QY 260 gLeuProArgGluAlaArgGluLeuArgGlyGlnArg 272
DB 901 AGGTCCCCCAGGGACCAAGGATCTCCATGAGCAGAGG 937

RESULT 8

AK087355

LOCUS

DEFINITION

AK087355 3865 bp mRNA linear HTC 05-DEC-2002
Mus musculus 0 day neonate lung cDNA, RIKEN full-length enriched
library, clone:E030049D17 product:similar to MAGIC ROUNDABOUT [Homo
sapiens], full insert sequence.

ACCESSION

AK087355

VERSION

AK087355.1

KEYWORDS

HTC; CAP trapper.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

Alignment Scores:

Pred. No.: 3, 48e-74 Length: 860
Score: 1081.50 Matches: 215
Percent Similarity: 79.78% Conservatives: 2
Best Local Similarity: 79.04% Mismatches: 11
Query Match: 73.32% Indels: 44
DB: 14 Gaps: 5

US-10-047-021-86_COPY_28_303 (1-276) x CB996189 (1-860)

Qy 1 GlnAepSerProProGlnLeuValHisProGlnAepGlnLeuPheGlnGlyProGly 20
Db 119 CAGGACTCCCGCCAGATCTAGTCCACCCAGGACCACTGTTCCAGGGCCCTGGC 178
Qy 21 ProAlaArgMetSerCysArgAlaSerGlyClnProProProThrIleArgTTPLeuLeu 40
Db 179 CCTCCAGAGTGAAGTCCCGAGCTCAGGCGAGCCAGCCCTCCACCATCGCTGGTGTG 238
Qy 41 AsnGlyGlnProLeuSerMetValProProAepProHisHisLeuLeuProAspGlyThr 60
Db 239 AATGGGCGAGCCCTGAGCATGCTGCGCCAGCCAGCCACACACCTCTCGCTGATGGGACC 298
Qy 61 LeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAepGlyGlnAlaLeuSerThr 80
Db 299 CTTCTGCTGTACAGCCCTCGCCGGGAGCATGCCACGATGGCCAGGCCCTGTCCACA 358
Qy 81 AspLeuGlyValThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100
Db 359 GACCTGGGTGCTACACATGTGAGGCCAGCAACCGCTTGGCAGCGGAGTCAGAGAGGC 418
Qy 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnLeuGlnProArgAspMetVal 120
Db 419 GCTGGCTGTCTGGCTGTCTCTCGGAGAGATTTCCAGATCCAGCCCTCGGACATGGTG 478
Qy 121 AlaValValGlyGlnGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluPro 140
Db 479 GCTGTGGTGGTGAGCAGTCTTACTCTGAATGTGGCGCCCTCGGGGCCACCCAGAGGCC 538
Qy 141 ThrValSerTrpTrpLeuAspGlyValProLeuAlaLeuGlnProGlyArgHisThrVal 160
Db 539 ACAGTCTCATGTGGTGAAGATGGGAAACCCCTCGCCCTCCAGCCCGGAGGACACAGTG 598
Qy 161 SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu**ThrTyMetCys 180
Db 599 TCCGGGGTCTCTGTGTGTCAGAGCAGAGAGAGTGCAGAGGACCTACATGTGT 658
Qy 181 ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArg-ValSerIleGlnG 200
Db 659 GTGGCCACCAACAGCGCAGGACATAGGAGAGCGCGCAGCGCGGGTTTCCATCCAGGA 718
Qy 200 uProGlnAspTyThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluAsnVa 220
Db 719 A----- 719
Qy 220 lThrLeuLeuAsnProAepProAlaGluGlyProLysProArgProAlaValTrpLeu** 240
Db 720 -----GCCCGAGGAACCTACCCGAGCGCCTGT----- 746
Qy 240 *TrpLysValSerGlyPro***Arg-----LeuPr 250
Db 747 -TGGGAGCTTTCTGGGCTGTGCGGAATTTTCAGCTGGGTAAATAATGTTGACACCTTGCC 805
Qy 250 o---AsnLeuThrArgProCys---SerGlyPro 259
Db 806 TGGAAACCCCGGGAATCCCTCCCAAGAGGGGCC 839

RESULT 7

AK004723

LOCUS

DEFINITION Mus musculus adult male lung cDNA, RIKEN full-length enriched library, clone:1200012D01 product:similar to MAGIC ROUNDABOUT [Homo sapiens], full insert sequence.

ACCESSION AK004723 GI:26334429
VERSION HTc; CAP trapper.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Mech. Enzymol. 303, 13-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischnmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G., Quackenbush, J., Schriml, L. M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barah, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyooka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohetsuki, S. and Hayashizaki, Y.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
MEDLINE 21085660
PUBMED 11217851
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
PUBMED 12033689
REFERENCE 6
AUTHORS Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D.,

REFERENCE
 1 (bases 1 to 826)
 AUTHORS
 NIH-MGC http://mgc.nci.nih.gov/
 TITLE
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL
 Unpublished
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: Dr. Stefan Hansson
 cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
 and advice from Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: NDAM348 row: c column: 24
 High quality sequence stop: 637.
 Location/Qualifiers

1. 826
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30331943"
 /tissue_type="pre-eclampsia placenta"
 /lab_host="DH10B Tona"
 /clone_lib="NIH MGC 148"
 /note="Organ: placenta; Vector: pBluescriptR; Site 1:
 all-XhoI; Site 2: BamH; Library is oligo-dT primed and
 directionally cloned using primer
 5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert
 size 2.3 kb and normalized to ROT 5. This is a primary
 library enriched for full-length clones and constructed
 using the Cap-trapper method (Carninci, in preparation).
 Library constructed by M. Brownstein (NIH/NHGRI,
 National Institutes of Health). Note: this is a NIH_MGC
 Library."

FEATURES

source

BASE COUNT 160 a 266 c 261 g 138 t 1 others
 ORIGIN
 Alignment Scores:
 Pred. No.: 1.02e-75 Length: 826
 Score: 1101.00 Matches: 216
 Percent Similarity: 91.98% Conservative: 2
 Best Local Similarity: 91.14% Mismatches: 14
 Query Match: 74.64% Indels: 5
 DB: 14 Gaps: 2

US-10-047-021-86_COPY_28_303 (1-276) x CB994099 (1-826)
 Qy 1 GlnAspSerProGlnPheValHisProGlnAspGlnLeuPheGlnGlyProGly 20
 Db 119 CAGACTCCCGCCCGCCAGATCTAGTCCACCCCGAGGACGAGCTGTTCCAGGGCCCTGGC 178
 Qy 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTrpLeuLeu 40
 Db 179 CCTGCCAGATGAGTGCAGGCTCAGCCAGCCAGCCACCTCCACCATCCGCTGTTGCTG 238
 Qy 41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60
 Db 239 AATGGGACGCCCTGAGCATGGTCCCGCCAGCCAGCCACCATCCCTCTGCTGATGGGACC 298
 Qy 61 LeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80
 Db 299 CTTCTGTGCTACAGCCCTGCGCGGGGACATGCCACGATGCGCCGCTGTCCACA 358
 Qy 81 AspLeuGlyValThrThrCysGluAlaSerHisArgLeuGlyThrAlaValSerArgGly 100
 Db 359 GACCTGGGTGCTACACATGTGAGGCCAGCAACCGCTTGGCAGCGGAGTCAGCAGAGGC 418
 Qy 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal 120
 Db 419 GCTCGCTGTCTGTGGCTGTCTCTCGGAGGAGTATTCAGATCCAGCTCGGGACATGGTG 478

Qy 121 AlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluPro 140
 Db 479 GCTGTGGTGGTGGAGCAGTCTTACTGTGAATGTGGCGCCCTGGGGCCACCCAGAGCCC 538
 Qy 141 ThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrVal 160
 Db 539 ACAGTCTCATGTGTGAAGATGGGAACCCCTGGCCCTCCAGCCCGGAAGGCACACAGTG 598
 Qy 161 SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu**ThrTyrMetCys 180
 Db 599 TCCGGGGGTCCTCTGCTGATGGCAGACAGAGAGAGTGCAGAAAGACCTTACATGTGT 658
 Qy 181 ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu 200
 Db 659 GTGGCCACCAACAGCGGCAAGACATANGAGAGCGCGCCACCCGGGTTTTCATCCAGGAG 718
 Qy 201 -ProGlnAspTyrThr-GluProVal-GluLeuLeu---AlaValArgIleGlnLeuGlu 218
 Db 719 CCCCAGGACTACACGGGAGCCTGTGGGAGCTTCTGGGCTGTGGCAATTTTCAGCTGGGAA 778
 Qy 219 AsnValThrLeuLeu---AsnProAspProAlaGluGlyProLys 232
 Db 779 AATGTGACATGGCTGGAAACCCCGATCTCTGGCAAGGGGCCCA 823

RESULT 6

LOCUS

DEFINITION

CB996189

AGENCOURT_13622686 NIH_MGC_148 Homo sapiens cDNA clone

IMAGE:30337143 5', mRNA sequence.

ACCESSION

CB996189

VERSION

CB996189.1 GI:30290709

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov

Tissue Procurement: Dr. Stefan Hansson

cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help

and advice from Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: NDAM361 row: 1 column: 16

High quality sequence stop: 578.

Location/Qualifiers

1. 860

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clones="IMAGE:30337143"

/tissue_type="pre-eclampsia placenta"

/lab_host="DH10B Tona"

/clone_lib="NIH MGC 148"

/notes="Organ: placenta; Vector: pBluescriptR; Site 1:
 all-XhoI; Site 2: BamH; Library is oligo-dT primed and
 directionally cloned using primer
 5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert
 size 2.3 kb and normalized to ROT 5. This is a primary
 library enriched for full-length clones and constructed
 using the Cap-trapper method (Carninci, in preparation).
 Library constructed by M. Brownstein (NIH/NHGRI,
 National Institutes of Health). Note: this is a NIH_MGC
 Library."

BASE COUNT 169 a 279 c 267 g 144 t 1 others

ORIGIN

ORIGIN

Alignment Scores:
 Pred. No.: 118-97 Length: 1201
 Score: 1387.00 Matches: 263
 Percent Similarity: 96.35% Conservative: 1
 Best Local Similarity: 95.99% Mismatches: 8
 Query Match: 94.03% Indels: 2
 DB: 9 Gaps: 0

US-10-047-021-86_COPY_28_303 (1-276) x AL553360 (1-1201)

Qy 1 GlnAspSerProGlnInLeuValHisProGlnAspGlnLeuPheGlnGlyProGly 20
 Db 162 CAGGACTCCCGCCCGCCAGATCTAGTCCACCCCGAGGACAGCTGTTCCAGGCGCCCTGGC 221
 Qy 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTrpLeuLeu 40
 Db 222 CCGTCCAGGATGAGCTGCAAGCCTCAGGCGGAGCCACCTCCACCATCCGCTGGTGGCTG 281
 Qy 41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60
 Db 282 AATGGCAGCCCTGAGCATGGTCCCGGAGCCACACACCATCTCCCTGCTGATGGGACC 341
 Qy 61 LeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80
 Db 342 CTCTCTGCTGTACAGCCCTCCCGGGGAGCATGCCACGATGGCCAGGCTCTGTCCACA 401
 Qy 81 AspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100
 Db 402 GACCTGGGTGTACACATGTGAGCCAGCAACCGCTTGGCAGCGCATGTAGCAGAGGC 461
 Qy 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal 120
 Db 462 GCTCGCTGTCTGGCTGTCTCCGGAGGATTTCCAGATCCAGCTCCGGGACATGGTG 521
 Qy 121 AlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluPro 140
 Db 522 GCTGTGGTGGTGAGCAGTTTACTCTGAATGTGGCGCGCCCTGGGGCCACCCAGAGCCC 581
 Qy 141 ThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGln-ProGlyArgHisThrVa 160
 Db 582 ACAGTCTCATGTGGAAGATGGAAACCCCTGGCCCTCCACGCGCGGAGGCACACAGT 641
 Qy 160 LserGlyCysLeuLeuMetAlaArgAlaGluLysSerAspGlu***ThrTyrMetCy 180
 Db 642 GTCCGGGGGGTCCCTGCTGTGATGGCAAGAGCAGAGAGATGACGAAGGACCTCATGTG 701
 Qy 180 sValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnI 200
 Db 702 TGTGGCCACCAACAGCGAGACATAGGAGAGCGCGCCACCCCGGGTTTCCATCCAGGA 761
 Qy 200 uProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluAsnVa 220
 Db 762 CCCCAGGACTACAGGAGCTGTGGAGCTTCTGGCTGTGGCAATTCAGCTGGAAATGT 821
 Qy 220 lThrLeuLeuAsnProAspProAlaGluGluProLysProArgProAlaValTrpLeu** 240
 Db 822 GACACTGTGTAACCGGATCTTCAGAGGGGCCCCAAGCCTAGACCGCGGGTGTGGCTCAG 881
 Qy 240 *TrpLysValSerGlyPro***ArgLeuProAsnLeuThrArgProCysSerGlyProA 260
 Db 882 CTGGAGGTCTAGTGGGCTCTGTGGCTTGGCCATCTTACACGGCTTGTTCAGGACCCA 941
 Qy 260 rgLeuProArgGluAlaArgGluLeuArgGlyGlnArg 272
 Db 942 GACTGCCCGGGAGGCGCAGGAGCTCTGTGGGCGAGG 979

RESULT 3

BM921911 1019 bp mRNA linear EST 12-MAR-2002
 LOCUS
 DEFINITION AGENCOURT 6706908 NIH_MGC_115 Homo sapiens CDNA clone IMAGE:5753515
 5', mRNA sequence.

ACCESSION

BM921911 GI:19372290

VERSION

BM921911.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 1019)

AUTHORS

NIH-MGC http://mgc.nci.nih.gov/.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L1AM12789 row: g column: 20
 High quality sequence stop: 697.
 Location/Qualifiers
 1..1019
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5753515"
 /lab_host="DH10B"
 /note="Organ: pooled brain, lung, testis; Vector:
 pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
 source anonymous pool of 6 male brains, age range 23-27; 1
 male lung, age 27; and 1 male testis, age 69. Library is
 oligo-dT primed and directionally cloned (EcoRV site is
 destroyed upon cloning). Average insert size 1.8 kb,
 insert size range 1-3 kb. Library is normalized and
 enriched for full-length clones and was constructed by C.
 Gruber (Invitrogen). Research Genetics tracking code
 021. Note: this is a NIH_MGC library."

FEATURES

BASE COUNT 201 a 331 c 321 g 162 t

ORIGIN

US-10-047-021-86_COPY_28_303 (1-276) x BM921911 (1-1019)

Alignment Scores:

Pred. No.: 118-94 Length: 1019
 Score: 1345.00 Matches: 254
 Percent Similarity: 97.70% Conservative: 1
 Best Local Similarity: 97.32% Mismatches: 4
 Query Match: 91.19% Indels: 2
 DB: 12 Gaps: 0

Qy

8 LeuValHisProGlnAspGlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArg 27

Db

16 CTAGTCCACCCCGGAGGACAGCTGTCCAGGGCCCTGGCCCTGCGAGGATGAGCTGCCAA 75

Qy

28 AlaSerGlyGlnProProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMet 47

Db

76 GCCTCAGCGCCAGCCACCTCCACCATCCGCTGGTGTGTAATGGGCGAGCCCTGAGCATG 135

Qy

48 ValProProAspProHisHisLeuLeuProAspGlyThrLeuLeuLeuGlnProPro 67

Db

136 GTGCCCCCAGACCCACACCATCTCTGCTGATGGACCTCTGCTGCTACAGCCCCCT 195

Qy

68 AlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCys 87

Db

196 GCCCGGGGACATGCCACGATGGCCAGGCCCTGTCCACAGACCTGGGTGTCTACACATGT 255

Qy

88 GluAlaSerAsnArgLeuGlyThrAlaValSerArgGlyAlaArgLeuSerValAlaVal 107

Db

256 GAGGCCAGCAACCGGCTTGGCAGCGAGTCAGCAGAGCGCGCTCGGCTGTCTGTGCTGTC 315

AUTHORS TITLE JOURNAL

Strausberg, R.
Direct Submission
Submitted (01-NOV-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
contact: amadane@systemsbio.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAC Plate: 84 Row: i Column: 5
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis, Genomescan gene prediction
This clone has the following problem: frame shifted.

FEATURES source

1. 3758
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5590503"
/tissue type="Ovary, pooled from 3 adults"
/clone_lib="NIH MGC_125"
/lab_host="DH10B"
/note="vector: pCMV-SPORT6"
772 a 1232 c 1046 g 708 t

BASE COUNT ORIGIN

Alignment Scores:
Pred. No.: 1.41e-100 Length: 3758
Score: 1432.00 Matches: 268
Percent Similarity: 98.53% Conservative: 1
Best Local Similarity: 98.17% Mismatches: 3
Query Match: 97.08% Indels: 1
DB: 11 Gaps: 0

US-10-047-021-86_COPY_28_303 (1-276) x BC039602 (1-3758)

Qy 1 GlnAspSerProGlnLeuValHisProGlnAspGlnLeuPheGlnGlyProGly 20
Db 110 CAGGACTCCCGCCCGCCAGATCTAGTCCACCCCGAGGACGAGTGTCCAGGCGCCCTGGC 169
Qy 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProProThrIleArgTrpLeuLeu 40
Db 170 CTTGCCAGGATGAGCTGCGCAAGCTTCAGGCGAGCCACCTCCGACCATCCGCTGGTTGCTG 229
Qy 41 AenGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60
Db 230 AATGGCGAGCCCTGAGCATGTGTCGCCCGGACACACACACCTCTCTGCTGATGGGACC 289
Qy 61 LeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80
Db 290 CTTCTGCTGTACAGCCCTCCCGGGGAGACATGCCACGATGGCCAGGCGCTGTCCACA 349
Qy 81 AspLeuGlyValTyThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100
Db 350 GACCTGGGTGTACACATGTGAGCGCCAGCAACCGCTTGGCAGCGAGTCAGCAGAGGC 409
Qy 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal 120
Db 410 GCTCGGCTGTCTGTGGCTGTCTCCGGGAGGATTTCCAGATCCAGCTCCGGGACATGGTG 469
Qy 121 AlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluPro 140

Db 470 GCTGTGTGTGGTGGAGCAGTTTACTCTGGAATGTGGGCGCCCTGTGGGCGCCACCCAGAGCCC 529
Qy 141 ThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrVal 160
Db 530 ACAGTCTCATGTGTGGAAGATGGAAACCCCTGCGCTCGAGCCCGGAGGCACACAGTGT 589
Qy 161 SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu***ThrTyMetCys 180
Db 590 TCCGGGGGGTCCCTGCTGATGGCAAGAGCAGAGAGAGTACGAGGAGGACCTACATGTGT 649
Qy 181 ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu 200
Db 650 GTGGCCACCAACAGCGCAGACATAGGAGAGCGCGCAGCGCGGTTCCTCATCCAGGAG 709
Qy 201 ProGlnAspTyThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluAsnVal 220
Db 710 CCCAGGAGCTACACGGAGCCTGTGGAGCTTCTGCTGTGCGAATTCAGCTGGAATAATGTG 769
Qy 221 ThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAlaValTrpLeu*** 240
Db 770 AACTGTCTGAACCGGATCTCTGAGAGGCGCCCAAGCCTAGACCGCGGTGTGCTCAGC 829
Qy 241 TrpLysValSerGlyPro***-ArgLeuProAsnLeuThrArgProCysSerGlyProAr 260
Db 830 TGAAGGTCAGTGGCCCTGCTGCGCTCGCCCAATCTTACACGGCGCTTGTTCAGGACCCAG 889
Qy 260 gLeuProArgGluAlaArgGluLeuArgGlyGlnArg 272
Db 890 ACTGCCCCGGGAGCCAGGAGGCTCCGTGGGCAGAG 926

RESULT 2

LOCUS AL553360
DEFINITION AL553360 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
clone CSODI075YP13 5-PRIME, mRNA sequence.
ACCESSION AL553360
VERSION AL553360.2 GI:31275174
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length CDNA libraries and normalization
JOURNAL Unpublished
COMMENT On Feb 15, 2001 this sequence version replaced gi:12893123.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6206.r For
more information about this cluster, see
<http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CSODI075CH07QPl&cluster=6206.r>. Contact :
Feng Liang Email : liang@lifetech.com URL :
<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI075CH07QPl.
Location/Qualifiers
1. 1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI075YP13"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 236 a 348 c 369 g 212 t 36 others

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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 31, 2004, 12:28:30 ; Search time 1674.59 Seconds
(without alignments)
4005.776 Million cell updates/sec

Title: US-10-047-021-86_COPY_28_303
Perfect score: 1475
Sequence: 1 QDSPQILVHPQDLFGQPG.....SGPRLPREARELRQRRNTG 276

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlp
-Q=/Cgn2_1/USPTO_spool_p/US10047021/runat_30012004_145453_24574/app_query.fasta_1.910
-DB=EST -QFMT=fastap -SUFFIX=first -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-LOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10047021.QCGN 1 1 4399 @runat_30012004_145453_24574 -NCPU=6 -ICPU=3
-NO_WMAP -LARGQUERY -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_ges_hum:*
18: em_ges_inv:*
19: em_ges_pln:*
20: em_ges_vrt:*
21: em_ges_fun:*
22: em_ges_mam:*
23: em_ges_mus:*
24: em_ges_pro:*
25: em_ges_rod:*
26: em_ges_phg:*
27: em_ges_vrl:*
28: gb_ges1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1432	97.1	3758	11	BC039602	BC039602 Homo sapi
2	1387	94.0	1201	9	AL553360	AL553360 AL553360
3	1345	91.2	1019	12	BM921911	BM921911 AGENCOURT
4	1132	76.7	922	13	BM921911	BM921911 AGENCOURT
5	1101	74.6	826	14	CB994099	CB994099 AGENCOURT
6	1081.5	73.3	860	14	CB996189	CB996189 AGENCOURT
7	1062.5	72.0	3689	11	AK004723	AK004723 Mus muscu
8	1062.5	72.0	3865	11	AK087355	AK087355 Mus muscu
9	1029.5	69.8	729	12	BI762862	BI762862 603048384
10	1013.5	68.7	941	13	BQ890126	BQ890126 AGENCOURT
11	1002.5	68.0	803	14	CB997292	CB997292 AGENCOURT
12	920	62.4	1087	12	BM914311	BM914311 AGENCOURT
13	918.5	62.3	797	14	CB961002	CB961002 AGENCOURT
14	897	60.8	1230	12	BM906521	BM906521 AGENCOURT
15	892.5	60.5	771	14	CB959649	CB959649 AGENCOURT
16	891.5	60.4	610	10	BG745318	BG745318 602723637
17	884	59.9	798	14	CB961529	CB961529 AGENCOURT
18	847	57.4	688	14	CB961818	CB961818 AGENCOURT
19	803	54.4	558	9	AL602474	AL602474 DKFZp6860
20	782	53.0	570	10	BE233526	BE233526 139756 MA
21	742.5	50.3	662	14	BY727209	BY727209 BY727209
22	732	49.6	502	13	BM964621	BM964621 DKFZp686M
23	704.5	47.8	620	10	BB664621	BB664621 BB664621
24	656	44.5	532	13	BM975138	BM975138 DKFZp6860
25	651	44.1	526	14	CA394658	CA394658 cs54c07.Y
26	647.5	43.9	631	10	BE376779	BE376779 601227331
27	642	43.5	501	13	BM947476	BM947476 DKFZp686B
28	577.5	39.2	529	4	BX520802	BX520802 RZPD Mus
29	576.5	39.1	551	9	AI116483	AI116483 ud74c05.Y
30	574.5	38.9	557	14	BY704924	BY704924 BY704924
31	574	38.9	344	9	AA577940	AA577940 nl20d01.s
32	567	38.4	438	13	BM947517	BM947517 DKFZp686F
33	566	38.4	450	9	AL039859	AL039859 DKFZp643AE
34	529	35.9	532	12	BI159602	BI159602 602920006
35	527	35.7	424	13	BM947517	BM947517 Homo sapi
36	527	35.7	426	2	HSM085795	Bx492967 Homo sapi
37	489.5	33.2	455	10	BB839755	BB839755 BB839755
38	452.5	30.7	1257	14	CB993951	CB993951 AGENCOURT
39	447	30.3	555	12	BI836220	BI836220 603085778
40	428.5	29.1	379	10	BB871780	BB871780 BB871780
41	426.5	28.9	441	13	BY285423	BY285423 BY285423
42	424.5	28.8	444	13	BY270114	BY270114 BY270114
43	412.5	28.0	782	14	CB527120	CB527120 UI-M-FY0-
44	409.5	27.8	586	14	CB585643	CB585643 AMGNNUC:N
45	405.5	27.5	781	14	CB527493	CB527493 UI-M-FY0-

ALIGNMENTS

RESULT 1
BC039602
LOCUS BC039602 3758 bp mRNA linear HTC 06-NOV-2002
DEFINITION Homo sapiens, Similar to roundabout homolog 4, magic roundabout
(Drosophila), clone IMAGE:5590503, mRNA.
ACCESSION BC039602
VERSION BC039602.1 GI:24660430
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3758)

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OM protein - protein search, using sw model

Run on: January 30, 2004, 15:51:24 ; Search time 29.0777 Seconds
(without alignments)
2449.385 Million cell updates/sec

Title: us-10-047-021-86_copy_28_303

Perfect score: 1475

Sequence: 1 QDSPPQILVHPQDLFGPG.....SGPRLPREARELQRENTG 276

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phase.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_rvirus.*

16: sp_bacteriap.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1311	88.9	1007	4 Q8WZ75	Q8WZ75 homo sapien
2	1303	88.3	792	4 Q8WZ75	Q8WZ75 homo sapien
3	1029.5	69.8	1016	11 Q8C310	Q8C310 mus musculus
4	748	50.7	702	4 Q8TEG1	Q8TEG1 homo sapien
5	448.5	30.4	1034	4 Q96MS0	Q96MS0 homo sapien
6	448.5	30.4	1651	11 Q55005	Q55005 rattus norv
7	446.5	30.3	1651	4 Q9Y6N7	Q9Y6N7 homo sapien
8	445.5	30.2	1612	11 Q89026	Q89026 mus musculus
9	442.5	30.0	330	13 Q90242	Q90242 gallus gall
10	432	29.3	1614	13 Q8UVD7	Q8UVD7 xenopus lae
11	420.5	28.5	1513	13 Q90270	Q90270 brachydanio
12	414.5	28.1	1344	11 Q92214	Q92214 mus musculus
13	404.5	27.4	1380	4 Q8HCK4	Q8HCK4 homo sapien
14	403.5	27.4	333	13 Q90241	Q90241 gallus gall
15	401.5	27.2	1389	13 Q90269	Q90269 brachydanio
16	401.5	27.2	1419	13 Q98SW3	Q98SW3 brachydanio

17	400.5	27.2	1675	13 Q98SW4	Q98SW4 brachydanio
18	395.5	26.8	1395	5 Q9W213	Q9W213 drosophila
19	395.5	26.8	1395	5 Q44924	Q44924 drosophila
20	394.5	26.7	227	11 Q8BJ59	Q8BJ59 mus musculus
21	394	26.7	1342	5 Q8GPP6	Q8GPP6 drosophila
22	394	26.7	1342	5 Q9VZ27	Q9VZ27 drosophila
23	354.5	24.0	1269	5 O01632	O01632 caenorhabdi
24	354.5	24.0	1273	5 O44928	O44928 caenorhabdi
25	348.5	23.6	376	13 Q90271	Q90271 brachydanio
26	346	23.5	1060	11 Q90213	Q90213 rattus norv
27	340	23.1	1406	5 Q8GPP7	Q8GPP7 drosophila
28	340	23.1	1483	5 Q9VQ08	Q9VQ08 drosophila
29	267.5	18.1	1496	4 Q92626	Q92626 homo sapien
30	261.5	17.7	1151	11 Q9QVN5	Q9QVN5 rattus norv
31	261.5	17.7	1174	11 Q91260	Q91260 rattus norv
32	261.5	17.7	1217	11 P97685	P97685 rattus norv
33	260.5	17.7	298	4 Q96HT1	Q96HT1 homo sapien
34	260.5	17.7	1041	4 Q94856	Q94856 homo sapien
35	259	17.6	1311	5 Q961K8	Q961K8 drosophila
36	259	17.6	1527	5 Q9VZ24	Q9VZ24 drosophila
37	253.5	17.2	1028	11 P97528	P97528 rattus norv
38	253	17.2	1535	5 Q23991	Q23991 drosophila
39	252.5	17.1	498	11 Q8BRT6	Q8BRT6 mus musculus
40	252.5	17.1	705	11 Q8CBD3	Q8CBD3 mus musculus
41	251	17.0	1272	13 Q90924	Q90924 gallus gall
42	251	17.0	1369	13 O42414	O42414 gallus gall
43	248.5	16.8	1026	11 Q62845	Q62845 rattus norv
44	245.5	16.6	1028	11 Q8C6X1	Q8C6X1 mus musculus
45	245	16.6	1427	13 Q91562	Q91562 xenopus lae

ALIGNMENTS

RESULT 1

Q8WZ75	ID	Q8WZ75	PRELIMINARY;	PRT;	1007 AA.
AC	Q8WZ75;				
DT	01-MAR-2002	(TrEMBLrel. 20, Created)			
DT	01-MAR-2002	(TrEMBLrel. 20, Last sequence update)			
DT	01-MAR-2003	(TrEMBLrel. 23, Last annotation update)			
DE	Magic roundabout.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=20530916; PubMed=11076864;				
RA	Huminecki L., Bicknell R.;				
RA	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.				
RL	EMBL; AF361473; AAL31867.1;				
DR	Genew; HGNC:17985; ROBO4				
DR	InterPro; IPR003961; FN_III.				
DR	InterPro; IPR007110; Ig-like.				
DR	InterPro; IPR003598; Ig_c2.				
DR	InterPro; IPR003006; Ig_MHC.				
DR	Pfam; PF00041; fn3; 2.				
DR	Pfam; PF00047; ig; 2.				
DR	SMART; SM00060; FN3; 2.				
DR	SMART; SM00408; IGC2; 1.				
DR	PROSITE; PS00835; IG_LIKE; 2.				
KW	Immunoglobulin domain.				
SQ	SEQUENCE 1007 AA; 107457 MW; E43F246C59BE1415 CRC64;				

Query Match 88.9%; Score 1311; DB 4; Length 1007;
Best Local Similarity 98.8%; Pred.No. 1e-104;
Matches 243; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QDSPQILVHPDQDLFOGPGPARMSCRASGPPPTIRWLLNGQPLSMVPPDPHLLPDGT 60
 DB 28 QDSPQILVHPDQDLFOGPGPARMSCRASGPPPTIRWLLNGQPLSMVPPDPHLLPDGT 87
 QY 61 LLLQPPARGHAHDGQALSTDLGVYTCESNRLGTAVSRGARLSAVLREDFOIQRDMV 120
 DB 88 LLLQPPARGHAHDGQALSTDLGVYTCESNRLGTAVSRGARLSAVLREDFOIQRDMV 147
 QY 121 AVVGEQFTLECGPPWGHPEPTVSWKDGKPLALQPGHRTVSGSLLMARAEKSDXTYMC 180
 DB 148 AVVGEQFTLECGPPWGHPEPTVSWKDGKPLALQPGHRTVSGSLLMARAEKSDXTYMC 207
 QY 181 VATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENTVLLNPDPAEGPKRPAVWLX 240
 DB 208 VATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENTVLLNPDPAEGPKRPAVWLX 267
 QY 241 WKVSGP 246
 DB 268 WKVSGP 273
 RESULT 2
 Q96JV6 PRELIMINARY; PRT; 792 AA.
 AC Q96JV6;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein FLJ14946.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RA Isoqai T., Oca T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
 RA Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,
 RA Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
 RA Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;
 RT "NEDO human cDNA sequencing project."
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK027852; BAB55411.1;
 DR InterPro; IPR003961; FN.III.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG.c2.
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF00041; fn3.2.
 DR Pfam; PF00047; ig.2.
 DR SMART; SM00060; FN3.2.
 DR SMART; SM00408; IGC2.1.
 DR PROSITE; PS00835; IG_LIKE; 2.
 KW Hypothetical protein; Immunoglobulin domain.
 SQ SEQUENCE 792 AA; 85419 MW; FC6DC05275B7B234 CRC64;

Query Match 88.3%; Score 1303; DB 4; Length 792;
 Best Local Similarity 98.4%; Pred. No. 3.7e-104;
 Matches 242; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 QDSPQILVHPDQDLFOGPGPARMSCRASGPPPTIRWLLNGQPLSMVPPDPHLLPDGT 60
 DB 28 QDSPQILVHPDQDLFOGPGPARMSCRASGPPPTIRWLLNGQPLSMVPPDPHLLPDGT 87
 QY 61 LLLQPPARGHAHDGQALSTDLGVYTCESNRLGTAVSRGARLSAVLREDFOIQRDMV 120
 DB 88 LLLQPPARGHAHDGQALSTDLGVYTCESNRLGTAVSRGARLSAVLREDFOIQRDMV 147
 QY 121 AVVGEQFTLECGPPWGHPEPTVSWKDGKPLALQPGHRTVSGSLLMARAEKSDXTYMC 180
 DB 148 AVVGEQFTLECGPPWGHPEPTVSWKDGKPLALQPGHRTVSGSLLMARAEKSDXTYMC 207

QY 181 VATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENTVLLNPDPAEGPKRPAVWLX 240
 DB 208 VATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENTVLLNPDPAEGPKRPAVWLX 267
 QY 241 WKVSGP 246
 DB 268 WKVSGP 273
 RESULT 3
 Q8C310 PRELIMINARY; PRT; 1016 AA.
 AC Q8C310;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Similar to MAGIC ROUNDABOUT.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Lung;
 RC MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium.
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573 (2002).
 DR EMBL; AK087355; BAC39850.1;
 SQ SEQUENCE 1016 AA; 108461 MW; DE70683C63AECDE8E CRC64;

Query Match 69.8%; Score 1029.5; DB 11; Length 1016;
 Best Local Similarity 78.5%; Pred. No. 2.2e-80;
 Matches 193; Conservative 20; Mismatches 32; Indels 1; Gaps 1;
 QY 2 DSPQILVHPDQDLFOGPGPARMSCRASGPPPTIRWLLNGQPLSMVPPDPHLLPDGT 61
 DB 39 DSPQILVHPDQDLFOGPGPARMSCRASGPPPTIRWLLNGQPLSMATPDHLLPDGT 98
 QY 62 LLLQPPARGHAHDGQALSTDLGVYTCESNRLGTAVSRGARLSAVLREDFOIQRDMV 120
 DB 99 LLHRPSVQGRPQDDQNLTSALLGVYTCESNRLGTAVSRGARLSAVLQEDFOIQRDVT 158
 QY 121 AVVGEQFTLECGPPWGHPEPTVSWKDGKPLALQPGHRTVSGSLLMARAEKSDXTYMC 180
 DB 159 AVVGESLVLECGPPWGYPKPSVSWKDGKPLVLQPGRTVSGDSLMSVRAEKNDSTGYMC 218
 QY 181 VATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENTVLLNPDPAEGPKRPAVWLX 240
 DB 219 MATNAGQRESRAARVSIQESQDKHELELAVRIQLENTVLLNPEPVRKPKGPGSVWLS 278
 QY 241 WKVSGP 246
 DB 279 WKVSGP 284

RESULT 4
 Q8TEG1 PRELIMINARY; PRT; 702 AA.
 AC Q8TEG1;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE FLJ00236 protein (Fragment).
 GN FLJ00236.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

```

Query Match      30.4%; Score 448.5; DB 4; Length 1034;
Best Local Similarity 43.1%; Pred. No. 3.8e-30;
Matches 109; Conservative 23; Mismatches 90; Indels 31; Gaps 8;

Qy      1 QDSPPOILVHPQDLFGQFGCPARMSCRASQPPPTIRWLLNGQPLSMVPPDP--HH-LLP 57
Db      60 EDAMPRIVQPPDLLVSRGEPATLPCRAEGRPNIEWYKNGARVATVREDPPRAHRLLLP 119

Qy      58 DGTLLLLQPARGHADGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLRDFFQIQPR 117
Db      120 SGALFF--PRIVH--GRRARDEGYTCVARNYLGAAASRNASLEVAVLRODFRQSPG 173

Qy      118 DMVAVVGEFTLECGPPGHWGHEPTVSNWKDGKPLALQAPGRHTVSGSLLMARAEKSDXT 177
Db      174 NVVAVGEPVAVLECPVPRGHPPEPSVSRKDGARLKEEGRTITRGGKLMMSHTLKSAGM 233

Qy      178 YMCVATNSAGHRESRAARYIQB-PODYTEPVELLAVRIQLENVTLNPDPAE----- 229
Db      234 YVCVASNMAGERESAAEVNVLERPSFLRPV-----NOVLADAPVTFLCEVKG 283

Qy      230 GPKPRPAVWLXWK 242
Db      284 DPPPR----LRWR 292

RESULT 6
O55005      PRELIMINARY;      PRT; 1651 AA.
AC O55005;
AD O55005;
DT 01-JUN-1998 (TEMBLrel. 06, Created)
DT 01-JUN-1998 (TEMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Transmembrane receptor Robol.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_Taxid=101116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spinal cord;
RX MEDLINE=98117249; PubMed=9458045;
RA Kidd T., Brose K., Mitchell K.J., Fetter R.D., Tessier-Lavigne M.,
RA Goodman C.S., Tear G.
RT "Roundabout controls axon crossing of the CNS midline and defines a
RL novel subfamily of evolutionarily conserved guidance receptors.";
RL Cell 92:205-215(1998)
DR ENBL; AF041082; AAC39960.1; -.
DR HSSP; P56276; 1TLK.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig c2.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00041; fn3; 3.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00060; FN3; 3.
DR SMART; SM00408; IGC2; 5.
DR PROSITE; PS50835; IG LIKE; 5.
DR K W Immunoglobulin domain; Receptor.
SQ SEQUENCE 1651 AA; 180747 MW; FA2452DD46E18687 CRC64;

Query Match      30.4%; Score 448.5; DB 11; Length 1651;
Best Local Similarity 42.2%; Pred. No. 6.7e-30;
Matches 92; Conservative 31; Mismatches 86; Indels 9; Gaps 2;

Qy      1 QDSPPOILVHPQDLFGQFGCPARMSCRASQPPPTIRWLLNGQPLSMVPPDPHH---LLP 57
Db      64 EDPPPRIVEPSDLIVSKGEPATLNCAEGRPTTIEWYKGGSRVETDKDPPSRHMLLP 123

Qy      58 DGTLLLLQPARGHADGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLRDFFQIQPR 117
Db      124 SCSLFFLR-----IVHGRKSRDEGYTCVARNYLGAEVSHNASLEVALIRDDFRNPS 177

Qy      118 DMVAVVGEFTLECGPPGHWGHEPTVSNWKDGKPLALQAPGRHTVSGSLLMARAEKSDXT 177

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Db 178 DMVAVGEPVMEQPRGHEPTISWKKGSPDLDDKDERITIRGGKLMITYTRKSDAGK 237
Qy 178 YMCVATNSAGHRESRAARVSIQEQDYTEPVELLAVRI 215
Db 238 YVCVGTNNVGERSEVAVELTVLERPSFVKRPSNLAVTV 275

RESULT 7
Q9Y6N7 PRELIMINARY; PRT; 1651 AA.
AC Q9Y6N7;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Roundabout 1.
GN ROBO1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98117249; PubMed=9458045;
RA Kidd T., Brose K., Mitchell K.J., Fetter R.D., Tessier-Lavigne M.,
RA Goodman C.S., Tear G.;
RT "Roundabout controls axon crossing of the CNS midline and defines a
RT novel subfamily of evolutionarily conserved guidance receptors.";
RL Cell 92:205-215(1998).
DR EMBL; AF040990; AAC39575.1; -.
DR HSP; P56276; 1TLK.
DR Genew; HGNC:10249; ROBO1.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00041; fn3; 3.
DR Pfam; PF00047; ig; 5.
DR SMART; SM00060; FN3; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
SQ SEQUENCE 1651 AA; 180929 MW; 9D98CD7CAB73074D CRC64;

Query Match 30.3%; Score 446.5; DB 4; Length 1651;
Best Local Similarity 41.7%; Pred. No. 1e-29;
Matches 91; Conservative 31; Mismatches 87; Indels 9; Gaps 2;

Qy 1 QDSPPQILVHPQDLFGQPGPARMSCRASQPPPTIRWLLNGQPLSMVPPDPHH---LLP 57
Db 64 EDFPRIVEHPHSDLIIVSKGEPATLNCKAEGRPPTIEWYKGERVETDKDDPRSHRM LLP 123
Qy 58 DGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRIGTAVSRGARLSVAVLRDFQIQPR 117
Db 124 SGLSFLFLR-----IVHGKSRPDEGVYVCVARNYLGEAVSHNASLEVAILEDFFRQNP 177
Qy 118 DMVAVGEPVMEQPRGHEPTISWKKGSPDLDDKDERITIRGGKLMITYTRKSDAGK 177
Db 178 DMVAVGEPVMEQPRGHEPTISWKKGSPDLDDKDERITIRGGKLMITYTRKSDAGK 237
Qy 178 YMCVATNSAGHRESRAARVSIQEQDYTEPVELLAVRI 215
Db 238 YVCVGTNNVGERSEVAVELTVLERPSFVKRPSNLAVTV 275

Query Match 30.3%; Score 446.5; DB 4; Length 1651;
Best Local Similarity 41.7%; Pred. No. 1e-29;
Matches 91; Conservative 31; Mismatches 87; Indels 9; Gaps 2;

Qy 1 QDSPPQILVHPQDLFGQPGPARMSCRASQPPPTIRWLLNGQPLSMVPPDPHH---LLP 57
Db 64 EDFPRIVEHPHSDLIIVSKGEPATLNCKAEGRPPTIEWYKGERVETDKDDPRSHRM LLP 123
Qy 58 DGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRIGTAVSRGARLSVAVLRDFQIQPR 117
Db 124 SGLSFLFLR-----IVHGKSRPDEGVYVCVARNYLGEAVSHNASLEVAILEDFFRQNP 177
Qy 118 DMVAVGEPVMEQPRGHEPTISWKKGSPDLDDKDERITIRGGKLMITYTRKSDAGK 177
Db 178 DMVAVGEPVMEQPRGHEPTISWKKGSPDLDDKDERITIRGGKLMITYTRKSDAGK 237
Qy 178 YMCVATNSAGHRESRAARVSIQEQDYTEPVELLAVRI 215
Db 238 YVCVGTNNVGERSEVAVELTVLERPSFVKRPSNLAVTV 275

Query Match 30.3%; Score 446.5; DB 4; Length 1651;
Best Local Similarity 41.7%; Pred. No. 1e-29;
Matches 91; Conservative 31; Mismatches 87; Indels 9; Gaps 2;

Qy 1 QDSPPQILVHPQDLFGQPGPARMSCRASQPPPTIRWLLNGQPLSMVPPDPHH---LLP 57
Db 64 EDFPRIVEHPHSDLIIVSKGEPATLNCKAEGRPPTIEWYKGERVETDKDDPRSHRM LLP 123
Qy 58 DGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRIGTAVSRGARLSVAVLRDFQIQPR 117
Db 124 SGLSFLFLR-----IVHGKSRPDEGVYVCVARNYLGEAVSHNASLEVAILEDFFRQNP 177
Qy 118 DMVAVGEPVMEQPRGHEPTISWKKGSPDLDDKDERITIRGGKLMITYTRKSDAGK 177
Db 178 DMVAVGEPVMEQPRGHEPTISWKKGSPDLDDKDERITIRGGKLMITYTRKSDAGK 237
Qy 178 YMCVATNSAGHRESRAARVSIQEQDYTEPVELLAVRI 215
Db 238 YVCVGTNNVGERSEVAVELTVLERPSFVKRPSNLAVTV 275

Query Match 30.3%; Score 446.5; DB 4; Length 1651;
Best Local Similarity 41.7%; Pred. No. 1e-29;
Matches 91; Conservative 31; Mismatches 87; Indels 9; Gaps 2;

Qy 1 QDSPPQILVHPQDLFGQPGPARMSCRASQPPPTIRWLLNGQPLSMVPPDPHH---LLP 57
Db 64 EDFPRIVEHPHSDLIIVSKGEPATLNCKAEGRPPTIEWYKGERVETDKDDPRSHRM LLP 123
Qy 58 DGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRIGTAVSRGARLSVAVLRDFQIQPR 117
Db 124 SGLSFLFLR-----IVHGKSRPDEGVYVCVARNYLGEAVSHNASLEVAILEDFFRQNP 138
Qy 118 DMVAVGEPVMEQPRGHEPTISWKKGSPDLDDKDERITIRGGKLMITYTRKSDAGK 177
Db 139 DMVAVGEPVMEQPRGHEPTISWKKGSPDLDDKDERITIRGGKLMITYTRKSDAGK 198
Qy 178 YMCVATNSAGHRESRAARVSIQEQDYTEPVELLAVRI 215
Db 199 YVCVGTNNVGERSEVAVELTVLERPSFVKRPSNLAVTV 236

RESULT 9
Q90Z42 PRELIMINARY; PRT; 330 AA.
AC Q90Z42;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Roundabout1 protein (fragment).
GN ROBO1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21366016; PubMed=11472852;
RA Vargesson N., Luria V., Messina I., Erskine L., Laufer B.;
RA "Expression patterns of Slit and Robo family members during vertebrate
RA limb development.";
RL Mech. Dev. 106:175-180(2001).
DR EMBL; AF364047; AAK94293.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00408; IGC2; 3.
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DR PROSITE; PS50835; IG LIKE; 3.
KW Immunoglobulin domain.
FT NON_TER 1
FT NON_TER 330 330
SQ SEQUENCE 330 AA; 36725 MW; 0613488F78CEBE61 CRC64;

Query Match 30.0%; Score 442.5; DB 13; Length 330;
Best Local Similarity 41.3%; Pred. No. 3.1e-30;
Matches 90; Conservative 32; Mismatches 87; Indels 9; Gaps 2;

QY 1 QDSPQILVHPDQQLFQGGPGPARMSCRASGQPPPTIRMLLNGQPLSMVPPDPHH---LLP 57
DB 19 EDFPPRIVEHPSDLIVSKGEPATLNCKAEGRPPTIWKYKGERVETDKDPRSHRMLLP 78
QY 58 DGTLLLLQPPARGHAHDGQALSTDLGVYTCASNRLGTAVSRGARLSVAVLRDFOIQR 117
DB 79 SGLSFLR-----IVHGKSRPDGCVVVCARNYLGEAVSNASLEVAILLRDFRQNP 132
QY 118 DMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRTVSGSLLMARAESDXT 177
DB 133 DMVAVGEPVAMECQPPRGHPPTISWKDKGTFLDDKDERITIRGGKLMITVTRKNDAG 192
QY 178 YMCVATNSAGHRESRAARVSIQEPDYTEPVELLAVRI 215
DB 193 YVCGTNMVGERESEVAELTVLERPSFVKRPSNLAIV 230

RESULT 10
Q8UVD7 PRELIMINARY; PRT; 1614 AA.
AC Q8UVD7;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Roundabout-1.
GN ROBO1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Connor R.M., Key B.;
RT "Dual role for Roundabout-1 in neural differentiation and axon
pathfinding in the Xenopus forebrain.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF461119; AAL66361.1; -.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00041; fn3; 3.
DR Pfam; PF00047; ig; 5.
DR SMART; SM00060; FN3; 3.
DR SMART; SM00408; IGC2; 5.
DR PROSITE; PS50835; IG LIKE; 5.
DR Immunoglobulin domain.
SQ SEQUENCE 1614 AA; 176733 MW; 01D2C3D6593F3935 CRC64;

Query Match 29.3%; Score 432; DB 13; Length 1614;
Best Local Similarity 40.6%; Pred. No. 1.7e-28;
Matches 89; Conservative 32; Mismatches 88; Indels 10; Gaps 3;

QY 1 QDSPQILVHPDQQLFQGGPGPARMSCRASGQPPPTIRMLLNGQPLSMVPPDPHH---LLP 57
DB 26 EDFPPRIVEHPSDLIVSKGEPATLNCKAEGRPPTIWKYKGERVETDKDPRSHRMLLP 85
QY 58 DGTLLLLQPPARGHAHDGQALSTDLGVYTCASNRLGTAVSRGARLSVAVLRDFOIQR 117
DB 86 SGLSFLR-----IVHGKIRPDGCVVVCARNYLGEAVSNASLEVAILLRDFRQNP 139
QY 118 DMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPL-ALQPGRTVSGSLLMARAESDXT 176

Query Match 28.5%; Score 420.5; DB 13; Length 1513;
Best Local Similarity 36.4%; Pred. No. 1.6e-27;
Matches 92; Conservative 38; Mismatches 92; Indels 31; Gaps 6;

QY 1 QDSPQILVHPDQQLFQGGPGPARMSCRASGQPPPTIRMLLNGQPLSMVPPDPHH---LLP 57
DB 26 EDFPPRIVEHPSDLIVSKGEPATLNCKAEGRPPTIWKYKGERVETDKDPRSHRMLLP 85
QY 58 DGTLLLLQPPARGHAHDGQALSTDLGVYTCASNRLGTAVSRGARLSVAVLRDFOIQR 117
DB 86 SGLSFLR-----IVHGKSRKPDGCVVVCARNYLGEAVSNASLEVAILLRDFRQNP 139
QY 118 DMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRTVSGSLLMARAESDXT 177
DB 140 DVVVAAGEPAILECVPVPRGHPPTIYWKOKVRIDEKDDRIKIRGGKLMISNTRKSDAG 199
QY 178 YMCVATNSAGHRESRAARVSI-QSPDYTEPV-----ELLAVRIQLENVLLNPPDAE 229
DB 200 YICVTNMVGERDSETAQTVFERTFLRRRTNQVLEEAVERFCVQV-----DPQFS- 254
QY 230 GPKPRPAVWLXWK 242
DB 255 -----IRWK 258

RESULT 12
Q9Z214 PRELIMINARY; PRT; 1344 AA.
ID Q9Z214
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 30, 2004, 15:45:39 ; Search time 9.53368 Seconds
(without alignments)
1361.423 Million cell updates/sec

Title: US-10-047-021-86_COPY_28_303

Perfect score: 1475

Sequence: 1 QDSPPPQLVHPQDLFGQFG.....SGPRLPREARELRGQRNTG 276

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query	ID	Description
1	232.5	15.8	1997	1	PTPF HUMAN
2	230.5	15.6	1040	1	AXOI_RAT
3	228	15.5	1040	1	AXOI_HUMAN
4	225	15.3	3707	1	PGSM_MOUSE
5	222	15.1	1912	1	PTPD_HUMAN
6	222	15.1	2029	1	LAR_DROME
7	221.5	15.0	1377	1	NEOI_RAT
8	215.5	14.6	1443	1	NEOI_CHICK
9	214.5	14.5	1461	1	NEOI_HUMAN
10	213.5	14.5	1036	1	AXOI_CHICK
11	212.5	14.4	1070	1	PTK7_HUMAN
12	209	14.2	1447	1	DCC_MOUSE
13	209	14.2	1493	1	NEOI_MOUSE
14	206	14.0	1447	1	DCC_HUMAN
15	203.5	13.8	4391	1	PGSM_HUMAN
16	202	13.7	837	1	NCM2_MOUSE
17	199.5	13.5	1302	1	NRG_DROME
18	195.5	13.3	1091	1	NCAL_CHICK
19	195.5	13.3	6632	1	UN89_CABEL
20	194.5	13.2	1284	1	NRCA_CHICK
21	193	13.1	837	1	NCM2_HUMAN
22	191.5	13.0	1914	1	KMLS_HUMAN
23	191	12.9	1260	1	CAML_MOUSE
24	186	12.6	416	1	RAGE_BOVIN
25	185	12.5	725	1	NCAL_MOUSE
26	185	12.5	1115	1	NCAL_MOUSE
27	185	12.5	1257	1	CAML_HUMAN
28	184	12.5	1051	1	PTK7_CHICK
29	183	12.4	858	1	NCAL_RAT
30	182.5	12.4	1010	1	CONT_CHICK
31	182	12.3	1259	1	CAML_RAT
32	181.5	12.3	333	1	AMAL_DROME
33	181.5	12.3	3375	1	UN52_CABEL

34	179	12.1	2012	1	DSCA_HUMAN
35	176	11.9	853	1	NCAL_BOVIN
36	176	11.9	2200	1	LAR_CABEL
37	175	11.9	1266	1	NGCA_CHICK
38	174.5	11.8	873	1	FAS2_DROME
39	173.5	11.8	761	1	NCAL_HUMAN
40	173.5	11.8	848	1	NCAL_HUMAN
41	172	11.7	404	1	RAGE_HUMAN
42	170.5	11.6	1018	1	CONT_HUMAN
43	168	11.4	1021	1	CONT_RAT
44	167.5	11.4	912	1	ICAS_RABIT
45	165.5	11.2	1020	1	CONT_MOUSE

ALIGNMENTS

RESULT 1	PTPF_HUMAN	STANDARD;	PRT; 1897 AA.
ID	PTPF_HUMAN	AC	P10586;
DT	01-JUL-1989	(Rel. 11, Created)	
DT	01-JUL-1989	(Rel. 11, Last sequence update)	
DT	15-SEP-2003	(Rel. 42, Last annotation update)	
DE	LAR protein precursor (leukocyte antigen related) (EC 3.1.3.48).		
GN	PTPRF OR LAR.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Tonsil;		
RX	MEDLINE=89035978; PubMed=2972792;		
RA	Streuli M., Krueger N.X., Hall L.R., Schloesman S.P., Saito H.;		
RT	"A new member of the immunoglobulin superfamily that has a cytoplasmic region homologous to the leukocyte common antigen.";		
RL	J. Exp. Med. 168:1523-1530(1988).		
RN	[2]		
RP	MUTAGENESIS.		
RX	MEDLINE=90048860; PubMed=2554325;		
RA	Streuli M., Krueger N.X., Tsai A.Y.M., Saito H.;		
RT	"A family of receptor-linked protein tyrosine phosphatases in humans and Drosophila.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 86:8698-8702(1989).		
RN	[3]		
RP	MUTAGENESIS.		
RX	MEDLINE=90316093; PubMed=1695146;		
RA	Streuli M., Krueger N.X., Thai T., Tang M., Saito H.;		
RT	"Distinct functional roles of the two intracellular phosphatase like domains of the receptor-linked protein tyrosine phosphatases LCA and LAR.";		
RL	EMBO J. 9:2399-2407(1990).		
CC	!- FUNCTION: IT IS POSSIBLE THAT DLAR IS A CELL ADHESION RECEPTOR. IT POSSESSES AN INTRINSIC PROTEIN TYROSINE PHOSPHATASE ACTIVITY (PTPASE).		
CC	!- FUNCTION: THE FIRST PTPASE DOMAIN HAS ENZYMATIC ACTIVITY. WHILE THE SECOND ONE SEEMS TO AFFECT THE SUBSTRATE SPECIFICITY OF THE FIRST ONE.		
CC	!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.		
CC	!- SUBCELLULAR LOCATION: Type I membrane protein.		
CC	!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.		
CC	!- SIMILARITY: Contains 8 fibronectin type III domains.		
CC	!- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		

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; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081817
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081952
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082569
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082700
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
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; PRIOR APPLICATION NUMBER: 60/085582
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; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 88.9%; Score 1311; DB 11; Length 985;
Best Local Similarity 98.8%; Pred. No. 3.7e-100;
Matches 243; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QDSPQILVHPQDQLFQGPGRMASCASGQPPPTIRWLLNGQPLSMVPPDPHLLPDGT 60
Db 6 QDSPQILVHPQDQLFQGPGRMASCASGQPPPTIRWLLNGQPLSMVPPDPHLLPDGT 65

Qy 61 LLLQPPARGHAHQALSTDLGVYTCEASNRGLTAVSRGARLSVAVLRDFQIQPRDMV 120
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Qy 121 AVGEOFTLECGPPWGHPEPTVSWKDGKPLALQPHRTVSGSLLMARAEKSDXTYMC 180
Db 126 AVGEOFTLECGPPWGHPEPTVSWKDGKPLALQPHRTVSGSLLMARAEKSDXTYMC 185

Qy 181 VATNSAGHRESRAARVSIQEPQDYTPVELLAVRIQLENVTLNPDPAEGPKPRPAVWLX 240
Db 186 VATNSAGHRESRAARVSIQEPQDYTPVELLAVRIQLENVTLNPDPAEGPKPRPAVWLX 245

Qy 241 WKVSGP 246
Db 246 WKVSGP 251

RESULT 12
US-09-978-403A-211
; Sequence 211, Application US/09978403A
; Publication No. US20030050240A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.

;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

;; FILE REFERENCE: P2630P1C17

;; CURRENT APPLICATION NUMBER: US/09/978,403A

;; CURRENT FILING DATE: 2002-03-19

;; PRIOR APPLICATION NUMBER: 09/918585

;; PRIOR FILING DATE: 2001-07-30

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;; PRIOR FILING DATE: 1997-10-17

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Query Match      88.9%; Score 1311; DB 11; Length 985;
Best Local Similarity 98.8%; Pred. No. 3.7e-100;
Matches 243; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QDSPPQILVHPDQQLFQCGPGPARMSCRASQGPPTIRWLLNGQPLSMVPPDPHLLPDGT 60
Db 6 QDSPPQILVHPDQQLFQCGPGPARMSCRASQGPPTIRWLLNGQPLSMVPPDPHLLPDGT 65

QY 61 LLLLOPPARGHAHQALSTDLGVYTCASNRLGTAVSARGARLSVAVLRDPFIQIPDMV 120
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QY 121 AVVGEQFTLECPGPHGPEPTVSWWKGKPLALQGRHTVSGSLLMARAESDXTYMC 180
Db 126 AVVGEQFTLECPGPHGPEPTVSWWKGKPLALQGRHTVSGSLLMARAESDXTYMC 185

QY 181 VATNSAGHRESRAARVSIQEPDYTEPVVELLAVRIQLENVTLNPDPAEGPKRPAVWLX 240
Db 186 VATNSAGHRESRAARVSIQEPDYTEPVVELLAVRIQLENVTLNPDPAEGPKRPAVWLS 245

QY 241 WKVSGP 246
Db 246 WKVSGP 251

RESULT 13
US-09-978-564A-211
; Sequence 211, Application US/09978564A
; Publication No. US20030050241A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Sheiton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC25
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60/084600	PRIOR FILING DATE: 1998-05-07
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60/085697	PRIOR APPLICATION NUMBER: 60/085697
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Query Match 88.9%; Score 1311; DB 11; Length 985;

Qy	1	QDSPPQIILVHPDQLFQSGPGPARMSCRASGQPPTTRWLLNGQPLSWPDPDHILLPDGT	60
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Qy	61	LILLLOPPARGHAHDQALSTDLGYITCEASNRLGTAVSRCARLSVAVLREDFOIQPRDMV	120
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Dd	66	LILLLOPPARGHAHDQALSTDLGYITCEASNRLGTAVSRCARLSVAVLREDFOIQPRDMV	125
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Qy	121	AVVGQPTFLCGCPGWGHPEPTVSWKDGKPLALOPGRHTVSGSLMARAKSDEXTYMC	180
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Qy	181	VATNSAGHRESRAARVSIOEPDYTEPVELLAVRIOLENVTLNLPDPAEGPKRPAPWLX	240
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RESULT 14
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; Sequence 211, Application US/09999833A
; Publication No. US20030054405A1
; GENERAL INFORMATION:
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; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnuyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Oiang

APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
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APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumaas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC65
CURRENT APPLICATION NUMBER: US/09/999,833A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085704
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 88.9%; Score 1311; DB 11; Length 985;
 Best Local Similarity 98.8%; Pred. No. 3.7e-100;
 Matches 243; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 QDSPPQILVHPQDQLFQCGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHLLPDGT 60
 DB 6 QDSPPQILVHPQDQLFQCGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHLLPDGT 65
 QY 61 LLLLOPPARGHAHDGQALSTDLGVYTCASNRLGTAVSRGARLSVAVLREDFOIQRDMV 120
 DB 66 LLLLOPPARGHAHDGQALSTDLGVYTCASNRLGTAVSRGARLSVAVLREDFOIQRDMV 125
 QY 121 AVVGEQFTLECGPWGHEPTVSWKDGKPLALQGRHTVSGSLLMARAKSDEXTVMC 180
 DB 126 AVVGEQFTLECGPWGHEPTVSWKDGKPLALQGRHTVSGSLLMARAKSDEXTVMC 185
 QY 181 VATNSAGHRESRAARVSIOEQDYTEPVVELLAVRIQLENVTLNPDPAEGPKRPVWLX 240
 DB 186 VATNSAGHRESRAARVSIOEQDYTEPVVELLAVRIQLENVTLNPDPAEGPKRPVWLX 245
 QY 241 WKVSGP 246
 DB 246 WKVSGP 251

RESULT 15
 US-09-981-915A-211
 ; Sequence 211, Application US/09981915A
 ; Publication No. US20030054986A1
 ; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Deenoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
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 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2630P1C12
 ; CURRENT APPLICATION NUMBER: US/09/981.915A
 ; CURRENT FILING DATE: 2001-10-16
 ; PRIOR APPLICATION NUMBER: 05/918585
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;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 88.9%; Score 1311; DB 11; Length 985;

Best Local Similarity 98.8%; Pred. No. 3.7e-100;

Matches 243; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Db 6 QDSPPQILVHPQDQLFQGGPARMSCRASGPPPTIRWLLNGQPLSMVPPDPHLLPDGT 65

Qy 61 LLLLQPPARGHADQALSTDLGVVYTCASNRGLGTAVSRGARLSVAVLRDEFQIQPRDMV 120

Db 66 LLLLQPPARGHADQALSTDLGVVYTCASNRGLGTAVSRGARLSVAVLRDEFQIQPRDMV 125

Qy 121 AVGGEQFTLECGPPWGHPEPTVSWKDKPLALQGRITVSGSLLMARAEKSDEXTYMC 180

Db 126 AVGGEQFTLECGPPWGHPEPTVSWKDKPLALQGRITVSGSLLMARAEKSDEXTYMC 185

Qy 181 VATNSAGHRESRAARVSIQEPQDYTEPVVELLAVRIQLENVTLLNPDPAEGPKPRPAVWLX 240

Db 186 VATNSAGHRESRAARVSIQEPQDYTEPVVELLAVRIQLENVTLLNPDPAEGPKPRPAVWLX 245

Qy 241 WKVSGP 246

Db 246 WKVSGP 251
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Search completed: January 30, 2004, 15:59:03
Job time : 29.1244 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 31, 2004, 11:38:39 ; Search time 2894.42 Seconds
(without alignments)
3900.967 Million cell updates/sec

Title: US-10-047-021-86_COPY_28_303
Perfect score: 1475
Sequence: 1 QDSPQILVHPDQLFQPG.....SGPRLPRELRGRRNTG 276

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlp
-Q/cgn2_1/USPTO_spool_p/US10047021/runat_30012004_145452_24562/app.query.fasta_1.910
-DB=GenEmbl -QFMT=fastap -SUFFIX=rg -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10047021@cgn 1 1 5066 @runat_30012004_145452_24562 -NCFU=6 -ICPU=3
-NO WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl: *
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2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
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9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
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14: gb.vi.*
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16: em.fun.*
17: em.hum.*
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19: em.mu.*
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21: em.or.*
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25: em.pl.*
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28: em.un.*

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41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1469	99.6	1346	6	BD074325	BD074325 50 human
2	1432	97.1	3267	6	AX405719	AX405719 Sequence
3	1432	97.1	3872	9	AF361473	AF361473 Homo sapi
4	1424	96.5	4262	6	BD012213	BD012213 Novel gen
5	1424	96.5	4262	6	BD160172	BD160172 Primer fo
6	1424	96.5	4262	9	AK027852	AK027852 Homo sapi
c 7	1232.5	83.6	186971	9	AP003501	AP003501 Homo sapi
8	1121	76.0	3467	9	BC014995	BC014995 Homo sapi
9	1061.5	72.0	2886	10	AY277635	AY277635 Rattus no
10	1057	71.7	756	6	BD150226	BD150226 Primer fo
11	869	58.9	4694	9	AK074163	AK074163 Homo sapi
12	827.5	56.1	209012	2	AC105958	AC105958 Mus muscu
c 13	827.5	56.1	214559	2	AC138284	AC138284 Mus muscu
c 14	795.5	53.9	223269	2	AC120636	AC120636 Rattus no
15	795.5	53.9	250318	2	AC109983	AC109983 Rattus no
16	450.5	30.5	4956	10	AF041082	AF041082 Rattus no
17	448.5	30.4	3384	6	AX714308	AX714308 Sequence
18	448.5	30.4	3384	9	AK056544	AK056544 Homo sapi
19	447.5	30.3	6922	10	MMU17793	Y17793 Mus musculu
20	446.5	30.3	4956	6	BD085989	BD085989 Method of
21	446.5	30.3	4956	9	AF040990	AF040990 Homo sapi
22	446.5	30.3	6789	9	HSDUT1	Z95705 Human DNA B
23	442.5	30.0	991	5	AF364047	AF364047 Gallus ga
24	432	29.3	6435	5	AF461119	AF461119 Xenopus l
25	423	28.7	4871	5	AF337035	AF337035 Danio rer
26	414.5	28.1	5259	10	AF060570	AF060570 Mus muscu
27	404.5	27.4	5598	9	AB046788	AB046788 Homo sapi
28	404.5	27.4	6215	6	AX556709	AX556709 Sequence
29	403.5	27.4	1565	5	AF364048	AF364048 Gallus ga
30	401.5	27.2	5067	5	AF304131	AF304131 Danio rer
31	401.5	27.2	5384	5	AF337036	AF337036 Danio rer
32	400.5	27.2	6860	5	AF304130	AF304130 Danio rer
33	396.5	26.9	6445	6	AX556703	AX556703 Sequence
34	395.5	26.8	4188	6	BD085986	BD085986 Method of
35	395.5	26.8	6440	3	AF040989	AF040989 Drosophil
36	394	26.7	4306	3	AF312580	AF312580 Drosophil
37	354.5	24.0	3822	3	AF041053	AF041053 Caenorhab
38	354.5	24.0	3894	6	BD085988	BD085988 Method of
39	348.5	23.6	1129	5	AF337034	AF337034 Danio rer
40	346	23.5	3650	10	AF182037	AF182037 Rattus no
41	345	23.4	4146	6	BD085987	BD085987 Method of
42	340	23.1	5381	3	AF312579	AF312579 Drosophil
43	299.5	20.3	186971	9	AP003501	AP003501 Homo sapi
c 44	292.5	19.8	16652	2	AC014298	AC014298 Drosophil
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ALIGNMENTS

RESULT 1

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BD074325      BD074325      1346 bp      DNA      linear      PAT 27-AUG-2002
LOCUS          50 human secreted proteins.
DEFINITION     BD074325
ACCESSION      BD074325
VERSION        BD074325.1 GI:22619928
KEYWORDS       JP 2001514024-A/30.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 1346)
AUTHORS        Moore,P.A., Ruben,S.M., Lafleur,D.W., Shi,Y., Rosen,C.A.,
Olsen,H.S., Ebner,R. and Brewer,L.A.
TITLE          50 human secreted proteins
JOURNAL        Patent: JP 2001514024-A 30 11-SEP-2001;
HUMAN GENOME SCIENCES INC
COMMENT        OS Homo sapiens (human)
PN JP 2001514024-A/30
PD 11-SEP-2001
PF 03-SEP-1998 JP 2000508394
PR 05-SEP-1997 US 60/057626 05-SEP-1997 US 60/057663 PR
05-SEP-1997 US 60/057669 12-SEP-1997 US 60/058667 PR
12-SEP-1997 US 60/058974 12-SEP-1997 US 60/058973 PR
12-SEP-1997 US 60/058666
PI PAUL A MOORE, STEVEN M RUBEN, DAVID W LAFLEUR, YANGGU SHI, CRAIG A
PI ROSEN
PI HENRIK S OLSEN, REINHARD EBNER, LAURIE A BREWER PC
C12N15/09,A61K38/00,A61K48/00,A61P17/02,A61P17/06,A61P19/00, PC
A61P19/02,
PC A61P29/00,A61P31/04,A61P31/12,A61P35/00,C07K14/435,C07K16/18,
PC C12N1/15,
PC C12N1/19,C12N1/21,C12N5/10,C12P21/02,C12Q1/68,G01N33/53,C12N15/ PC
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PC A61K37/02,C12N5/00
CC n equals a,t,g, or c
CC n equals a,t,g, or c
FH Key source
FT source
FT Location/Qualifiers
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/organism="Homo sapiens (human)"
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BASE COUNT 318 a 379 c 376 g 267 t 6 others
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Score: 1469.00 Matches: 276
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.59% Indels: 0
DB: 6 Gaps: 0
US-10-047-021-86_COPY_28_303 (1-276) x BD074325 (1-1346)
QY 1 GlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGly 20
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DB 112 CAGGACTCCCGCCCGACAGTCTTAGTCCACCCAGGACGAGTCTCCAGGCGCTGGC 171
|||||
QY 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProProThrIleArgTrpLeuLeu 40
|||||
DB 172 CCGCCAGAGTGGAGTGGCGGCTTCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 231
|||||
QY 41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60
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DB 232 AATGGGAGCCCTGAGCATGTGGCCCGACCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 291
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QY 61 LeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80
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SRSPGVLLPDTSTFYGLIAELPSTPARPSQVAVRRLPQAQLSSPCSSSDSL
OSRGLSPRLSLAPAEAWAKKQELQHANSPPLRGSHSLERACELGNRGSNLS
OSGAVPALVAMRALGPKLLSSNELVTRHLPAPLPFHPPTTQOQTPPVAPQA
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ALCRLSSEETPRNSVMPRAPSPPTTYGYISVPTASEFTDMGRTGGVPGKGVV
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BASE COUNT 628 a 1101 c 927 g 611 t

ORIGIN

Alignment Scores:
Pred. No.: 8,49e-76 Length: 3267
Score: 1432.00 Matches: 268
Percent Similarity: 98.53% Conservative: 1
Best Local Similarity: 98.17% Mismatches: 3
Query Match: 97.08% Indels: 1
DB: 6 Gaps: 0

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QY 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTrpLeuLeu 40
DB 176 CCGTGCAGGATGAGCTGCAGGCTCAGGCGCAGCCACCTCCACCATCGCTGCTGCTG 235
QY 41 AnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60
DB 236 AATGGCAGCCCTGAGCATGTGCGCCCGCAGACCCACACACCTCCTGCTGATGGGACC 295
QY 61 LeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80
DB 296 CTTCTGCTGCTACAGCCCTGCGCGGAGCATGCCAGATGGCGAGCCCTGTCCACA 355
QY 81 AspLeuGlyValThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100
DB 356 GACCTGGGTGTCTACACATGTGAGCGCAGCAACCGCTTGGCAGCGAGTACAGAGAGGC 415
QY 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal 120
DB 416 GCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 475
QY 121 AlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluPro 140
DB 476 GCTGTGTTGGGTGAGCAGTTTACTCTGGAATGTGGGCGCCCTCGGGGCCACCCAGAGCCC 535
QY 141 ThrValSerTrpTrpLeuAspGlyHisProLeuAlaLeuGlnProGlyArgHisThrVal 160
DB 536 ACAGTCTCATGTGGNAAGATGGGAACCCCTGGCCCTCCAGCCCGGAGGACACAGTG 595
QY 161 SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu***ThrTyrMetCys 180
DB 596 TCCGGGGGCTGCTGCTGATGCAAGAGCAGAGAGAGTGCAGAGGAGACCTACATGTGT 655
QY 181 ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu 200
DB 656 GTGGCCACCAACAGCGCAGACATAGGAGAGCCGCGCAGCCCGGCTTTCATCCAGGAG 715
QY 201 ProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluAsnVal 220
DB 716 CCCAGGACTACAGGAGCTGTGGAGCTTCTGGCTGTGCGAATTCAGTGGAAATGTG 775
QY 221 ThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAlaValTrpLeu*** 240

DB 776 ACATGCTGAACCGGATCCTGCGAGGGGCCCCAAGCCCTAGACCGCGGTGTGGCTCAGC 835
QY 241 TrpLysValSerGlyPro***ArgLeuProAsnLeuThrArgProCysSerGlyProArg 260
DB 836 TGGAGGTCAGTGGCCCTGCTGCGGCTGCCCAATCTTACACGGCCTTGTTCAGGACCCAG 895
QY 260 GLeuProArgGluAlaArgGluLeuArgGlyGlnArg 272
DB 896 ACTGCCCGGAGGCGCAGGAGCTCCGTGGGCAGAG 932

RESULT 3
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LOCUS Homo sapiens magic roundabout mRNA, complete cds.
DEFINITION AF361473
ACCESSION AF361473
VERSION AF361473.1 GI:16930357
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3872)
AUTHORS Huminiacki, L. and Bicknell, R.
TITLE In silico cloning of novel endothelial-specific genes
JOURNAL Genome Res. 10 (11), 1796-1806 (2000)
MEDLINE 20530916
PUBMED 11076864
REFERENCE 2 (bases 1 to 3872)
AUTHORS Huminiacki, L. and Bicknell, R.
TITLE Direct Submission
JOURNAL Submitted (15-MAR-2001) ICRF, Institute of Molecular Medicine, John
Radcliffe Hospital, Oxford OX3 9DS, UK
FEATURES
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Location/Qualifiers
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SEHGPTWLEOLATRIKPREVIATCGVALLLLGTAVCIHRRRRARVHLPGLYRYTS
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BASE COUNT 850 a 1245 c 1063 g 714 t

ORIGIN

Alignment Scores:
Pred. No.: 9,98e-76 Length: 3872
Score: 1432.00 Matches: 268
Percent Similarity: 98.53% Conservative: 1
Best Local Similarity: 98.17% Mismatches: 3
Query Match: 97.08% Indels: 1
DB: 9 Gaps: 0

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Qy 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTrpLeu 40
Db 211 CCTGCAGGATGAGTGCACAGCTTCAGGCGAGCCACCTCCACCATCCGCTGGTGTGTG 270
Qy 41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60
Db 271 AATGGCAGCCCTGAGCATGCTGCGCCCGCCAGCCACACACCTCTGCTGCTGATGGGACC 330
Qy 61 LeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80
Db 331 CTTCTGCTGTACAGCCCGCTGCGCGGGAGATGCCACGATGGCGAGCCCTGTCCACA 390
Qy 81 AspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100
Db 391 GACCTGGGTGTCTACATGTGAGCCAGCAACCGCTTGGCAGCGCAGTCAGCAGAGGC 450
Qy 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnInLeuGlnProArgAspMetVal 120
Db 451 GCTCGCTGTCTGTGGCTGTCTCTCGGAGGATTTCCAGATCCAGCTCGGAGCATGGTG 510
Qy 121 AlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpTrpGlyHisProGluPro 140
Db 511 GCTGTGTGGGTGAGCAGTCTTACTCTGGAATGTGGCGCGCTGCGGGCCACCCAGAGCCC 570
Qy 141 ThrValSerTrpTrpLysAspGlyValProLeuAlaLeuGlnProGlyArgHisThrVal 160
Db 571 ACAGTCTCATGTGGTGAAGATGGGAACCCCTGCGCCCTCCAGCCCGGAAGGCACACAGTG 630
Qy 161 SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu***ThrTyrMetCys 180
Db 631 TCCGGGGGTCTCTGCTGATGCGAGAGCAGCAGAGAGTGTGACGAGGACCTCATATGTGT 690
Qy 181 ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu 200
Db 691 GTGGCCACCAACAGCGCAGGACATAGGAGAGCGCGCAGCGCGCGGTTCATCCAGGAG 750
Qy 201 ProGlnAspTyrThrGluProValGluLeuLeuAlaValAlaGlnLeuGlnAsnVal 220
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Qy 241 TrpLysValSerGlyPro***ArgLeuProAsnLeuThrArgProCysSerGlyProAr 260
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Qy 260 gLeuProArgGluAlaArgGluLeuArgGlyGlnArg 272
Db 931 ACTGCCCGGAGGCCAGGAGCTCCGTGGGACAGG 967

RESULT 4
BD012213
LOCUS BD012213 4262 bp DNA linear PAT 02-AUG-2002
DEFINITION Novel genes encoding protein kinase or protein phosphatase.
ACCESSION BD012213
VERSION BD012213.1 GI:22092402
KEYWORDS WO 0109345-A/11.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 4262)
Ota,T., Isegai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K., Otsuki,T.,
Funahashi,S., Seno,C. and Nezu,J.
Novel genes encoding protein kinase or protein phosphatase
Patent: WO 0109345-A/11 08-FEB-2001.
HELIX RESEARCH INSTITUTE, TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA,
KOJI HAYASHI, KAORU SAITO, JUNICHI YAMAMOTO, SHIZUKO ISHII, OMOYASU
SUGIYAMA, AI WAKAMATSU, KEIICHI NAGAI, TETSUJI OTSUKI, OTSUKI SHINICHI
FUNAHASHI, HIAKI SENO, JUNICHI NEZU
OS Homo sapiens (human)
PN WO 0109345-A/11
PD 08-FEB-2001
PF 28-JUL-2000 WO 2000JP005060
PR 29-JUL-1999 JP 99P 248036, 11-JAN-2000 JP 00P 118776 PR
02-MAY-2000 JP 00P 183767, 18-OCT-1999 US 60/159590 PR
17-FEB-2000 US 60/183322
PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, PI
KAORU SAITO,
JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
PI KEIICHI NAGAI, TETSUJI OTSUKI, SHINICHI FUNAHASHI, CHIAKI SENO,
PI JUNICHI NEZU
PC C12N15/54, C12N15/55, C12N9/12, C12N9/16, C12N5/10, C12N1/21 PC
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PC G01N33/53, G01N33/566
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FT CDS 873 a 1333 c 1209 g 847 t
BASE COUNT
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Alignment Scores:
Pred. No.: 3,24e-75 Length: 4262
Score: 1424.00 Matches: 267
Percent Similarity: 98.17% Conservative: 1
Best Local Similarity: 97.80% Mismatches: 4
Query Match: 96.54% Indels: 1
DB: 6 Gaps: 0
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Qy 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTrpLeu 40
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Qy 41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60
Db 241 AATGGCAGCCCTGAGCATGCTGCGCCCGCCAGCCACACCTCTGCTGCTGATGGGACC 300
Qy 61 LeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80
Db 301 CTTCTGCTGTACAGCCCGCTGCGCGGGAGCATGCCACGATGGCGAGCCCTGTCCACA 360
Qy 81 AspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100
Db 361 GACCTGGGTGTCTACATGTGAGGCGCAGCAACCGCTTGGCAGCGCAGTCAGCAGAGGC 420
Qy 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnInLeuGlnProArgAspMetVal 120
Db 421 GCTCGCTGTCTGTGGTGTCTCTCGGAGGATTTCCAGATCCAGCTCCAGACATGGTG 480
Qy 121 AlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpTrpGlyHisProGluPro 140
Db 481 GCTGTGTGGGTGAGCAGTCTTACTCTGGAATGTGGCGCGCTGCGGGCCACCCAGAGCCC 540
Qy 141 ThrValSerTrpTrpLysAspGlyValProLeuAlaLeuGlnProGlyArgHisThrVal 160
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Db 541 ACAGTCTCATGTGGAAAGATGAGAAACCCCTGGCCCTCCAGCCGGAGGCACACAGTG 600
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Db 601 TCCGGGGGGTCTCTGCTGATGCAAGACGACGAGAGAGTGACAGAGGACCTACATGTGT 660
Qy 181 ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu 200
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Qy 221 ThrLeuLeuAsnProAspProAlaGluGlyProLysProAspProAlaValTyrLeu*** 240
Db 781 ACACGTCTGTAACCCGGATCTGCAGAGGCCCCCAAGCCTAGACCCGGGTGTGGCTCAGC 840
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Qy 260 gluProArgGluAlaArgGluLeuArgGlyClnArg 272
Db 901 ACTGCCCGGGAGGCCAGGAGCTCCGTGGGCAGAGG 937

RESULT 5

BD160172 4262 bp DNA linear -PAT 17-JAN-2003
LOCUS Primer for synthesizing full-length cDNA and use thereof.
DEFINITION BD160172
ACCESSION BD160172.1 GI:27865930
VERSION JP 2002191363-A/15015.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.,
Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.
TITLE Primer for synthesizing full-length cDNA and use thereof
JOURNAL Patent: JP 2002191363-A 15015 09-JUL-2002;
HELIX RESEARCH INSTITUTE
COMMENT OS Homo sapiens (human)
PN JP 2002191363-A/15015
PD 09-JUL-2002
PF 28-JUL-2000 JP 2000280990
PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
PI KEIICHI NAGAI, TETSUJI OTSUKI
PI
PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
10, C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH key

FEATURES

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BASE COUNT 873 a 1333 c 1209 g 847 t
ORIGIN

Alignment Scores:

Pred. No.: 3 248-75 Length: 4262
Score: 1424.00 Matches: 267
Percent Similarity: 98.11% Conservative: 1
Best local Similarity: 97.80% Mismatches: 4
Query Match: 96.54% Indels: 1
DB: Gaps: 0

US-10-047-021-86_copy_28_303 (1-276) x BD160172 (1-4262)

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Qy 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProProThrIleArgTyrLeuLeu 40
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Qy 41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60
Db 241 AATGGCAGCCCTGAGCATGTGTCGCCCCAGACCCACACCACTCTCTGCTGATGGGACC 300
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Db 301 CTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCACAGATGGCCAGGCCCTGTCCACA 360
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Db 361 GACCTGGGTGCTACACATGTGAGGCCAGCAACCGGCTTGGCACCGCAGTCAGCAGAGGC 420
Qy 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal 120
Db 421 GCTGGCTGTCTGTGGCTGTCTCTCGGGAGGATTTCCAGATCCAGCTCGAGACATGGTG 480
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Db 481 GCTGGTGGGTGAGCAGTCTTACTCTGGAATGTGGGGCGCCCTGGGGGCCACCCAGAGCCC 540
Qy 141 ThrValSerTyrTyrLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrVal 160
Db 541 ACAGTCTCATGTGGAAAGATGAGAAACCCCTGGCCCTCCAGCCCGGAGGCACACAGTG 600
Qy 161 SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu***ThrTyrMetCys 180
Db 601 TCCGGGGGGTCCCTGCTGATGGCAAGACGACAGAGAGTGACGAAGGACCTTACATGTGT 660
Qy 181 ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu 200
Db 661 GTGGCCACCAACAGCGCAGGACACAGGAGAGCCGCGCAGCCGGTTCATCCAGGAG 720
Qy 201 ProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluAsnVal 220
Db 721 CCCAGGACTACACGAGCCTGTGAGCTTCTGGCTGTGCGAATTCAGCTGGAATGTG 780
Qy 221 ThrLeuLeuAsnProAspProAlaGluGlyProLysProArGProAlaValTyrLeu*** 240
Db 781 ACACGTCTGTAACCCGGATCTTCAGAGGCCCCCAAGCCTAGACCCGGGTGTGGCTCAGC 840
Qy 241 TrpLysValSerGlyPro***ArgLeuProAsnLeuThrArgProCysSerGlyProAr 260
Db 841 TGGAAAGTCACTGGGCCCTGCTGCGCTGCGCAATCTTACACGGCTTGTTCAGGACCCAG 900
Qy 260 gluProArgGluAlaArgGluLeuArgGlyClnArg 272
Db 901 ACTGCCCGGGAGGCCAGGAGCTCCGTGGGCAGAGG 937

RESULT 6

AK027852 4262 bp mRNA linear PRI 01-AUG-2002
LOCUS Homo sapiens cDNA FLJ14946 fis, clone PLACE2000034, weakly similar
DEFINITION to LAR PROTEIN PRECURSOR (EC 3.1.3.48).
ACCESSION AK027852
VERSION AK027852.1 GI:14042831
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, Y.,

Nishikawa, T., Nagai, K., Sugano, S., Takahashi-Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Nabekura, T., Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagahara, K., Masuho, Y. and Oshina, A.
NEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 4262)
Isogai, T. and Otsuki, T.
Direct Submission
Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection; Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.

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BASE COUNT 873 a 1333 c 1209 g 847 t

ORIGIN

Alignment Scores:

Pred. No.: 3.24e-75 Length: 4262
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Best Local Similarity: 97.80% Mismatches: 4
Query Match: 96.54% Indels: 1
DB: 9 Gaps: 0

US-10-047-021-86_COPY_28_303 (1-276) x AK027852 (1-4262)

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Qy 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProThriLeArgTrpLeuLeu 40
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Qy 41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60
241 AATGGGAGCCCTGAGCATGGTGGCCCGACACCCACACACCTTCCTGCTGATGGGACC 300

Qy 61 LeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80

Db 301 CTTCGTGCTGTACAGCCCTGCGGGGAGCATGCCACGATGGCCAGGCGCTGTCCACA 360
Qy 81 AspleuclyValTyThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100
Db 361 GACCTGGGTGTCTACATGTGAGGCCAGCAACCGGCTTGGCAGCGGAGTCCAGAGGC 420
Qy 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal 120
Db 421 GCTCGGCTGTCTGGGTGCTCTCCGGAGAGATTCCAGATCCAGCCTCGAGACATGGTG 480
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Db 541 ACAGTCTCATGGTGGAAAGATGAGAAACCCCTGGCCCTCCAGCCCGGAGGACACACAGTG 600
Qy 161 SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu***ThrTyMetCys 180
Db 601 TCCGGGGGGTCCCTGCTGATGGCAAGACAGAGAGTGCAGNAGGAGCCTACATGTGT 660
Qy 181 ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu 200
Db 661 GTGGCCACCAACAGCGCAGGACACAGGAGGCGCGCAGCGCGGGTTCATCCAGGAG 720
Qy 201 ProGlnAspTyThrGluProValGluLeuAlaValArgIleGlnLeuGluAsnVal 220
Db 721 CCCAGGACTACACGAGGCGCTGTGGAGCTTCTGGCTGTGGCAATTCAGCTGGAAATGTG 780
Qy 221 ThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAlaValTrpLeu*** 240
Db 781 ACCTGCTGAACCCGGATCTTCAGAGGGCCCCCAGCCTAGACCGCGGTGTGCTCAGC 840
Qy 241 TrpLysValSerGlyPro***ArgLeuProAsnLeuThrArgProCysSerGlyProAr 260
Db 841 TGAAGGTGAGTGGCCCTGCTGGCGCTGCCCAATCTTACACGGCCTTGTTCAGGACCCAG 900
Qy 260 gLeuProArgGluAlaArgGluLeuArgGlyGlnArg 272
Db 901 ACTGCCCCGGAGGCCAGGAGCTCCGTGGGCGAGAG 937

RESULT 7

AP003501/c 186971 bp DNA linear PRI 08-MAR-2002

LOCUS Homo sapiens genomic DNA, chromosome 11q, clone:RP11-664I21,
complete sequence.

ACCESSION AP003501

VERSION AP003501.2 GI:19263048

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
Homo sapiens genomic DNA
Published Only in Database (2001)
2 (bases 1 to 186971)
Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (11-APR-2001) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: hattori@gsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/, Tel: 81-45-503-9111, Fax: 81-45-503-9170)
On Mar 7, 2002 this sequence version replaced gi:13603460.
FEATURES
Location/Qualifiers
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Percent Similarity: 48.46% Conservative: 1
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Query Match: 83.56% Indels: 282
DB: 9 Gaps: 4

US-10-047-021-86_COPY_28_303 (1-276) x AP003501 (1-186971)

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QY 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTrpLeu 40
D 32270 CCTGCCAGGATGAGCTGCCAAGCCTCAGGCGCCAGCCACCTCCACCATCCGCTGGTGGTG 32211
QY 41 AsnGlyGlnProLeuSerMetValProProAspProHisLeuLeuProAspGlyThr 60
D 32210 AATGGCAGCCCTGAGCATGTGTCGCCCGCCAGACCCACACACCTCTGCTGATGGGACC 32151
QY 61 LeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80
D 32150 CTTCTGCTGCTACAGCCCTGTCGCCGGGACATGCCACGATGGCCAGGCGCCCTGTCCACA 32091
QY 81 AspLeuGlyValTyThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100
D 32090 GACCTGGGTGTGTACACATGTGAGGCCAGCAACCGGCTTGGCAGCGCAGTCAGCAGAGGC 32031
QY 101 AlaArgLeuSerValAla----- 106
D 32030 GCTCGGCTGTGTGCTGTGAGGCTTGGAGGGGAGGCTTCAGGGTGGGGCAACCTGG 31971
QY 106 ----- 106
D 31970 GTGGAGACATCTGAGCTGAATGTTCAAGGGAACATCTGAGAGGTGAGTGGGATACCTGTG 31911
QY 106 ----- 106
D 31910 AGCAGAGGCTGGGCTGGAAGGCTTGGGAGGGCAAGCTGGGGGGGCTGGCCCTAAATG 31851
QY 106 ----- 106
D 31850 GGAGGCCAGAGGTGGGCAAGCAGAGAGGGGCAAGAGTGTATAGGGAGAGAGAGAGG 31791
QY 107 -----ValLeuArgGluAspPheGln 113
D 31790 CTTGGGCCCTGCTCCGTGTACCTTCCATCTCTCCCCACAGTCTCTCCGGGAGGATTTCCAG 31731
QY 114 IleGlnProArgAspMetValAlaValValGlyGlnPheThrLeuGluCysGlyPro 133
D 31730 ATCCAGCCTCGGACATGTGCTGTGGTGGGTGAGCAGTCTTACTCTGGAATGTGGGCG 31671
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D 31670 CCTGGGGCCACCCAGAGCCCAAGTCTCATGTGTGAAGAAGTGGGAACCCCTGGCCCTC 31611
QY 154 GlnProGlyArgHisThrVal----- 160
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QY 169 ArgAlaGluLysSerAspGlu***ThrTyMetCysValAlaThrAsnSerAlaGlyHis 188
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D 30771 TCCAGGTTCAGTGGCCCTGCTGGGCTGCCCATCTTACAGGCTTGTTCAGAGCCCGAG 30712
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RESULT 8

BC014995

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3467)

Srausberg, R.

Direct Submission

JOURNAL

BC014995 Homo sapiens, clone IMAGE:4850025, mRNA. linear PRI 12-SEP-2002

BC014995.1 GI:21955407

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3467)

Srausberg, R.

Direct Submission

Submitted (01-OCT-2001) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. Mark Watson

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Genome Sequence Centre,

BC Cancer Agency, Vancouver, BC, Canada

info@bcgsc.bc.ca

Steven Chan, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanana Jones, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saedi, Jacqueline Schein, Duane Smalhus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IPAL Plate: 34 Row: a Column: 19.

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BASE COUNT
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US-10-047-021-86_COPY_28_303 (1-276) x BC014995 (1-3467)

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Qy 97 ValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnPro 116
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Db 182 CGGACATGCTGTGCTGTGGTGTGAGCAGTTTACTCTGGAATGTGGCGCCCTCGGGGC 241
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AY277635
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DEFINITION Rattus norvegicus ROBO4 (Robo4) mRNA, complete cds.
ACCESSION AY277635
VERSION AY277635.1 GI:30575794
KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 2886)
AUTHORS Roberts,K.G. and Stewart,L.M.
TITLE Direct Submission
JOURNAL Submitted (15-APR-2003) CRT Development Laboratory, Cancer Research
Technology, Suite 23, Dominion House, 59 Bartholomew Close, London,
England EC1A 7BE, United Kingdom
FEATURES
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Score: 1057.00 Matches: 205
Percent Similarity: 97.17% Conservatives: 1
Best Local Similarity: 96.70% Mismatches: 6
Query Match: 71.66% Indels: 2
DB: 6 Gaps: 0
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Db 541 ACAGTCTCATGTGGAAGATGAGAAACCTCTGGCCCTCCAGCCCGGAGGACACACAGTG 600
Qy 161 SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu***ThrTyrMetCys 180
Db 601 TCCGGGGGTCTCTGTGATGTCAGAGCAGCAGAGAGTGTGAGAGGACCTACATGTGT 660
Qy 181 ValAlaThrAnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu 200
Db 661 GTGGC-ACCAACAGCGCAGGACACAGGAGAGCGCGGCCACC-CGGGTTTNCATTCCAGGAG 718
Qy 201 ProGlnAepTyrThrGluProValGlnLeuLeuAla 212
Db 719 CCCANGACTACAGGAACCTGTGGAACCTTTGGCT 754
RESULT 11
AK074163
LOCUS AK074163 Homo sapiens mRNA for FLJ00236 protein. linear PRI 15-FEB-2002
DEFINITION AK074163
ACCESSION AK074163
VERSION AK074163.1 GI:18676673
KEYWORDS fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Jikuya,H., Takano,J., Nomura,N., Kikuno,R., Nagase,T. and Ohara,O.
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QY 163 GlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu***ThrTyrMetCysValAla 182
 Db 238 GGGTCCCTGCTGATGGCAAGACGAGAGAGAGTGCAGAGGACCTACATGTGTGTGGCC 297
 QY 183 ThrAnSerAlaGlyHisArgGluSerArgAlaAlaAArgValSerIleGlnGluProGln 202
 Db 298 ACCAAGCGGAGGACATAGGAGAGCGCGGAGCGCGGGTTCATCCAGAGAGCCCGAG 357
 QY 203 AspTyrThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluAsnValThrLeu 222
 Db 358 GACTACACGAGCCGTGTGGAGTCTTGGCTGTGGCAATTCAGCTGGAAAATGTGACATG 417
 QY 223 LeuAsnProAspProAlaGluGlyProLysProArgProAlaValTrpLeu***TrpLys 242
 Db 418 CTGAACCCGGATCTCTGCAGAGCGGCCCAAGCCCTAGACCGCGGTGTGGCTCAGCTGGAAG 477
 QY 243 ValSerGlyPro***ArgLeuProAsnLeuThrArgProCysSerGlyProArgLeuPr 262
 Db 478 GTCACTGGCCCTGTGGCGCTGCCCAATCTTACAGCGGCTTGTTCAGGACCCAGACTGCC 537
 QY 262 OhArgGluAlaArgGluLeuArgGlyGlnArg 272
 Db 538 CCGGAGGCGGAGGAGGAGCTCCGTGGCGAGG 568

RESULT 12
 AC105958 209012 bp DNA linear HTG 04-MAR-2003
 LOCUS Mus musculus clone RP24-325P4, WORKING DRAFT SEQUENCE, 9 unordered
 DEFINITION pieces.
 ACCESSION AC105958
 VERSION AC105958.6 GI:28827995
 KEYWORDS HTG; HTGS; PHASE1; HTGS DRAFT.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Birren,B., Nusbaum,C. and Lander,E.
 Mus musculus, clone RP24-325P4
 Unpublished
 2 (bases 1 to 209012)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
 Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukhgalter,B.,
 Brown,A., Camarata,J., Campolano,A., Chang,J.J., Chazaro,B.,
 Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
 Cooke,P., DeArelano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
 Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,
 Ginde,S., Gord,S., Goyette,M., Graham,L., Hulme,W., Iliev,I., Johnson,R.,
 Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K.,
 Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,
 MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
 McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J.,
 Meneus,L., Mihova,T., Mienga,V., Murphy,T., Naylor,J., Nguyen,C.,
 Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D.,
 Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
 Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
 Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
 Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
 Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
 Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
 Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission
 Submitted (11-JAN-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 209012)

Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
 Anderson,S., Archchi,H.M., Barna,N., Bastien,V., Bloom,T.,
 Boguslavsky,L., Boukhgalter,B., Camarata,J., Chang,J.J., Choepel,Y.,
 Collymore,A., Cook,A., Cooke,P., Corum,B., DeArelano,K.,
 Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
 Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,

Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,
 Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
 Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
 Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., MacLean,C.,
 Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,
 Meldrim,J., Meneus,L., Mihova,T., Mienga,V., Murphy,T., Naylor,J.,
 Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
 O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
 Ruchupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,
 Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C.,
 Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
 Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,
 Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
 Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission
 Submitted (04-MAR-2003) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Mar 4, 2003 this sequence version replaced gi:28201704.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence submissions@genome.wi.mit.edu

----- Project Information

Center project name: L19390

Center clone name: 325_P4

----- Summary Statistics

Sequencing vector: Plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 208525 bases at least Q40

Consensus quality: 207512 bases at least Q30

Consensus quality: 207947 bases at least Q20

Insert size: 182000; agarose-fp

Insert size: 208212; sum-of-contigs

Quality coverage: 11.1 in Q20 bases; agarose-fp

Quality coverage: 9.7 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently

* consists of 9 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1 38270: contig of 38270 bp in length

* 38271 38370: gap of 100 bp

* 38371 39590: contig of 1220 bp in length

* 39591 39690: gap of 100 bp

* 39691 47174: contig of 7484 bp in length

* 47175 47274: gap of 100 bp

* 47275 61618: contig of 14344 bp in length

* 61619 61718: gap of 100 bp

* 61719 86099: contig of 24381 bp in length

* 86100 86199: gap of 100 bp

* 86200 112506: contig of 26307 bp in length

* 112507 112606: gap of 100 bp

* 112607 143181: contig of 30575 bp in length

* 143182 143281: gap of 100 bp

* 143282 179163: contig of 35882 bp in length

* 179164 179263: gap of 100 bp

* 179264 209012: contig of 29749 bp in length.

* 179264 209012: contig of 29749 bp in length.

Location/Qualifiers

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/mol_type="genomic DNA"

/db_xref="taxon:10090"

/clone="RP24-325P4"

/clone_lib="RPCI-24 Male Mouse BAC"

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Score: 827.50 Matches: 204
Percent Similarity: 37.56% Conservative: 24
Best Local Similarity: 33.61% Mismatches: 43
Query Match: 56.10% Indels: 336
DB: 2 Gaps: 5

US-10-047-021-86_COPY_28_303 (1-276) x AC105958 (1-209012)
Qy 2 AspSerProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGlyPro 21
Db 8818 GATTCTCACCCAGATCTTAGTTCACCCCGAGGACAGCTACTTCAGGGCTCTGGCCCA 8877
Qy 22 AlaArgMetSerCysArgAlaSerGlyGlnProProProThrIleArgTrpLeuAsn 41
Db 8878 GCCAAGATGAGGTGCAGATCTCCGGCCCAACACCTCCACTATCCCGCTGCTGTAAT 8937
Qy 42 GlyGlnProLeuSerMetValProProAspProHisHisAspGlyGln---AlaLeuSerThr 61
Db 8938 GGGCAGCCCTCAGCATGGCCACCCAGACCTACTATACCTTTTCCGGATGGACCCCTC 8997
Qy 62 LeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGln---AlaLeuSerThr 80
Db 8998 CTGTTACATCGCCCTCTGTCCAGGCGGCCACAGATGACCAACATCTCTCAGCA 9057
Qy 81 AspLeuGlyValThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100
Db 9058 ATCTGGGTGTCTACATGTGAGGCCAGCAACCGGCTGGGCACAGCAGTGAAGCCGGGT 9117
Qy 101 AlaArgLeuSerValAla----- 106
Db 9118 GCTAGGCTGTCTGGCTGGTGAAGCTTGGGAGGGTAGGCCCGGAGGGAAGCAGAGTTAG 9177
Qy 106 ----- 106
Db 9178 GCTGAGATGCTTGTCTCCAGGGAATACGAGAGTCTGTCTGTGAAGGGAGCGAGGACTG 9237
Qy 106 ----- 106
Db 9238 AGGGTCTTGGATGGAGAACTAGTGTAACTAGAGATAGAGGGGCAAGGAAGTGGTAGAG 9297
Qy 106 ----- 106
Db 9298 CAGAATTGGGTAAAGCATGTTCCGATAAGCCATCCATGTTAGATGTTAGAGGACTCAGG 9357
Qy 107 -----ValLeuArgGluAspPhe 112
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Db 9358 GTGGGTAGACGTGCTTCTGCTGCTGATTTGCTGACTTCCCAATAGTCTCTCCAGGAGACTTC 9417
Qy 113 GlnIleGlnProArgAspMetValAlaValValGlyGlnPheThrLeuGluCysGly 132
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Db 9418 CAGATCCACCTCGGGACACAGTGGCGGTGGTGGAGAGAGCTTGGTCTTGTAGTGGT 9477
|||||:|||||
Qy 133 ProProTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAla 152
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Db 9478 CTTCCCTGGGGCTACCCAAACCTCGGTCTCTATGTTGGTGAAGACGGGAACCCCTGGTC 9537
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Qy 153 LeuGlnProGlyArgHis----- 158
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Db 9538 CTCAGCCAGGAGGGCGCACAGTGAAGAACCCCAATCTCTGGGAACCTCTTTTGGCCATAC 9597
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Qy 158 ----- 158
Db 9598 ATCATCTGTCTCTGGGCGACATTTGAGCAACTGACCCACCTCCCAACCTCTAAGCTTCTCAA 9657
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Qy 159 -----Thr-ValSerGlyGlySerLeuLeuMetAl 168
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Db 9658 ATTGAAGACTTCATGGAGTATCTGAACCTGCACAGGTATCTGGGATTCCTGTGTTGTC 9717
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Qy 168 aArgAlaGluLysSerAspGlu***ThrTyrMetCysValAlaThrAsnSerAlaGlyHi 188
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Db 9718 AAGAGCAGAGAAGAAATGACTCGGGGACCTATATGTGTATGTCACCAACAATGCTGGCA 9777
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Qy 188 sArgGluSerArgAlaAlaArgValSerIleGln----- 199
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Db 9778 ACGGAGAGCCGACAGCAGCGGGTGTCTATCCAGGGTAAAGACAGGAGTCACTTACAATC 9837
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Qy 199 ----- 199
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Qy 199 ----- 199
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Qy 200 ----GluProGlnAspTyrThrGluProValGluLeuAlaValArgIleGlnLeuG1 218
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Qy 218 uAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAlaValTr 238
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Db 10378 AATGTGACCTGCTGAACCCCGAACCTGTAAAGGTCCCAAGCTGGGCCATCCGTGTG 10437
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Qy 238 pLeu***TrpLys----- 242
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QY 243 -----ValserGlyPro***- 247
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 QY 268 LeuArgGlyGlnArg 272
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RESULT 13
 AC138284/C
 LOCUS
 DEFINITION Mus musculus chromosome 9 clone RP23-356D13 map 9, WORKING DRAFT
 AC138284
 VERSION HTG; HTGS PHASE1; HTGS DRAFT.
 KEYWORDS Mus musculus (house mouse)
 SOURCE
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Birren,B., Nusbaum,C. and Lander,E.
 1 (bases 1 to 214559)
 Mus musculus chromosome 9, clone RP23-356D13
 Unpublished
 2 (bases 1 to 214559)
 Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
 Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhgalter,B.,
 Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
 Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
 Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,
 Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hafez,N.,
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 Matthews,C., McCarthy,M., Meldrim,J., Meneus,L., Mihova,T.,
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 Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J.,
 Peterson,K., Phunkhanger,P., Pierre,N., Raymond,C., Retta,R.,
 Rise,C., Rogov,P., Roman,J., Roy,A., Schauer,S., Schupback,R.,
 Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N.,
 Stojanovic,N., Talamas,J., Tesfaye,S., Theodore,J., Topham,K.,
 Travers,M., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X.,
 Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
 Direct Submission
 Submitted (20-DEC-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 214559)
 Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
 Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
 Boguslavskiy,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y.,
 Collymore,A., Cook,A., Cooke,P., Corum,B., DeArellano,K.,
 Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
 Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,
 Graham,L., Grand-Pierre,N., Hafez,N., Hapcoplan,D., Hagos,B.,
 Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
 Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
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 Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,
 Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J.,
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 Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C.,
 Spencer,B., Stange-Thomann,N., Stojanovic,N., Strubbs,M.,
 Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,
 Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
 Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
 Direct Submission

JOURNAL
 COMMENT
 Submitted (23-MAR-2003) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Mar 23, 2003 this sequence version replaced gi:28460994.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L28797
 Center clone name: 356.D.13
 ----- Summary Statistics
 Sequencing vector: plasmid; n/a; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 213654 bases at least Q40
 Consensus quality: 213955 bases at least Q30
 Consensus quality: 214104 bases at least Q20
 Insert size: 210000; agarose-fp
 Insert size: 214159; sum-of-contigs
 Quality coverage: 10.7 in Q20 bases; agarose-fp
 Quality coverage: 10.5 in Q20 bases; sum-of-contigs

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 5 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 * 1 5437: contig of 5437 bp in length
 * 5438 5537: gap of 100 bp
 * 5538 134170: contig of 128633 bp in length
 * 134171 134270: gap of 100 bp
 * 134271 159037: contig of 24767 bp in length
 * 159038 159137: gap of 100 bp
 * 159138 212279: contig of 53142 bp in length
 * 212280 212379: gap of 100 bp
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 Pred. No.: 212b-38 Length: 214559
 Score: 827.50 Matches: 204
 Percent Similarity: 37.56% Conservative: 24

TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
 Boguslavskiy,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y.,
 Collymore,A., Cook,A., Cooke,P., Corum,B., DeArellano,K.,
 Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
 Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,
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 Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., MacLean,C.,
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 Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J.,
 Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
 O'Neill,D., Oliver,J., Peterson,K., Phunkhanger,P., Pierre,N.,
 Rachupka,A., Ramaasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,
 Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C.,
 Spencer,B., Stange-Thomann,N., Stojanovic,N., Strubbs,M.,
 Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,
 Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
 Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
 Direct Submission

Best Local Similarity: 33.61% Mismatches: 43
Query Match: 56.10% Indels: 336
DB: 2 Gaps: 5

US-10-047-021-86_COPY_28_303 (1-276) x AC138284 (1-214559)

Qy 2 AspSerProGlnLeuValHisProGlnAspGlnLeuPheGlnGlyProGlyPro 21
Db 188584 GATCTCCACCCAGATCTTAGTTCACCCAGGACAGCTACTTCCAGGGCTCTGGCCCA 188525
Qy 22 AlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTrpLeuLeu 41
Db 188524 GCCAAGATGAGTGAGATCCGGCCAAACCACTCCCACTATCCGCTGCTGAAT 188465
Qy 42 GlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThrLeu 61
Db 188464 GGGCAGCCCTCAGCATGCCACCCAGCTTACATTAACCTTTTCCGGATGGGACCCCTC 188405
Qy 62 LeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGln---AlaLeuSerThr 80
Db 188404 CTGTTACATCGCCCTCTGTCCAGGACGGCCACAGATGACCAACATCTCTCAGCA 188345
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Db 188344 ATCTGGGTGTCTACACATGTGAGGCCAGCAACCGCTGGGCACAGCAGTGTGAGCGGGT 188285
Qy 101 AlaArgLeuSerValAla----- 106
Db 188284 GCTAGGCTGTCTGTGGCTGGTGGAGGCTGGGAGGTAGCCCGAGGGGGAAGCAGAGTTAG 188225
Qy 106 ----- 106
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Qy 106 ----- 106
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Qy 106 ----- 106
Db 188104 CAGAAATGGGTAAGCATGTTCCGATTAAGCCATCATGTTAGGATGTTTAGAAGGACTCAGG 188045
Qy 107 -----ValLeuArgGluAspPhe 112
Db 188044 GTGGGTACAGCTGTTCTCTGTGATTTGCTGACTTCCCAATAGTCTCCAGGAGACTTC 187985
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Db 187984 CAGATCCAACTCCGGACACAGTGGCCGCTGGTGGGAGAGAGCTTGTCTTTGAGTGTGT 187925
Qy 133 ProProTrpGlyHisProGluProThrValSerTrpTrpTyrAspGlyLysProLeuAla 152
Db 187924 CTTCCCTGGGGTACCCAAAACCTCTGCTCTCATGTTGGTGAAGACGGGAAACCTCTGTC 187865
Qy 153 LeuGlnProGlyArgHis----- 158
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Qy 158 ----- 158
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Qy 159 -----Thr-ValSerGlySerLeuLeuMetAl 168
Db 187744 ATTGAAGACTTCTAGGAGTATCTGAACCTGACAGGTATCTGGGATTCCTCGATGGTGTCT 187685
Qy 168 aArgAlaGluLysSerAspGlu***ThrTyrMetCysValAlaThrAsnSerAlaGlyHi 188
Db 187684 AAGACAGAGAGATGATCTCGGGACCTATATGTATGTCGCCAACCAACATGTGTGGCA 187625
Qy 188 aArgGluSerArgAlaAlaArgValSerIleGln----- 199
Db 187624 ACGGAGAGCCGAGCAGCGGGTGTCTATCCAGGGTAAGGACAGGAGTCTATCTACAATC 187565

Qy 199 ----- 199
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Db 187084 CACAGAATCCAGGACCAAGGAACATCTAGAGCTTCTGGCTGTGCTATTCAGTCTGGA 187025
Qy 218 uAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAlaValTr 238
Db 187024 AAATGTGACCTGTCTAAACCCGAACTGTAAAGGTCCCAAGCTGGCCATCCGTGTG 186965
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Qy 248 ArgLeuProAsnLeuThrArgProCysSerGlyProArgLeuProArgGluAlaArgGlu 267
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RESULT 14

AC120636/c

LOCUS

DEFINITION

Rattus norvegicus clone CH230-136D4, *** SEQUENCING IN PROGRESS

AC120636

VERSION

AC120636.4 GI:25138029

KEYWORDS

HTG; HTGS PHASE2; HTGS DRAFT; HTGS_ENRICHED.

SOURCE

Rattus norvegicus (Norway rat)

ORGANISM

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

REFERENCE

1 (bases 1 to 223269)

AUTHORS

Muzny,D,Marie., Metzker,M, Lee., Abramson,S., Adams,C., Alder,J., Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,

Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Dengon, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Frazer, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregiorgis, B., Geer, K., Gill, R., Grady, M., Guerra, M., Guevara, W., Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hughes, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpach, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kwis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, W., Liu, W., London, P., Longacre, S., Lopez, J., Lorensuhewa, L., Loulseged, H., Lorado, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindaratne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhinney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Parks, K., Nwakoelameh, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, F., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savary, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sison, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steidle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Umami, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willison, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.

TITLE
JOURNAL
REFERENCE
AUTHORS

Direct Submission
Unpublished
2 (bases 1 to 223269)
Worley, K.C.
Direct Submission
Submitted (09-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 223269)
Rat Genome Sequencing Consortium.

REFERENCE
AUTHORS
TITLE
JOURNAL

Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

COMMENT

On Nov 20, 2002 this sequence version replaced gi:23667909.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Aclis (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature

table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GXDD
Center clone name: CH230-136D4
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 201827 bases at least Q40
Consensus quality: 204782 bases at least Q30
Consensus quality: 206701 bases at least Q20
Estimated insert size: 209571; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 1 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 223269: contig of 223269 bp in length.

FEATURES

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1. 223269
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end_sequence:BH352255"
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164341. 165851
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221935. 223269
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BASE COUNT 59410 a 47952 c 46732 g 54018 t 15157 others
ORIGIN
Alignment Scores:
Pred. No.: 1.7e-36 Length: 223269
Score: 795.50 Matches: 204
Percent Similarity: 36.64% Conservative: 21
Best Local Similarity: 33.22% Mismatches: 46
Query Match: 53.93% Indels: 344
DB: 2 Gaps: 5

US-10-047-021-86_COPY_28_303 (1-276) x AC120636 (1-223269)

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Db 202611 GCCAAGATGAGTTGCAGAGCATCGGGCCACCACTTCCCACTATCCGCTGCTGTAAT 202552
Qy 42 GlyGlnProLeuSerMetValProProAspProHisIleLeuProAspGlyThrIleu 61
Db 202551 GGGCAGCCCTCAGCATGCGGACCCGACCTACATTACCTCCAATCAGATGGGACCTC 202492

Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuewa, L., Loulseged, H., Lozado, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindartine, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhiney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montanayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munitasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwaokelimeh, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Umani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wiczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished

2 (bases 1 to 250318)

Worley, K.C.

Direct Submission

Submitted (09-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 250318)

Rat Genome Sequencing Consortium.

Direct Submission

Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 15, 2002 this sequence version replaced gi:23266067. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GRFO

Center clone name: CH230-85A24

----- Summary Statistics

Assembly program: Phrap; version 0.990329

Consensus quality: 230810 bases at least Q40

Consensus quality: 233159 bases at least Q30

Consensus quality: 234781 bases at least Q20

Estimated insert size: 236162; sum-of-contigs estimation

Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.

FEATURES

source

1 250318: contig of 250318 bp in length.

Location/Qualifiers

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end sequence: BH302237"

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/note="wgs_end_extension"

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BASE COUNT 66941 a 51524 c 51351 g 66227 t 14275 others

ORIGIN

Alignment Scores:

Pred. No.: 1.9e-36 Length: 250318

Score: 795.50 Matches: 204

Percent Similarity: 36.64% Conservative: 21

Best Local Similarity: 33.22% Mismatches: 46

Query Match: 53.93% Indels: 344

DB: 2 Gaps: 5

US-10-047-021-86_COPY_28_303 (1-276) x AC109983 (1-250318)

Qy 2 AspSerProGlnIleLeuValHisProGlnaspGlnLeuPheGlnGlyProGlyPro 21

Db 129886 GATTCTCCACCCAGATCTTAGTTTCATCCCGAGACAGTACTTTCAGGGCTCCGGCGG 129945

Qy 22 AlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTrpLeuLeuAen 41

Db 129946 GCCAAGATGAGTTGCAGAGCATCGGGCCACCACTTCCCACTATCCGCTGCTGTAAT 130005

Qy 42 GlyGlnProLeuSerMetValProProaspProHisIleLeuLeuProAspGlyThrLeu 61

Db 130006 GGGCAGCCCCCTCAGATGGCGACCCAGACCTTACCTTACCTTACATGAGTGGGACCTC 130065

Qy 62 LeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGln---AlaLeuSerThr 80

Db 130066 CTGTACATCGCGCCCTTACCCTATGGACGGCGGCGGCAAGACAGACCATTTCTCTCAGCA 130125

Qy 81 AspLeuGlyValThrThrCysGluAlaSerAenArgLeuGlyThrAlaValserArgGly 100

Db 130126 ATCTGGGTGTCTACATGTGAGCCAGCAACCGGCTGGGCACAGCAGTGGCGGGGT 130185

Qy 101 AlaArgLeuSerValAla----- 106

Db 130186 GCTAGGCTGTCTGTGGC-TGGTGAGGCTTGGGAGGTAGGCTCAGGGGTGAGGCAGAGTTA 130244

Qy 106 ----- 106

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Db 130305 CGGCTCTGGGATGAAGGTTAAACTAGACATAAACGGGCAAGAAACCGGTACAGCAGAAC 130364
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Db 130365 TGGGTAAGCGGCTTAGGTAAGCAAGAGACTCGGGTGGGTAGACATGCTTCTCGTGTAT 130424
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Db 130425 CCGCTGACCTCCCAATAGTCTCCAGGAGACTTCGGATCCAACCTCGGGACACAGTG 130484
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Qy 199 ----- 199

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Qy 207 oValGluLeuLeuAlaValArgIleGlnLeuGluAsnValThrLeuLeuAsnProAspPr 227
Db 131445 TCTAGAGCTTCTGGCTTTCGAATTCAGCTGGAAATGTGACCTGTCTGAACCCAGAACC 131504
Qy 227 oAlaGluGlyProIysProArgProAlaValTrpLeu***TrpIys----- 242
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Qy 242 ----- 242
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Qy 243 ----- ValSerGlyPro***ArgLeuProAsnLeuThrArgProCysSerGlyProArg 260
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Db 131685 GGGACCCCGAGGACAGGGATCTCCATGGACAGAGG 131720
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Job time : 3137.42 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 31, 2004, 11:37:09 ; Search time 220.228 Seconds
(without alignments)
3383.062 Million cell updates/sec

Title: US-10-047-021-86_COPY_28_303
Perfect score: 1475
Sequence: 1 QDSPPQLVHPDQLFQPG.....SGPLPREARELRGRRNTG 276

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTC spool_P/US10047021/runat_30012004.145452.24552/app.query.fasta_1.910
-DB=1_Geneseq_19Jun03 -QMT=fascap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10047021 @CGN 1.1 605 @runat_30012004.145452.24552 -NCPU=6 -ICPU=3
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_19Jun03:*
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25: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1469	99.6	1346	20	AA51721 DNA encoding a hum
2	1469	99.6	1346	24	ABQ92573 Human secreted pro
3	1432	97.1	3267	24	ABN59723 Novel human coding
4	1432	97.1	3715	24	ABK87137 cDNA human ECSM4 p
5	1432	97.1	3716	20	AAZ34069 Human PRO860 nucle
6	1432	97.1	3716	21	AAC78502 Human PRO860 (UNQ4
7	1432	97.1	3716	25	ABX92441 cDNA encoding huma
8	1432	97.1	3808	22	AA501695 Human TANGO 330 fo
9	1424	96.5	4262	22	AAH18180 Human cDNA sequenc
10	1424	96.5	4262	22	AAH78073 Nucleotide sequenc
11	1077	73.0	3042	22	AA501694 Human TANGO 330 fo
12	1062.5	72.0	3688	24	ABK87138 cDNA mouse ECSM4 p
13	1057	71.7	756	22	AAH08234 Human cDNA clone (
14	446.5	30.3	4291	20	AAV69278 Human T85 cDNA. H
15	446.5	30.3	4956	20	AA555770 Human Robo 1 polyp
16	446.5	30.3	4956	20	AA57253 Human ROBO1 cDNA.
17	404.5	27.4	6215	24	AAAL49658 Human neurotransmi
18	396.5	26.9	6445	24	AAAL49652 Human neurotransmi
19	395.5	26.8	4188	20	AA555767 Drosophila Robo 1
20	395.5	26.8	4188	20	AA57250 Drosophila ep. ROB
21	395.5	26.8	4355	23	ABL22881 Drosophila melanog
22	354.5	24.0	3894	20	AA555769 C. elegans Robo po
23	354.5	24.0	3894	20	AA57252 C. elegans Robo cd
24	347	23.5	2499	23	ABL09471 Drosophila melanog
25	345	23.4	4146	20	AA555768 Drosophila Robo 2
26	345	23.4	4146	20	AA57251 Drosophila ep. ROB
27	307	20.8	2658	23	ABL09371 Drosophila melanog
28	292.5	19.8	8410	23	ABL22880 Drosophila melanog
29	276.5	18.7	5510	21	AAZ51671 Human PS3 target m
30	276.5	18.7	5510	24	ABK83723 Human cDNA differe
31	276.5	18.7	5510	24	ABN95260 Gene #1758 used to
32	276.5	18.7	5510	25	ABX08782 Angiogenesis-assoc
33	276.5	18.7	5530	22	ABA08831 Human peroxidasin
34	276.5	18.7	6814	24	AB570409 Human bone remodel
35	276.5	18.7	6847	20	AA579922 Melanoma associate
36	276.5	18.7	6847	24	ABQ88160 Human osteoblast d
37	275.5	18.7	4694	22	AAK51847 Human polynucleoti
38	267.5	18.1	4080	25	AA449595 Human cytoskeleton
39	267.5	18.1	4131	25	ABT16046 NOVX related polyn
40	267.5	18.1	4360	25	AA449596 Human cytoskeleton
41	267.5	18.1	4739	22	AAK51848 Human polynucleoti
42	265.5	18.0	5093	24	AAAL39621 Human secreted pro
43	259	17.6	5164	23	ABL01909 Drosophila melanog
44	256	17.4	4548	24	AAI64283 Human transient ax
45	256	17.4	11796	25	ABX10231 Human cDNA encodin

ALIGNMENTS

RESULT 1
AA51721
ID AA51721 standard; DNA; 1346 BP.
XX
AC AA51721;
XX
DT 17-JUN-1999 (first entry)
XX
DE DNA encoding a human secreted protein.
XX
KW Human secreted protein; cancer; immune disorder; infection;
KW inflammatory disorder; skin disorder; tumour; atherosclerosis;
KW restenosis; autoimmune disorder; Alzheimer's disease;
KW peripheral neuropathy; trauma; spinal cord injury; allergy;
KW hematopoietic disorder; skeletal disorder; neurological disorder;
KW arthritic disorder; asthma; immunodeficiency disease; AIDS;
KW transplant rejection; ss.

```

XX OS Homo sapiens.
XX WO9911293-A1.
XX PD 11-MAR-1999.
XX PF 03-SEP-1998; 98WO-US18360.
XX PR 12-SEP-1997; 97US-00589974.
XX PR 05-SEP-1997; 97US-0057626.
XX PR 05-SEP-1997; 97US-0057663.
XX PR 12-SEP-1997; 97US-0058666.
XX PR 12-SEP-1997; 97US-0058667.
XX PR 12-SEP-1997; 97US-0058667.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Brewer LA, Ebner R, Lafleur DW, Moore PA, Olsen HS;
XX PI Rosen GA, Ruben SM, Shi Y;
XX DR WPI; 1999-204988/17.
XX DR P-PSDB; AAY12934.
XX PT New isolated human genes and the secreted polypeptides they encode
XX PT - useful for diagnosis and treatment of e.g. neurological disorders,
XX PT tumours, immune disorders, inflammation or haematological disorders
XX PS Claim 1; Page 165-166; 215pp; English.
XX CC AAX51701-55 encode human secreted proteins. The polynucleotides and
XX CC their corresponding secreted polypeptides are useful for preventing,
XX CC treating or ameliorating medical conditions, e.g. by protein or gene
XX CC therapy. Pathological conditions can also be diagnosed by determining
XX CC the amount of the new polypeptides in a sample or by determining the
XX CC presence of mutations in the new polynucleotides. Specific uses are
XX CC described for each polynucleotide, based on which tissues they are
XX CC most highly expressed in, and include developing products for the
XX CC diagnosis or treatment of cancer, immune disorders, infection,
XX CC inflammatory disorders, skin disorders, tumours, atherosclerosis,
XX CC restenosis, autoimmune disorders, Alzheimer's disease, peripheral
XX CC neuropathies, trauma, spinal cord injuries, allergy, hematopoietic
XX CC disorders, skeletal disorders neurological disorders, arthritic
XX CC disorders, asthma, immunodeficiency diseases, AIDS and transplant
XX CC rejection. The polypeptides are also useful for identifying their
XX CC binding partners.
XX SQ Sequence 1346 BP; 318 A; 379 C; 376 G; 267 T; 6 other;

Alignment Scores:
Pred. No.: 9.12e-91 Length: 1346
Score: 1469.00 Matches: 276
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.59% Indels: 0
DB: 20 Gaps: 0

US-10-047-021-86_COPY_28_303 (1-276) x AAX51721 (1-1346)

Qy 1 GlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGly 20
Db 112 CAGGACTCCCGCCCCAGATCTTAGTCCACCCCGAGGACGAGTGTCCAGGGCCCTGGC 171
Qy 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProProThrIleArgTrpLeuLeu 40
Db 172 CTGCCAGGATGAGTGCAGCCTCAGGCTCAGGCACCCACCTCCACCATCCGCTGGTGTG 231
Qy 41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60
Db 232 AATGGGAGCCCTTGGATGGTGGCCCGACACCCACACACCTCCCTGCTGGTGGAC 291
Qy 61 LeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80

Db 292 CTTCTGCTGTACAGCCCTGCGCGGACATGCCACCATGGCCAGGCGCTGTCCACA 351
Qy 81 AspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100
Db 352 GACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCAGCGCAGTCCAGCAGGC 411
Qy 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal 120
Db 412 GCTCGGCTGTCTGTGGCTGTCTCCGGGAGATTTCCAGATCCAGCTCCGGACATGGTG 471
Qy 121 AlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluPro 140
Db 472 GCTGTGGTGGTGGAGCAGTTTACTCTGGAATGTGGCGCGCTGGGGCCACCCAGAGGCC 531
Qy 141 ThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrVal 160
Db 532 ACAGTCTCATGGTGGAAAGATGGGAAACCCCTCGCCCTCCAGCCCGGAGGACACAGTG 591
Qy 161 SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu***ThrTyrMetCys 180
Db 592 TCCGGGGGTCTCTGTGATGGCAAGCAGACAGAGTACGANGGACCTACATGTGT 651
Qy 181 ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu 200
Db 652 GTGCCACCAACAGCGCAGCAGACACAGGAGCGCGCGCGGTTTCCATCCAGGAG 711
Qy 201 ProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluAsnVal 220
Db 712 CCCAGGACTACACAGGAGCCTGTGGAGCTTCTGGCTGTGGAAATTCAGCTGGAAAAATGTG 771
Qy 221 ThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAlaValTrpLeu*** 240
Db 772 ACCTCTGAACCCGGATCTCTGCAAGGCCCCAGCCTAGACCGCGGTGTGGCTCARG 831
Qy 241 TrpLysValSerGlyPro***ArgLeuProAsnLeuThrArgProCysSerGlyProArg 260
Db 832 TGGAAAGTCAAGTGGCCCTTGGCCCTGCCCAATCTTACACGGCTTGTTCAGGACCCAGA 891
Qy 261 LeuProArgGluAlaArgGluLeuArgGlyGlnArgAsnThrGly 276
Db 892 CTGCCCCGGAGGCCAGGAGCTCCGTGGGCGAGAGGAGGAACACAGGA 939

RESULT 2
ABQ92573
ID ABQ92573 standard; cDNA; 1346 BP.
XX AC ABQ92573;
XX DT 12-NOV-2002 (first entry)
XX DE Human secreted protein encoding cDNA SEQ ID NO 31.
XX KW Human; neurotropic; neuroprotective; cytostatic; dermatological; virucide;
XX KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
XX KW antiparkinsonian; antiischemic; antianemic; antiarthritic; cancer;
XX KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
XX KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
XX KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
XX KW neurological disease; infection; nephrotropic; gene therapy; vaccine;
XX KW gene; ss.
XX OS Homo sapiens.
XX PN WO200257420-A2.
XX PD 25-JUL-2002.
XX PF 17-JAN-2002; 2002WO-US01109.
XX PR 18-JAN-2001; 2001US-262066P.
XX PA (HUMA-) HUMAN GENOME SCI INC.

```

XX Moore PA, Ruben SM, LaFleur DW, Shi Y, Rosen CA, Olsen H;
PI Ebner R, Brewer LA;
XX
DR WPI: 2002-599716/64.
DR P-PSDB; ABP62033.
XX
XX New polynucleotides and polypeptides useful for diagnosing, prognosing,
PT treating or preventing e.g. neurodegenerative, central nervous system,
PT autoimmune, respiratory, reproductive, or inflammatory diseases or
PT disorders
XX
PS Claim 1; Page 713-714; 785pp; English.
XX
XX The invention relates to novel genes (ABQ92553-ABQ92607) and proteins
CC (ABP62013-ABP62153) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemia;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
XX
SQ Sequence 1346 BP; 318 A; 379 C; 376 G; 267 T; 6 other;

Alignment Scores:
Pred. No.: 9,128-91 Length: 1346
Score: 1469.00 Matches: 276
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.59% Indels: 0
DB: 24 Gaps: 0

US-10-047-021-86_COPY_28_303 (1-276) x ABQ92573 (1-1346)

Qy 1 GlnAepSerProGlnLeuValHisProGlnAepGlnLeuPheGlnGlyProGly 20
Db 112 CAGGACTCCCGCCCGACATCTTAGTCCACCCAGGAGGAGTCTTCCAGGCGCTGGC 171
Qy 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProProThriLeArgTrpLeuLeu 40
Db 172 CCGTGCAGGATGAGCTGCCGAGCCTCAGGCCAGCCACCTCCACCATCCGCTGGTGTCTG 231
Qy 41 AenGlyGlnProLeuSerMetValProProAepProHisHisLeuLeuProAepGlyThr 60
Db 232 AATGGCAGCCCTGAGCATGTGTCGCCAGACCCACACCATCTCTGCTGATGGGACC 291
Qy 61 LeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAepGlyGlnAlaLeuSerThr 80
Db 292 CTCTGCTGTACAGCCCGCTGCCCGGGAGATGCCACGATGGCCAGGCGCTGTCCACA 351
Qy 81 AepLeuGlyValThrCysGluAlaSerAenArgLeuGlyThrAlaValSerArgGly 100
Db 352 GACCTGGGTGTCTACACATGTGAGGCCAGCAACCGCTTGGCAGCGAGTCAGCAGAGGC 411
Qy 101 AlaArgLeuSerValAlaValLeuArgGluAepPheGlnLeuGlnProArgAepMetVal 120
Db 412 GCTCGGCTGTCTGTGGCTGTCTCGGAGGAGTTCAGATGCCAGCTCCGGAGCATGTG 471
Qy 121 AlaValValGlyGlnGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluPro 140
Db 472 GCTGTGGTGGTGACAGTTTACTCTGGATGTGGCGCCCGCTGGGGCCACCCAGAGGCC 531
Qy 141 ThrValSerTrpTrpLysAepGlyProLeuAlaLeuGlnProGlyArgHisThrVal 160
Db 532 ACAGTCTCATGTGGAAGATGGGAAACCCCTGGGCCCTCCAGCCCGGAGGACACACAGTG 591

Qy 161 SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAepGlu***ThrTyMetCys 180
Db 592 TCCGGGGGTCCTGCTGATGGCAAGAGCAGAGAGAGTGCACGAAGGACCTACATGTGT 651
Qy 181 ValAlaThrAenSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu 200
Db 652 GTGGCCCAACACAGCGCAGGACACAGGAGAGCGCGCAGCCCGGTTTCCATCCAGAG 711
Qy 201 ProGlnAepTyThrGluProValGluLeuAlaValArgIleGlnLeuGluAenVal 220
Db 712 CCCGAGACTACAGGAGCCTGTGGAGCTTCTGGCTGTGGCAATTCAGCTGGAAATGTG 771
Qy 221 ThrLeuLeuAenProAepProAlaGluGlyProLysProAepProAlaValTrpLeu*** 240
Db 772 ACACCTCTGAACCGGATCCTGTGAGAGGCCCAAGCCTAGACCGCGGTGTGGCTCARG 831
Qy 241 TrpLysValSerGlyPro***ArgLeuProAenLeuThrArgProCysSerGlyProArg 260
Db 832 TGGAAAGTCAAGTGGCCCTNTGCGCCTGCCCAATCTTACACGCGCTTGTTCAGGACC 891
Qy 261 LeuProArgGluAlaArgGluLeuArgGlyGlnArgAenThrGly 276
Db 892 CTGCCCCGGAGGCCAGGAGCTCCGTGGCGAGGAGGAGAACACAGGA 939
RESULT 3
ID ABN59723 standard; cDNA; 3267 BP.
XX
AC ABN59723;
XX
DT 28-JUN-2002 (first entry)
XX
DE Novel human coding sequence SEQ ID NO: 134.
XX
KW Human; antianaemic; vulnery; antiinflammatory; immunomodulator;
KW antinfertility; cerebroprotective; cytostatic; rheumatic; gene therapy;
KW neuroprotective; antiparkinsonian; protein therapy; EST;
KW expressed sequence tag; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200222660-A2.
XX
PD 21-MAR-2002.
XX
PF 10-SEP-2001; 2001WO-US26015.
XX
PR 11-SEP-2000; 2000US-0659671.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren P;
PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;
XX
DR WPI: 2002-292408/33.
DR P-PSDB; ABB97310.
XX
PT An isolated polynucleotide for treating diseases associated with its
PT encoded polypeptide such as cancer and multiple sclerosis -
XX
PS Claim 1; SEQ ID NO 134; 509pp; English.
XX
CC The present invention provides the protein and coding sequences of 444
CC novel human proteins. These were isolated from expressed sequences tags
CC (ESTs). They can be used to stimulate cell growth, to regulate
CC haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth
CC e.g. in burn treatment, to regulate the immune system e.g. to treat
CC multiple sclerosis, to regulate activin or inhibit e.g. to treat
CC infertility, to regulate haemostasis or thrombolysis e.g. to treat
CC stroke and cancer, to screen for drugs, to treat inflammatory conditions
CC e.g. rheumatoid arthritis, and to treat nervous system disorders e.g.
CC parkinson's disease. The present sequence is a coding sequence of the

CC invention.

XX Sequence 3267 BP; 628 A; 1101 C; 927 G; 611 T; 0 other;

Alignment Scores:

Pred. No.: 7.36e-88 Length: 3267
Score: 1432.00 Matches: 268
Percent Similarity: 98.53% Conservative: 1
Best Local Similarity: 98.17% Mismatches: 3
Query Match: 97.08% Indels: 1
DB: 24 Gaps: 0

US-10-047-021-86_COPY_28_303 (1-276) x ABN59723 (1-3267)

Qy 1 GlnAspSerProGlnIleuValHisProGlnAspGlnLeuPheGlnGlyProGly 20
Db |||||
Qy 116 CAGGACTCCCGCCCGCCAGATCTAGTCACCCCGAGGACGAGTGTTCAGGGCCCTGGC 175
Db |||||
Qy 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTrpLeuLeu 40
Db |||||
Qy 176 CTGCGCAGGATGAGTGCAGAGCCTCAGGCCAGCCCTCCACCATCCGCTGGTGTG 235
Db |||||
Qy 41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60
Db |||||
Qy 236 AATGGCAGCCCTCAGCATGTGTCGCCCGGAGCATGCCACGATGGCCGCTGTCCACA 295
Db |||||
Qy 61 LeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80
Db |||||
Qy 296 CTTCTGTCTACAGCCCGCTGCCCGGGAGCATGCCACGATGGCCGCTGTCCACA 355
Db |||||
Qy 81 AspLeuGlyValTyThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100
Db |||||
Qy 356 GACCTGGGTGTACACATGTGAGCCGACGACCGCTGGCAGCGCAGTCCAGCAGGC 415
Db |||||
Qy 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal 120
Db |||||
Qy 416 GCTCGGTGTCTGTGGTGTCTCTCCGGAGGATTTCCAGATCCAGCCTCGGGACATGGTG 475
Db |||||
Qy 121 AlaValValGlyGlnGlnPheThrLeuGluCysGlyProProTrpGlyHisProGlyPro 140
Db |||||
Qy 476 GCTGTGGTGGTGAGCAGTTTACTCTGTGAATGTGGCGCCCTGGGGCCACCCAGAGCCC 535
Db |||||
Qy 141 ThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrVal 160
Db |||||
Qy 536 ACAGTCTCATGTGGAAAGATGGGAACCCCTGGCCCTCCAGCCCGGAGGCACACAGTG 595
Db |||||
Qy 161 SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu***ThrTyMetCys 180
Db |||||
Qy 596 TCCGGGGGTCCTGTGTATGGCAAGAGCAGAGAAGAGTGCAGAGGGACCTACATGTGT 655
Db |||||
Qy 181 ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu 200
Db |||||
Qy 656 GTGGCCACCAAGCGCAGGACATAGGAGAGCGCGCAGCCCGGGTTTCATCCAGGAG 715
Db |||||
Qy 201 ProGlnAspTyThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluAsnVal 220
Db |||||
Qy 716 CCCAGGACTACAGGACCTGTGGAGCTTCTGCTGTGCAATTCAGCTGGAAATGTG 775
Db |||||
Qy 221 ThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAlaValTrpLeu*** 240
Db |||||
Qy 776 ACACCTGTGAACCGGATCTCTGACAGAGGGCCCCAAGCCTAGACCGGGGCTGTGCTCAGC 835
Db |||||
Qy 241 TrpLysValSerGlyPro***ArgLeuProAsnLeuThrArgProCysSerGlyProAr 260
Db |||||
Qy 836 TGGAAAGGTCAGTGGCCCTGTGCGCCTGCCCAATCTTACAGGGCTTGTTCAGGACCCAG 895
Db |||||
Qy 260 gLeuProArgGluAlaArgGluLeuArgGlyGlnArg 272
Db |||||
Qy 896 ACTGCCCGGAGGCCAGGAGCTCCGTGGGCAGAGG 932
Db |||||

RESULT 4

ABK87137

ID ABK87137 standard; cDNA; 3715 BP.

XX ABK87137;
XX
XX
DT 07-OCT-2002 (first entry)
XX
XX cDNA human ECSM4 protein.
XX
XX Human; endothelial cell-specific molecule 4; ECSM4; neovasculature;
XX imaging vascular endothelium; proliferative disease; cancer;
XX psoriasis; diabetic retinopathy; atherosclerosis; menorrhagia;
XX endothelial damage; tumour neovasculature; cardiac disease;
XX endometriosis; hypoxic condition; angiogenesis; cytostatic;
XX cardiant; gene; ss.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX CDS 70..3384
XX FT /*tag= a
XX FT /product= "ECSM4"
XX
XX W020236771-A2.
XX
XX 10-MAY-2002.
XX
XX 06-NOV-2001; 2001WO-GB04906.
XX
XX 06-NOV-2000; 2000US-245566P.
XX 07-MAR-2001; 2001US-273662P.
XX
XX (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
XX
XX Bicknell R, Huminiecki L;
XX
XX WPI; 2002-508120/54.
XX P-PSDB; AAU99419.
XX
XX Novel endothelial cell-specific molecule polypeptide 1 or 4, useful for
XX imaging, diagnosing and treating a condition involving vascular
XX endothelium e.g. cancer, cardiac disease, endometriosis, diabetes
XX
XX Disclosure; Fig 12; 248pp; English.
XX
XX The present invention relates to endothelial cell-specific molecule 4
XX (ECSM4), and the polynucleotide sequences encoding it. The ECSM4
XX proteins are useful for imaging vascular endothelium in the body of
XX an individual, and for diagnosing and treating a proliferative
XX disease or condition involving the vascular endothelium (preferably,
XX neovasculature) such as cancer, psoriasis, diabetic retinopathy,
XX atherosclerosis or menorrhagia. The ECSM4 proteins are also useful in
XX the manufacture of diagnostic or prognostic agent for such conditions.
XX The proteins are also useful for detecting endothelial damage or
XX activation, detecting a tumour or tumour neovasculature, cardiac
XX disease, or endometriosis by detecting the amount of ECSM4 present in
XX a sample. The polynucleotide sequences encoding ECSM4 are useful in
XX gene therapy for treating a hypoxic condition such as cancer, cardiac
XX disease, endometriosis or atherosclerosis and in the manufacture of
XX medicaments for treating the above disease. The sequences are useful
XX for modulating angiogenesis in an individual. The present sequence
XX encodes human ECSM4 protein.
XX
XX Sequence 3715 BP; 725 A; 1239 C; 1053 G; 698 T; 0 other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 8.42e-88 Length: 3715
XX Score: 1432.00 Matches: 268
XX Percent Similarity: 98.53% Conservative: 1
XX Best Local Similarity: 98.17% Mismatches: 3
XX Query Match: 97.08% Indels: 1
XX DB: 24 Gaps: 0
XX
XX US-10-047-021-86_COPY_28_303 (1-276) x ABK87137 (1-3715)

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QY 1 GlnAspSerProProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGly 20
Db 151 CAGGACTCCCGCCCGCCAGATCTAGTCCACCCCGCAGGACAGCTGTTCAGGGCCCTGGC 210
QY 21 ProAlaAatMetSerCysArgAlaSerGlyGlnProProThrIleArgTrpLeuLeu 40
Db 211 CTGTCAGGATGAGTGCACCAAGCCTCAGCCAGCAGCAGCTCCACCATCGCTGGTGTGTG 270
QY 41 AenGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60
Db 271 NATGGGAGCCCTGAGCATGTGTCGCCAGCAGCAGCAGCAGCAGCTCTGCCTGATGGGACC 330
QY 61 LeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80
Db 331 CTTCTGCTCTACAGCCCTCCCGGGGACATGTCACAGTGGCAGGCGCTGTCCACA 390
QY 81 AspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100
Db 391 GACCTGGGGTGTACACATGTGAGGCCAGCAACCGGCTTGGCAGCGCATGACGAGAGGC 450
QY 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal 120
Db 451 GCTGGGCTCTGTGGTGTCTCTCGGGAGGATTTCCAGATCCAGCCTCGGCACATGGTG 510
QY 121 AlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluPro 140
Db 511 GCTGTGGTGGTGAGCAGTTTACTCTGGAATGTGGGCGCCCTCGGGCCACCCAGAGGCC 570
QY 141 ThrValSerTrpTrpLeuAspGlyCysProLeuAlaLeuGlnProGlyArgHisThrVal 160
Db 571 ACAGTCTCATGTGTGAAGATGGGAACCCCTGGGCCCTCCAGCCCGGAAGGCACACAGTG 630
QY 161 SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu**ThrTyrMetCys 180
Db 631 TCCGGGGGTCCTCTGCTGATGTGCAGAGCAGAGAGATGACAGAGGACCTACATGTGT 690
QY 181 ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu 200
Db 691 GTGGCCACCAACAGCGCAGGACATAGGAGAGAGCCGCGAGCCGGTTCATCCAGGAG 750
QY 201 ProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluAsnVal 220
Db 751 CCCCAGGACTACACGAGCCTGTGAGCTTCTGGCTGTGCGAATTCAGCTGGAAATGTG 810
QY 221 ThrLeuLeuAsnProAspProAlaGluGlyProLysProAspProAlaValTrpLeu** 240
Db 811 ACACCTGCTGAACCCGATCTCGAGAGGCCCCCAAGCCTAGACCGCGGTGTGGCTCAGC 870
QY 241 TrpLysValSerGlyPro***ArgLeuProAsnLeuThrArgProCysSerGlyProAr 260
Db 871 TGGAGGTCAGTGGGCTGTGCTGGCTGCCCCAATCTTACACGGCTTGTTCAGGACCCAG 930
QY 260 GlnProArgGluAlaArgGluLeuArgGlyGlnArg 272
Db 931 ACTGCCCGGGAGGCGAGGAGCTCGTGGGCAGAGG 967

RESULT 5
AAZ34069
ID AAZ34069 standard; cDNA; 3716 BP.
XX
AC AAZ34069;
XX
XX
DT 07-DEC-1999 (first entry)
DE
DE Human PRO860 nucleotide sequence.
XX
KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
KW secreted protein; transmembrane protein; ss.
XX
OS Homo sapiens.
XX
PN WO9946281-A2.
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XX 16-SEP-1999.
PD
XX 08-MAR-1999; 99WO-US05028.
PF
XX 10-MAR-1998; 98US-0077450.
PR 11-MAR-1998; 98US-0077632.
PR 11-MAR-1998; 98US-0077641.
PR 11-MAR-1998; 98US-0077649.
PR 12-MAR-1998; 98US-0077791.
PR 13-MAR-1998; 98US-0078004.
PR 17-MAR-1998; 98US-0040220.
PR 20-MAR-1998; 98US-0078886.
PR 20-MAR-1998; 98US-0078910.
PR 20-MAR-1998; 98US-0078936.
PR 20-MAR-1998; 98US-0078939.
PR 25-MAR-1998; 98US-0078939.
PR 26-MAR-1998; 98US-0079294.
PR 26-MAR-1998; 98US-0079656.
PR 27-MAR-1998; 98US-0079663.
PR 27-MAR-1998; 98US-0079664.
PR 27-MAR-1998; 98US-0079689.
PR 27-MAR-1998; 98US-0079728.
PR 27-MAR-1998; 98US-0079786.
PR 30-MAR-1998; 98US-0079920.
PR 30-MAR-1998; 98US-0079923.
PR 31-MAR-1998; 98US-0080105.
PR 31-MAR-1998; 98US-0080107.
PR 31-MAR-1998; 98US-0080165.
PR 31-MAR-1998; 98US-0080194.
PR 01-APR-1998; 98US-0080327.
PR 01-APR-1998; 98US-0080328.
PR 01-APR-1998; 98US-0080333.
PR 01-APR-1998; 98US-0080334.
PR 08-APR-1998; 98US-0081049.
PR 08-APR-1998; 98US-0081070.
PR 08-APR-1998; 98US-0081071.
PR 09-APR-1998; 98US-0081195.
PR 09-APR-1998; 98US-0081203.
PR 09-APR-1998; 98US-0081229.
PR 15-APR-1998; 98US-0081817.
PR 15-APR-1998; 98US-0081838.
PR 15-APR-1998; 98US-0081952.
PR 15-APR-1998; 98US-0081955.
PR 21-APR-1998; 98US-0082568.
PR 21-APR-1998; 98US-0082569.
PR 22-APR-1998; 98US-0082700.
PR 22-APR-1998; 98US-0082704.
PR 22-APR-1998; 98US-0082804.
PR 23-APR-1998; 98US-0082767.
PR 23-APR-1998; 98US-0082796.
PR 27-APR-1998; 98US-0083336.
PR 28-APR-1998; 98US-0083332.
PR 29-APR-1998; 98US-0083392.
PR 29-APR-1998; 98US-0083495.
PR 29-APR-1998; 98US-0083496.
PR 29-APR-1998; 98US-0083499.
PR 29-APR-1998; 98US-0083500.
PR 29-APR-1998; 98US-0083545.
PR 29-APR-1998; 98US-0083554.
PR 29-APR-1998; 98US-0083558.
PR 29-APR-1998; 98US-0083559.
PR 30-APR-1998; 98US-0083742.
PR 05-MAY-1998; 98US-0084366.
PR 06-MAY-1998; 98US-0084414.
PR 06-MAY-1998; 98US-0084441.
PR 07-MAY-1998; 98US-0084598.
PR 07-MAY-1998; 98US-0084600.
PR 07-MAY-1998; 98US-0084627.
PR 07-MAY-1998; 98US-0084637.
PR 07-MAY-1998; 98US-0084639.
PR 07-MAY-1998; 98US-0084640.
PR 07-MAY-1998; 98US-0084643.
PR 13-MAY-1998; 98US-0085323.
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PR 13-MAY-1998; 98US-0085338.
 PR 13-MAY-1998; 98US-0085339.
 PR 15-MAY-1998; 98US-0085573.
 PR 15-MAY-1998; 98US-0085579.
 PR 15-MAY-1998; 98US-0085580.
 PR 15-MAY-1998; 98US-0085582.
 PR 15-MAY-1998; 98US-0085689.
 PR 15-MAY-1998; 98US-0085697.
 PR 15-MAY-1998; 98US-0085700.
 PR 15-MAY-1998; 98US-0085704.
 PR 18-MAY-1998; 98US-0086023.
 PR 22-MAY-1998; 98US-0086392.
 PR 22-MAY-1998; 98US-0086414.
 PR 22-MAY-1998; 98US-0086430.
 PR 22-MAY-1998; 98US-0086486.
 PR 28-MAY-1998; 98US-0087096.
 PR 28-MAY-1998; 98US-0087106.
 PR 30-JUL-1998; 98US-0094651.
 PR 11-SEP-1998; 98US-0100038.
 XX
 DA (GETH) GENENTECH INC.
 XX
 XX Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
 PT P-PSDB; AAY41716.
 DR
 DR WPI; 1999-551358/46.
 XX
 PT New secreted and transmembrane polypeptides and their polynucleotides,
 PT useful for treating blood coagulation disorders, cancers and cellular
 PT adhesion disorders -
 XX
 XX Claim 2; Fig 76; 530pp; English.
 XX
 CC The present invention describes secreted and transmembrane polypeptides
 CC and their polynucleotides. The nucleotide sequences are useful as
 CC sources of probes, primers, for chromosome mapping, and for generation
 CC of antisense sequences. They can also be used to create transgenic
 CC animals. The proteins can be used to treat a variety of diseases and
 CC disorders, depending on their function. Diseases that may be treated
 CC include blood coagulation disorders, cancers and cellular adhesion
 CC disorders. They may also be used to raise antibodies. AAZ33891 to
 CC AAZ34338, and AAY41685 to AAY41774 represent polynucleotide and
 CC polypeptide sequence given in the exemplification of the present
 CC invention.
 XX
 XX SQ Sequence 3716 BP; 757 A; 1225 C; 1032 G; 702 T; 0 other;
 Alignment Scores:
 Pred. No.: 8.42e-88 Length: 3716
 Score: 1432.00 Matches: 268
 Percent Similarity: 98.53% Conservative: 1
 Best Local Similarity: 98.17% Mismatches: 3
 Query Match: 97.08% Indels: 1
 DB: 20 Gaps: 0
 US-10-047-021-86_COPY_28_303 (1-276) x AAZ34069 (1-3716)
 Qy 1 GlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGly 20
 Db 73 CAGGACTCCCGCCCCAGATCCTAGTCCACCCCGAGGACCATGTTCCAGGGCCCTGGC 132
 Qy 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTrpLeuLeu 40
 Db 133 CCTGCCAGGATGAGTGCACAGCCTCAGGCCAGCCACCTCCACCATCCGCTGGTGTG 192
 Qy 41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60
 Db 193 AATGGCAGCCCTGAGCATGCTGCCCCAGACCCACACCATCTCTGCTGATGGGACC 252
 Qy 61 LeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80
 Db 253 CTTCTGCTGTACAGCCCCCTGCGCGGGAGATGCCCCACGATGCGGCGCCCTGTCCACA 312

Qy 81 AspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgly 100
 Db 313 GACCTGGTCTTACACATGTGAGGCCAGCAACCGGCTTGGCAGCGCAGTCAGCAGGC 372
 Qy 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal 120
 Db 373 GCTCGGCTGTCTGGCTGCTCTCCGGGAGGATTTCCAGATCCAGACCTCGGAGACATG 432
 Qy 121 AlaValValGlyGlnGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluPro 140
 Db 433 GCTGTGGTGGGTGAGCAGTCTTACTTGGAAATGTGGGCCGCCCTGGGGCCACCCAGAGCCC 492
 Qy 141 ThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrVal 160
 Db 493 ACAGTCTCATGTGGAAAGATGGAAACCCCTGGCCCTCCAGCCCGGAGGACACACAGTG 552
 Qy 161 SerGlyGlySerLeuLeuMetAlaArgAlaGlyLysSerAspGlu***ThrTyrMetCys 180
 Db 553 TCCGGGGGCTCCCTGCTGATGGCAAGAGCAGAGAGAGTGCAGGAAGGACCTACATGTGT 612
 Qy 181 ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu 200
 Db 613 GTGGCCACCAACAGCGCAGGACATAGGGAGAGCGCGCAGCCCGGGTTTCCATCCAGAG 672
 Qy 201 ProGlnAspTyrThrGluProValGluLeuAlaValArgIleGlnLeuGluAsnVal 220
 Db 673 CCCAGGACTACACGGAGCCTGTGGAGCTTCTGGCTGTGCAATTACAGTGGAAATGTG 732
 Qy 221 ThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAlaValTrpLeu*** 240
 Db 733 ACATGCTGAACCCGGATCCTGCAGAGGGGCCCAAGCCTAGACCGCGCGGTGTGGCTCAGC 792
 Qy 241 TrpLysValSerGlyPro***ArgLeuProAsnLeuThrArgProCysSerGlyProAr 260
 Db 793 TGAAGGTCAGTGCCCTGTGGCGCTGCTGGCCAAATCTTACAGCGCCTTGTTCAGGACCCAG 852
 Qy 260 gLeuProArgGluAlaArgGluLeuArgGlyGlnArg 272
 Db 853 ACTGCCCGGAGGCCAGGAGCTCCGTGGCAGAGG 889
 RESULT 6
 AAC78502
 ID AAC78502 standard; cDNA; 3716 BP.
 XX
 XX AAC78502;
 AC
 XX
 DT 08-FEB-2001 (first entry)
 XX
 DE Human PRO860 (UNQ421) nucleotide sequence SEQ ID NO:210.
 XX
 KW Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;
 KW expressed sequence tag; detection; cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200053756-A2.
 XX
 PD 14-SEP-2000.
 XX
 PF 18-FEB-2000; 2000WO-US04341.
 XX
 PR 08-MAR-1999; 99WO-US05028.
 PR 12-MAR-1999; 99US-0123957.
 PR 29-MAR-1999; 99US-0126773.
 PR 21-APR-1999; 99US-0130232.
 PR 28-APR-1999; 99US-0131445.
 PR 14-MAY-1999; 99US-0134287.
 PR 23-JUN-1999; 99US-0141037.
 PR 26-JUL-1999; 99US-0145698.
 PR 29-OCT-1999; 99US-0162506.
 PR 30-NOV-1999; 99WO-US28313.
 PR 02-DEC-1999; 99WO-US28551.

PR 02-DEC-1999; 99WO-US28565.
PR 16-DEC-1999; 99WO-US30095.
PR 30-DEC-1999; 99WO-US31243.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
XX
XX
PA (GETH) GENENTECH INC.
XX
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Pazzara N, Filvaroff E, Fong S, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi CU, Gurney AL, Hillan KJ;
PI Kijavini IJ, Kuo SS, Napier WA, Pan J, Paoni NF, Roy MA;
PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
XX
XX
DR WPI; 2000-611443/58.
DR P-PSDB; AAB44272.
XX
XX
PT Novel PRO polypeptides and polynucleotides used in detection methods,
PT to target bioactive molecules to specific cells, and to modulate
PT cellular activities -
XX
XX
PS Claim 2; Fig 76; 636pp; English.
XX
CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed
CC sequence tag) sequences which encode secreted or transmembrane PRO
CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic
CC activity. The polynucleotides and polypeptides can be used for detecting
CC the presence of PRO polypeptides in samples, for linking bioactive
CC molecules to cells and for modulating biological activities of cells,
CC using the polypeptides for specific targeting. The polypeptide targeting
CC can be used to kill the target cells, e.g. for the treatment of cancers.
CC The polypeptide pairs provide specific targeting of bioactive molecules
CC to cells. AAC78600 to AAC78987 represent PCR primers and probes used in
CC the isolation of the PRO polynucleotide sequences.
XX
SQ Sequence 3716 BP; 757 A; 1225 C; 1032 G; 702 T; 0 other;

Alignment Scores:
Pred. No.: 8,42e-88 Length: 3716
Score: 1432.00 Matches: 268
Percent Similarity: 98.53% Conservative: 1
Best Local Similarity: 98.17% Mismatches: 3
Query Match: 97.08% Indels: 1
DB: 21 Gaps: 0

US-10-047-021-86_COPY_28_303 (1-276) x AAC78502 (1-3716)

QY 1 GlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGly 20
DB 73 CAGGACTCCCGCCCCAGATCTAGTCCACCCCGAGGACCGAGTCTTCAGGGCCCTGGC 132

QY 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTrpLeuLeu 40
DB 133 CCTGCCAGGTGAGTGCACAGCCTCAGGCAGCCACCTCCACCATCGCTGGTGTG 192

QY 41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60
DB 193 AATGGGAGCCCTCAGCATGTGTGCCCGGACATGCGAGTGGCCAGCCCTCTCCATGGGACC 252

QY 61 LeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80
DB 253 CTTCTGCTGTACAGCCCTGCGGAGCATGCGAGTGGCCAGCCCTGTCCACA 312

QY 81 AspLeuGlyValTyThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgly 100
DB 313 GACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCAGCGAGTCAGCAGAGGC 372

QY 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal 120
DB 373 GCTCGGCTGTCTGTGGTGTCTCTCCGGGAGGATTTCCAGATCCAGCCTCGGACATGGTG 432

QY 121 AlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluPro 140
DB 433 GCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGCGCCCTGGGGCCACCCAGAGGCC 492

QY 141 ThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrVal 160
DB 493 ACAGTCTCATGTGGTGGAAAGATGGGAAACCCCTGGCCCTTCCAGCCCGGAAGCACACAGTG 552

QY 161 SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu***ThrTyMetCys 180
DB 553 TCCGGGGGGTCCCTGCTGATGGCAAGAGCAGAGAGAGTGCAGAGGACCTCATGTGT 612

QY 181 ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu 200
DB 613 GTGGCCACCAACAGCGCAGGACATAGGAGAGCGCGCAGCGCGGTTTCCATCCAGGAG 672

QY 201 ProGlnAspTyThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluAsnVal 220
DB 673 CCCAGGACTACACGGAGCCTGTGGAGCTTCTGGCTGTGCCAATTTACGTGGAATGTG 732

QY 221 ThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAlaValTrpLeu*** 240
DB 733 ACAGTGTGAACCCGGATCTCTGCAGAGGGCCCCAAGCCTAGACCGCGGTGTGGCTCAGC 792

QY 241 TrpLysValSerGlyPro***-ArgLeuProAsnLeuThrArgProCysSerGlyProAr 260
DB 793 TGGAAAGGTCACTGGCCCTGTGCTGCCCTGCCCAATCTTACACGGCTTGTTCAGGACCCAG 852

QY 260 gLeuProArgGluAlaArgGluLeuArgGlyGlnArg 272
DB 853 ACTGCCCCGGGAGGCCAGGGAGCTCCGTGGGCAGAGG 889

RESULT 7
ABX92441
ID ABX92441 standard; cDNA; 3716 BP.
XX
XX ABX92441;
XX
XX
DT 08-MAY-2003 (first entry)
XX
XX
DE cDNA encoding human PRO860 polypeptide.
XX
XX
KW Human; PRO polypeptide; secreted and transmembrane protein;
KW immune disorder; diabetes; hyper-insulinaemia; hypo-insulinaemia;
KW cardiac insufficiency; nervous system disorder; kidney disorder;
KW bone disorder; cartilage disorder; arthritis; tumour; wound healing;
KW genetic disorder; cytostatic; antidiabetic; anti-inflammatory;
KW antiarthritic; anti-tumour; vulnery; antianaemic; dermatological;
KW cardiant; gene; ss.
XX
XX Homo sapiens.
XX
XX US2002169284-A1.
XX
XX 14-NOV-2002.
XX
XX 16-OCT-2001; 2001US-0978697.
XX
XX 07-OCT-1998; 98WO-US21141.
XX 20-NOV-1998; 98WO-US24855.
XX 05-JAN-1999; 99WO-US00106.
XX 08-MAR-1999; 99WO-US05028.
XX 10-MAR-1999; 99WO-US05190.
XX 14-MAY-1999; 99WO-US10733.
XX 02-JUN-1999; 99WO-US12252.
XX 30-NOV-1999; 99WO-US28313.
XX 02-DEC-1999; 99WO-US28551.
XX 02-DEC-1999; 99WO-US28565.
XX 16-DEC-1999; 99WO-US30095.
XX 30-DEC-1999; 99WO-US31243.
XX 30-DEC-1999; 99WO-US31274.
XX 05-JAN-2000; 2000WO-US00219.
XX 06-JAN-2000; 2000WO-US00277.

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PR 06-JAN-2000; 200WO-US00376.
PR 11-FEB-2000; 200WO-US03565.
PR 18-FEB-2000; 200WO-US04341.
PR 24-FEB-2000; 200WO-US05004.
PR 02-MAR-2000; 200WO-US05841.
PR 10-MAR-2000; 200WO-US06319.
PR 21-MAR-2000; 200WO-US07532.
PR 30-MAR-2000; 200WO-US08439.
PR 17-MAY-2000; 200WO-US13705.
PR 22-MAY-2000; 200WO-US14042.
PR 30-MAY-2000; 200WO-US14941.
PR 02-JUN-2000; 200WO-US15264.
PR 28-JUL-2000; 200WO-US20710.
PR 24-AUG-2000; 200WO-US23328.
PR 01-DEC-2000; 200WO-US32678.
PR 20-DEC-2000; 200WO-US34956.
PR 28-FEB-2001; 200WO-US06520.
PR 22-MAR-2001; 200WO-US09552.
PR 25-MAY-2001; 200WO-US17092.
PR 01-JUN-2001; 200WO-US17800.
PR 20-JUN-2001; 200WO-US19692.
PR 29-JUN-2001; 200WO-US21066.
PR 09-JUL-2001; 200WO-US21735.
PR 17-OCT-1997; 97US-062250P.
PR 03-NOV-1997; 97US-064249P.
PR 13-NOV-1997; 97US-065311P.
PR 21-NOV-1997; 97US-066364P.
PR 10-MAR-1998; 98US-077450P.
PR 11-MAR-1998; 98US-077632P.
PR 11-MAR-1998; 98US-077641P.
PR 11-MAR-1998; 98US-077649P.
PR 12-MAR-1998; 98US-077791P.
PR 13-MAR-1998; 98US-078004P.
PR 20-MAR-1998; 98US-078886P.
PR 20-MAR-1998; 98US-078910P.
PR 20-MAR-1998; 98US-078936P.
PR 25-MAR-1998; 98US-079294P.
PR 26-MAR-1998; 98US-079656P.
PR 27-MAR-1998; 98US-079663P.
PR 27-MAR-1998; 98US-079664P.
PR 27-MAR-1998; 98US-079689P.
PR 27-MAR-1998; 98US-079728P.
PR 27-MAR-1998; 98US-079786P.
PR 30-MAR-1998; 98US-079920P.
PR 30-MAR-1998; 98US-079923P.
PR 26-MAY-1981; 81US-0267213.
PR 17-MAR-1998; 98US-0040220.
PR 26-JUN-1998; 98US-0105413.
PR 07-OCT-1998; 98US-0168978.
PR 02-NOV-1998; 98US-0184216.
PR 06-NOV-1998; 98US-0187368.
PR 07-DEC-1998; 98US-0202054.
PR 22-DEC-1998; 98US-0218517.
PR 05-MAR-1999; 99US-0254465.
PR 10-MAR-1999; 99US-0265686.
PR 12-APR-1999; 99US-0284291.
PR 14-MAY-1999; 99US-0311832.
PR 14-MAY-1999; 99US-0380137.
PR 25-AUG-1999; 99US-0380138.
PR 25-AUG-1999; 99US-0380142.
PR 08-NOV-2000; 2000US-0709238.
PR 27-NOV-2000; 2000US-0723749.
PR 20-DEC-2000; 2000US-0747259.
PR 22-MAR-2001; 2001US-0816744.
PR 22-MAR-2001; 2001US-0816920.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 01-JUN-2001; 2001US-0872035.
PR 05-JUN-2001; 2001US-0874503.
PR 14-JUN-2001; 2001US-0882636.
PR 19-JUN-2001; 2001US-0886342.
PR 30-JUL-2001; 2001US-0918585.

XX PA (GETH ) GENENTECH INC.
XX PI Ashkenazi A, Baker KP, Botstein D, Desnoyers L, Eaton D;
PI Ferrara N, Filvaroff E, Fong S, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillian KJ;
PI Kijavini IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;
PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
XX WPI; 2003-288163/28.
DR P-PSDB; ABU61102.
XX
XX Novel secreted and transmembrane polypeptides and polynucleotides
XX encoding them useful for treating cancer, kidney diseases, bone,
XX cartilage disorders and immune deficiencies -
XX
XX Claim 2; Fig 76; 459pp; English.
XX
XX The present invention relates to the isolation of novel human PRO
XX polypeptides, and the polynucleotide sequences encoding them. The
XX PRO polypeptides are secreted and transmembrane proteins. The PRO
XX polypeptides are useful for detecting other PRO polypeptides, for
XX linking bioactive molecules to cells expressing PRO polypeptides,
XX for modulating biological activities of cells expressing PRO
XX polypeptides, and for identifying agonists or antagonists. The
XX bioactive molecule may be a toxin, radiolabel or antibody, and causes
XX apoptosis or death of the cell. The PRO polypeptides are useful for
XX treating immune disorders, diabetes or hyper- or hypo-insulinaemia,
XX cardiac insufficiency, nervous system disorders, kidney disorders,
XX bone and cartilage disorders or arthritis, tumours, and wound healing.
XX The polynucleotide sequences encoding PRO polypeptides are useful as
XX hybridisation probes, in chromosome and gene mapping, in the generation
XX of antisense RNA and DNA, in the preparation of PRO polypeptides, for
XX generating transgenic animals or knockout animals, and for the genetic
XX analysis of individuals with genetic disorders, and in gene therapy.
XX The present sequence data for this patent was obtained in electronic
XX format directly from the USPTO web site at
XX seqdata.uspto.gov/psipsDIDENTry.html.
XX
XX Sequence 3716 BP; 757 A; 1225 C; 1032 G; 702 T; 0 other;

Alignment Scores:
Pred. No.: 8.42e-88 Length: 3716
Score: 1432.00 Matches: 268
Percent Similarity: 98.53% Conservatives: 1
Best Local Similarity: 98.17% Mismatches: 3
Query Match: 97.08% Indels: 1
DB: 25 Gaps: 0

US-10-047-021-86_COPY_28_303 (1-276) x ABX92441 (1-3716)
Qy 1 GlnAspSerProGlnInlLeuValHisProGlnAspGlnLeuPheGlnGlyProGly 20
Db 73 CAGGACTCCCGCCGCGCCAGATCCTAGTCCACCCAGGAGGAGTGTTCAGAGGGCCCTGGC 132
Qy 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProProThrIleArgTrpLeuLeu 40
Db 133 CCTGCCAGAGTAGCTGCCAAGCCTCAGGCCAGGCCACCTCCACATCCGCTGGTGTCTG 192
Qy 41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60
Db 193 AATGGGCGAGCCCTGAGCATGGTGTGCCCCAGAGCCACACACCTCTGCTGATGGGACC 252
Qy 61 LeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80
Db 253 CTTCTGCTGTACAGCCCTCTGCCCGGGGAGCATGCCACCATGAGCCAGGCTGTCCACA 312
Qy 81 AsnLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100
Db 313 GACCTGGGTGTCTACATGTGAGGCCAGCAACCGGTGTGACGGCAGTCAGGAGGAGGC 372
Qy 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnInlLeuGlnProArgAspMetVal 120
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Db 373 GCTCGCTCTCTGTGGCTCTCTCGGGAGGATTTCCAGATCCAGCTCGGACATGGTG 432
QY 121 AlaValValGlyGluGlnPheThrLeuGluCysGlyProProTyrGlyHisProGluPro 140
Db 433 GCTGTGGTGGTGAGCAGATTTACTCTGGAAATGTGGCCCGCTCGGGCCACCCAGAGCCC 492
QY 141 ThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrVal 160
Db 493 ACAGTCTCATGTGTGGAAGATGGAAACCCCTGGCCCTCCAGCCCGGAAGGCACACAGTG 552
QY 161 SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu***ThrTyrMetCys 180
Db 553 TCCGGGGGTCCCTGCTGTATGCAAGAGCAGAGAGAGTGCAGAAAGGACCTACATGTGT 612
QY 181 ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu 200
Db 613 GTGGCCACCAACAGCCAGCAGCATAGGGAGCCGCGCAGCCGGTTTCCATCCAGGAG 672
QY 201 ProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluVal 220
Db 673 CCCAGGACTACACGGAGCTGTGGAGCTTCTGGCTGTGCGAATTCAGCTGGAATGTG 732
QY 221 ThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAlaValTrpLeu*** 240
Db 733 ACACGTCTGAACCGGATCTCTCAGAGGGCCCAAGCCTTAGACCGCGGTGTGGCTCAGC 792
QY 241 TrpLysValSerGlyPro***ArgLeuProAsnLeuThrArgProCysSerGlyProAr 260
Db 793 TGGAAAGGTCAAGTGGCCCTCTCGCGCTGCCCAATCTTACAGGCGCTTGTTCAGGACCCAG 852
QY 260 GlnProArgGluAlaArgGluLeuArgGlyGlnArg 272
Db 853 ACTGCCCGGGAGGCCAGGAGCTCCGTGGGACAGGG 889
RESULT 8
AAS01695
ID AAS01695 standard; cDNA; 3808 BP.
XX
AC AAS01695;
XX
DT 18-JUL-2001 (first entry)
DE Human TANGO 330 form 2 cDNA sequence.
XX
KW Human; TANGO 315; clone Jthx181e12; TANGO 330; TANGO 437; TANGO 480;
KW cellular process regulator; gene therapy; astrocyte; cancer; ss;
KW Roundabout; adrenal cortex; hypoadrenalism; hyperadrenalism; neoplasia;
KW cell proliferative disorder; neurological disorder; Alzheimer's disease.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 9..1451
FT /tag= a
FT /product= "TANGO 330 form 2 protein"
FT /note= "The ORF is specifically claimed"
FT sig_peptide 9..68
FT /tag= b
FT mat_peptide 69..1448
FT /tag= c
XX
WO200123523-A2.
XX
PN 05-APR-2001.
XX
PD 02-OCT-2000; 2000WO-US27202.
XX
PR 30-SEP-1999; 99US-0409634.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Kirst S, Wrighton N, Fraser CC;
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XX WPI; 2001-235372/24.
DR P-PSDB; AAU00501.
XX
PT Isolated secreted proteins and their encoding nucleic acids are used
PT for diagnosis and treatment of e.g. bacterial and viral infections,
PT autoimmune diseases and inflammatory disorders -
XX
PS Claim 2; Fig 14; 261pp; English.
XX
CC The present sequence encoding for human TANGO 330 form 2 is
CC isolated from cDNA clone Jthx181e12 from a human astrocyte cDNA
CC library. TANGO 330 is 1 of 4 novel human transmembrane proteins
CC which also includes TANGO 315 (AAU00498-AAU00499), TANGO 437 (AAU00502)
CC and TANGO 480 (AAU00503). The nucleic acids encoding these proteins
CC are useful as modulating agents in regulating a variety of cellular
CC processes and can be used to express the proteins in a host cell in
CC gene therapy applications. Antisense nucleic acid molecules and
CC expression vectors containing the TANGO nucleic acids are also described.
CC Diagnostic assays can be used to detect genetic alterations in the TANGO
CC nucleic acids and to identify compounds that bind to or modulate activity
CC of the TANGO proteins. Anti-TANGO antibodies are used diagnostically to
CC monitor protein levels in tissue as a clinical testing procedure.
CC TANGO 330 shows homology to human Roundabout. TANGO 330 nucleic acids
CC and proteins may be used to diagnose, treat and monitor disorders of the
CC adrenal cortex e.g. hypoadrenalism, hyperadrenalism, and neoplasia. They
CC can also be used to treat cell proliferative disorders (e.g. cancer),
CC and neurological disorders e.g. Alzheimer's disease.
XX
SQ Sequence 3808 BP; 773 A; 1244 C; 1041 G; 750 T; 0 other;
```

```
Alignment Scores:
Pred. No.: 8,64e-88 Length: 3808
Score: 1432.00 Matches: 268
Percent Similarity: 98.53% Conservative: 1
Best Local Similarity: 98.17% Mismatches: 3
Query Match: 97.08% Indels: 1
DB: 22 Gaps: 0
US-10-047-021-86_COPY_28_303 (1-276) x AAS01695 (1-3808)
QY 1 GlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGly 20
Db 183 CAGGACTCCCGCCCGCCAGATCTAGTCCACCCAGGACCAGCTGTTCCAGGCGCTGCGC 242
QY 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTrpLeuLeu 40
Db 243 CCTGCCAGGATGAGCTGCCAAGCCTCAGGCCAGCCACCTCCACCATCCGCTGGTTGCTG 302
QY 41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60
Db 303 AATGGGAGCCCTCGAGCATGTGTGCCCCCAGACCACACACCTCTCGCTGATGGGACC 362
QY 61 LeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80
Db 363 CTCTCTGCTGTACAGCCCGCTCGCCGGGACATGCCCCAGCATGGCCAGGCCCTGTCCACA 422
QY 81 AspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100
Db 423 GACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCACCGCAGTCAGCAGAGGC 482
QY 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal 120
Db 483 GCTCGGCTGTCTGTGGCTGTCTCTCGGAGGATTTCCAGATCCAGCCCTCGGGACATGGTG 542
QY 121 AlaValValGlyGluGlnPheThrLeuGluCysGlyProProTyrGlyHisProGluPro 140
Db 543 GCTGTGGTGGTGAGCAGTTTACTCTGGAATGTGGCCCGCTCGGGCCACCCAGAGCCC 602
QY 141 ThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrVal 160
Db 603 ACAGTCTCATGTGTGGAAGATGGGAAACCCCTGGCCCTTCCAGCCCGGAAGGCACACAGTG 662
```

Qy 161 SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu***ThrTyrMetCys 180
Db TCCGGGGGTCCTCTGATGCAAGACAGAGAAGAGTGAGGAAGGACCTACATGTGT 722
Qy 181 VallatThrAenSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu 200
Db GTGGCCACCAACAGCGAGGACATAGGAGAGCGCGAGCCGGGTTTCCATCCAGGAG 782
Qy 201 ProGlnAepTyrThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluAsnVal 220
Db CCCAGAGACTACCGGAGCCCTGTGAGCTTCTGGCTGTGCGAATTCAGCTGGAAATGTG 842
Qy 221 ThrLeuLeuAenProAspProAlaGluGlyProLysProArgProAlaValTyrLeu*** 240
Db ACATGTGTGAACCGGATCTTCGAGAGGCGCCCAAGCTAGACCGCGGTGTGCTCAGC 902
Qy 241 TrpLysValSerGlyPro***-ArgLeuProAsnLeuThrArgProCysSerGlyProAr 260
Db TGAAGGTGTCAGTGGCCCTGTGCGCTGCCCAATCTACAGCGGCTTGTTCAGGACCCAG 962
Qy 260 gLeuProArgGluAlaArgGluLeuArgGlyGlnArg 272
Db ACTGCCCGGAGGCCAGGGAGCTCCGTGGGCGAGG 999

RESULT 9

AAH18180
ID AAH18180 standard; cDNA; 4262 BP.
AC AAH18180;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human cDNA sequence SEQ ID NO:18084.
XX

KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX

OS Homo sapiens.
XX

PN EP1074617-A2.
XX

PD 07-FEB-2001.
XX

PF 28-JUL-2000; 2000EP-0116126.
XX

PR 29-JUL-1999; 99JP-0248036.
XX

PR 27-AUG-1999; 99JP-0300253.
XX

PR 11-JAN-2000; 2000JP-0118776.
XX

PR 02-MAY-2000; 2000JP-0183767.
XX

PR 09-JUN-2000; 2000JP-0241899.
XX

XX (HELI-) HELIX RES INST.
XX

XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX WPI; 2001-318749/34.
XX

XX Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs -
XX

PS Claim 8; SEQ ID 18084; 2537bp + CD ROM; English.
XX

XX The present invention describes primer sets for synthesizing 5602
CC full-length cDNAs defined in the specification. Where a primer set
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a

CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence and the 3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to
CC AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.
XX

SQ Sequence 4262 BP; 873 A; 1333 C; 1209 G; 847 T; 0 other;

Alignment Scores:

Pred. No.: 3,38e-87 Length: 4262
Score: 1424.00 Matches: 267
Percent Similarity: 98.17% Conservative: 1
Best Local Similarity: 97.80% Mismatches: 4
Query Match: 96.54% Indels: 1
DB: 22 Gaps: 0

US-10-047-021-86_COPY_28_303 (1-276) x AAH18180 (1-4262)

Qy 1 GlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGly 20
Db 121 CAGGACTCCCGCCCGCCAGATCCTAGTCCACCCCGAGGACGAGCTGTTCCAGGGCCCTTGGC 180
Qy 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTyrLeuLeu 40
Db 181 CTGCGCAGATGAGCTGCCAAGCTCAGGCGAGCCACCTCCACCATCCGCTGTTGCTG 240
Qy 41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60
Db 241 AATGGCGAGCCCTGAGCATGTGTGCCCCCAGAGACACACACCTCTCTGCTGTATGGGACC 300
Qy 61 LeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80
Db 301 CTCTGCTGTCTACAGCCCCCTGCCGGGAGCATGCCACCATGGCCAGGCGCTGTCCACA 360
Qy 81 AspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100
Db 361 GACCTGGGTGTCTACACATGTGAGGCCAGCACACCGGCTTGGCAGCGCAGTCAGCAGAGC 420
Qy 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal 120
Db 421 GCTCGGCTGTCTGTGGTGTCTCCGGGAGGATTTCCAGATCCAGACCTCCGAGACATGGTG 480
Qy 121 AlaValValGlyGlnGlnPheThrLeuGluCysGlyProProTyrGlyHisProGluPro 140
Db 481 GCTGTGGTGGGTGAGCAGTCTTACTCTGGAATGTGGCGCCCTCTGGGGCCACCCAGAGCCC 540
Qy 141 ThrValSerTyrTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrVal 160
Db 541 ACAGTCTCATGGTGGAAAGATGAGAAACCCCTGGCCCTCCAGCCCGAGGACACACAGTG 600
Qy 161 SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu***ThrTyrMetCys 180
Db 601 TCCGGGGGGTCCCTGTCTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 660
Qy 181 ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu 200
Db 661 GTGGCCACCAACAGCGCAGACACAGGAGAGCGCGCGCGCGGTTTCCATCCAGAG 720
Qy 201 ProGlnAepTyrThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluAsnVal 220
Db 721 CCCAGGACTACAGGAGCTTGTGGAGCTTCTGGCTGTGCGAATTCAGCTGGAAATGTG 780
Qy 221 ThrLeuLeuAenProAspProAlaGluGlyProLysProArgProAlaValTyrLeu*** 240
Db 781 ACATGTGTAACCGGATCTTCGAGAGGCGCCCAAGCTAGACCGCGGCTGTGCTCAGC 840

cell proliferative disorder; neurological disorder; Alzheimer's disease.

OS Homo sapiens.

XX Key Location/Qualifiers
FH CDS 2..2806

FT /*tag= a

FT /partial

FT /product= "TANGO 330 form 1 protein"

FT /note= "The ORF is specifically claimed. This sequence

FT lacks a start codon"

FT variation

FT replace (4,C)

FT /*tag= b

FT variation

FT replace (5,T)

FT /*tag= c

FT variation

FT replace (9,T)

FT /*tag= d

FT variation

FT replace (159,A)

FT /*tag= e

XX WO200123523-A2.

XX 05-APR-2001.

XX 02-OCT-2000; 2000WO-US27202.

XX 30-SEP-1999; 99US-0409634.

XX (MILL-) MILLENNIUM PHARM INC.

XX KIRST S, WRIGHTON N, FRASER CC;

XX WPI; 2001-235372/24.

XX P-PSDB; AAU00500.

PT Isolated secreted proteins and their encoding nucleic acids are used
PT for diagnosis and treatment of e.g. bacterial and viral infections,
PT autoimmune diseases and inflammatory disorders -

PS Claim 2; Fig 13; 261pp; English.

XX The present sequence encoding for human TANGO 330 form 1 is
XX isolated from cDNA clone jthAa060g22 from a human adrenal gland
XX cDNA library. TANGO 330 is 1 of 4 novel human transmembrane proteins
XX which also includes TANGO 315 (AAU00498-AAU00499); TANGO 437 (AAU00502)
XX and TANGO 480 (AAU00503). The nucleic acids encoding these proteins
XX are useful as modulating agents in regulating a variety of cellular
XX processes and can be used to express the proteins in a host cell in
XX gene therapy applications. Antisense nucleic acid molecules and
XX expression vectors containing the TANGO nucleic acids are also described.
XX Diagnostic assays can be used to detect genetic alterations in the TANGO
XX nucleic acids and to identify compounds that bind to or modulate activity
XX of the TANGO proteins. Anti-TANGO antibodies are used diagnostically to
XX monitor protein levels in tissue as a clinical testing procedure.
XX TANGO 330 shows homology to human Roundabout. TANGO 330 nucleic acids
XX and proteins may be used to diagnose, treat and monitor disorders of the
XX adrenal cortex e.g. hypoadrenalism, hyperadrenalism, and neoplasia. They
XX can also be used to treat cell proliferative disorders (e.g. cancer),
XX and neurological disorders e.g. Alzheimer's disease.

SQ Sequence 3042 BP; 607 A; 1008 C; 859 G; 568 T; 0 other;

Alignment Scores:

Pred. No.: 7.25e-64 Length: 3042
Score: 1077.00 Matches: 207
Percent Similarity: 97.20% Conservative: 1
Best Local Similarity: 96.73% Mismatches: 4
Query Match: 73.02% Indels: 2
DB: 22 Gaps: 0

US-10-047-021-86_COPY_28_303 (1-276) x AAS01694 (1-3042)

OY 61 LeuLeuLeuLeuGln-ProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerTh 80

Db 43 CTCTGCTCATATGCGCCCTGCGGGGACATGCCACGATGGCCGAGCCCTGTCCAC 102
OY 80 rAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgG1 100
Db 103 AGACCTGGGTGTCTACACATGTGAGCCAGCAACCGGCTTGGCAGCGCATGTCAGCAGG 162
OY 100 YAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVa 120
Db 163 CGCTGGCTGTCTGTGGCTGTCTCTCGGAGGATTTCCAGATCCAGCTCGGACATGGT 222
OY 120 lAlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluPr 140
Db 223 GGCTGTGTGGGTGAGCAGTTTACTCTGGAATGTGGGCGCCCTGGGGCCACCCAGAGCC 282
OY 140 oThrValSerTrpTrpIysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrVa 160
Db 283 CACAGTCTCATGTGTGGAAGATGGAAACCCCTGGCCCTCCAGCCCGGAAGGCACAGT 342
OY 160 lSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu**ThrTyrMetCy 180
Db 343 GTCCGGGGGTCCCTGCTGATGGCAGAGCAGAGAGATGACGAAGGACCTACATGTG 402
OY 180 sValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnG1 200
Db 403 TGTGGCCACCAACAGCGCAGCAGATAGGAGAGCGCGCAGCGCGGTTCCTCATCCAGGA 462
OY 200 uProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluAsnVa 220
Db 463 GCCCCAGGACTACACGAGGCTGTGGAGCTTCTGGCTGTGCGAATTCAGTGGGAAAATGT 522
OY 220 lThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAlaValTrpLeu** 240
Db 523 GACACTGCTGAACCCGGATCTGCAGAGGGCCCCCAGCCCTAGACCGCGCGGTGGCTCAG 582
OY 240 *TrpLysValSerGlyPro***-ArgLeuProAsnLeuThrArgProCysSerGlyProA 260
Db 583 CTGGAAGTCTAGTGGCCCTGCTGCGCTGCCCAATCTTACACGGCCTTGTTCAGGCCCA 642
OY 260 rgLeuProArgGluAlaArgGluLeuArgGlyGlnArg 272
Db 643 GACTGCCCGGAGCGCCAGGAGCTCCGTGGCAGAGG 680
RESULT 12
ABK87138
ID ABK87138 standard; cDNA; 3688 BP.
XX AC ABK87138;
XX DT 07-OCT-2002 (first entry)
XX DE cDNA mouse ECSM4 protein.
XX KW Mouse; endothelial cell-specific molecule 4; ECSM4; neovasculture;
XX KW imaging vascular endothelium; proliferative disease; cancer;
XX KW psoriasis; diabetic retinopathy; atherosclerosis; menorrhagia;
XX KW endothelial damage; tumour neovasculture; cardiac disease;
XX KW endometriosis; hypoxic condition; angiogenesis; cytostatic;
XX KW cardiant; gene; ss.
XX OS Mus sp.
XX PH Key Location/Qualifiers
FT CDS 6..3053
FT /*tag= a
FT /note= "ECSM4 #1"
FT CDS 3393..3512
FT /*tag= b
FT /note= "ECSM4 #2"
FT CDS 3579..3683
FT /*tag= c
FT /note= "ECSM4 #3"
XX

PN WO200236771-A2.
XX PD 10-MAY-2002.
XX PF 06-NOV-2001; 2001WO-GB04906.
XX PR 06-NOV-2000; 2000US-245566P.
XX PR 07-MAR-2001; 2001US-273662P.
XX PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
XX PI Bicknell R, Huminiecki L;
XX DR P-PSDB; AAU99420, AAU99421, AAU99422.
XX PT Novel endothelial cell-specific molecule polypeptide 1 or 4, useful for
PT imaging, diagnosing and treating a condition involving vascular
PT endothelium e.g. cancer, cardiac disease, endometriosis, diabetes
XX PS Disclosure; Fig 13; 248pp; English.
XX CC The present invention relates to endothelial cell-specific molecule 4
CC (ECSM4), and the polynucleotide sequences encoding it. The ECSM4
CC proteins are useful for imaging vascular endothelium in the body of
CC an individual, and for diagnosing and treating a proliferative
CC disease or condition involving the vascular endothelium (preferably,
CC neovasculature) such as cancer, psoriasis, diabetic retinopathy,
CC atherosclerosis or hemorrhagia. The ECSM4 proteins are also useful in
CC the manufacture of diagnostic or prognostic agent for such conditions.
CC The proteins are also useful for detecting endothelial damage or
CC activation, detecting a tumour or tumour neovasculature, cardiac
CC disease, or endometriosis by detecting the amount of ECSM4 present in
CC a sample. The polynucleotide sequences encoding ECSM4 are useful in
CC gene therapy for treating a hypoxic condition such as cancer, cardiac
CC disease, endometriosis or atherosclerosis and in the manufacture of
CC medicaments for treating the above disease. The sequences are useful
CC for modulating angiogenesis in an individual. The present sequence
CC encodes mouse ECSM4 protein.
XX SQ Sequence 3688 BP; 801 A; 1115 C; 1011 G; 761 T; 0 other;

Alignment Scores:
Pred. No.: 8 49e-63 Length: 3688
Score: 1062.50 Matches: 204
Percent Similarity: 83.52% Conservatives: 24
Best Local Similarity: 74.73% Mismatches: 43
Query Match: 72.03% Indels: 2
DB: 24 Gaps: 1

US-10-047-021-86_COPY_28_303 (1-276) x ABR07138 (1-3688)

QY 2 AspSerProGlnLeuValHisProGlnAspGlnLeuPheGlnGlyProGlyPro 21
Db 120 GATTCTCCACCCAGATCTAGTTCACCCAGGACCACTACTTCAGGGCTCTGGCCA 179

QY 22 AlaArgMetSerCysArgAlaSerGlyGlnProProProThrIleArgTrpLeuAsn 41
Db 180 GCCAAGATGAGTGCAGATCATCCCGGCCAACCACTCCCACTATCCGCTGGCTGTAAT 239

QY 42 GlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThrLeu 61
Db 240 GGGGAGCCCTCAGATGATGCCACCCAGACCTACATTACCTTTGCCGGATGGGACCTC 299

QY 62 LeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGln---AlaLeuSerThr 80
Db 300 CTGTTACATCGGCCCTCTGTCCAGGACCGGCCCAAGATGACCAACATCTCTCAGCA 359

QY 81 AspLeuGlyValThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100
Db 360 ATCCTGGGTGTACACATGTGAGGCCAGCAACCGCTGGGCACAGCATGTAGCCGGGT 419

QY 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnLeuGlnProArgAspMetVal 120

Db 420 GCTAGGCTGTCTGTGGCTGTCTCCAGGAGACTTCCAGATCCAACTCCGGACAGTG 479

QY 121 AlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluPro 140
Db 480 GCCGTGGTGGGAGAGAGCTTGGTCTCTGAGTGTGTCTCTCCCTGGGGCTACCCAAAACCC 539

QY 141 ThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrVal 160
Db 540 TCGGTCTCATGTGGAAAGACGGGAACCCCTGGTCTCCAGCCAGGAGGCGCACAGTA 599

QY 161 SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu***ThrTrpMetCys 180
Db 600 TCTGGGATTCCTGATGTCTCAAGACAGAGAAGATGACTCGGGGACCTATATGTGT 659

QY 181 ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu 200
Db 660 ATGGCCACCAACATGTCTGGGCAACGGGAGAGCCGAGCAGCGGTGTCTATCCAGGAA 719

QY 201 ProGlnAspTyThrGluProValGluLeuAlaValArgIleGlnLeuGluAsnVal 220
Db 720 TCCAGGACCAACAGGACATCTAGAGCTTCTGGCTGTTCGATTCAGCTGGAAATGTG 779

QY 221 ThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAlaValTrpLeu*** 240
Db 780 ACCCTGTCTAAACCCGAACTGTAAAGTCCCAAGCTCCGAGCCATCGTGTGGCTCAGC 839

QY 241 TrpLysValSerGlyPro***ArgLeuProAsnLeuThrArgProCysSerGlyProAr 260
Db 840 TGGAAGGTGAGCGGCCCTGTGTCACCTCTCGATCATACACAGCTCTGTTCAGGACTCAG 899

QY 260 gLeuProArgGluAlaArgGluLeuArgGlyGlnArg 272
Db 900 AGTCCCCCAGGACCAAGGATCTCCATGGACAGAGG 936

RESULT 13
ID AAH08234 standard; cDNA; 756 BP.
XX AC AAH08234;
XX DT 26-JUN-2001 (first entry)
XX DE Human cDNA clone (5'-primer) SEQ ID NO:5069.
XX KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX OS Homo sapiens.
XX PN EP1074617-A2.
XX PD 07-FEB-2001.
XX PF 28-JUL-2000; 2000EP-0116126.
XX PR 29-JUL-1999; 95JP-0248036.
XX PR 27-AUG-1999; 95JP-0300253.
XX PR 11-JAN-2000; 2000JP-0118776.
XX PR 02-MAY-2000; 2000JP-0183767.
XX PR 09-JUN-2000; 2000JP-0241899.
XX PA (HELI-) HELIX RES INST.
XX PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
XX PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX DR WPI; 2001-318749/34.
XX PT Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
XX full-length cDNAs -

PS Claim 1; SEQ ID 5069; 2537pp + CD ROM; English.

XX The present invention describes primer sets for synthesising 5602
CC full-length cDNAs defined in the specification. Where a primer set
CC comprises: (a) an oligo-dr primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesising polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to
CC AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.

SQ Sequence 756 BP; 147 A; 242 C; 236 G; 128 T; 3 other;

Alignment Scores:

Pred. No.: 3.81e-63 Length: 756
Score: 1057.00 Matches: 205
Percent Similarity: 97.17% Conservative: 1
Best Local Similarity: 96.70% Mismatches: 6
Query Match: 71.66% Indels: 2
DB: 22 Gaps: 0

US-10-047-021-86_COPY_28_303 (1-276) x AAH08234 (1-756)

Qy 1 GlnAspSerProGlnIleValHisProGlnAspGlnLeuPheGlnGlyProGly 20
Db 121 CAGGACTCCCGCCCGCCAGATCTAGTCACCCCGCCAGGACCGCTTCCAGGGCCCTGGC 180
Qy 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProProThrIleArgTrpLeuLeu 40
Db 181 CCTGCCAGATGAGTGCAGAGCTCAGCCAGCCACCTCCACCATCCGCTGGTGTG 240
Qy 41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60
Db 241 AATGGCGAGCCCTGAGCATGGTGCCTCCAGACCCACACACCTCTCTGCTGATGGGACC 300
Qy 61 LeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80
Db 301 CTTCCTGCTGCTACAGCCCTCCCGGGGAGATGCCACAGATGGCCAGCCCTGTCCACA 360
Qy 81 AspLeuGlyValThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100
Db 361 GACCTGGGTGTCTACACATGTGAGCCAGCAACCGCTTGCACGGCAGTCCAGCAGAGGC 420
Qy 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal 120
Db 421 GCTCGGCTGTCTGTGGCTGTCTCCGGGAGGATTTCCAGATCCAGCCCTCCGAGACATGGTG 480
Qy 121 AlaValValGlyGluGlnPheThrLeuGluCysGlyProProThrGlyHisProGluPro 140
Db 481 GCTGTGGGTGGTGAGCAGTTTACTCTGGAATGTGGCGCCCTCCGGGGCCACCCAGAGCCC 540
Qy 141 ThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrVal 160
Db 541 ACAGTCTCATGTTGAAGATGAGAAACCCCTTGGCCCTCCAGCCCGGAGGACACACAGTG 600
Qy 161 SerGlyGlySerLeuLeuMetAlaArgAlaGlnLysSerAspGlu***ThrTyMetCys 180
Db 601 TCCGGGGGGTCTCTGCTGATGGCAAGAGCAGAGAGAGTGACGAAGGAGCCTACATGTGT 660

Qy 181 ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu 200
Db 661 GTGGC-ACCACAGCGCAGGACACACAGGAGAGCGGACACC-CGGGTTTNCATTCAGAG 718
Qy 201 ProGlnAspTyrThrGluProValGluLeuAla 212
Db 719 CCCGANGACTACACGGAACCTGTGGAACTTTTGCT 754

RESULT 14

AAV69278
ID AAV69278 standard; cDNA; 4291 BP.
XX AC AAV69278;
XX DT 01-MAR-1999 (first entry)
XX DE Human T85 cDNA.
XX KW T85; FMHB-6D4; FMHV-SD4; human; neurological disorder; therapy;
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT CDS 958..3219 /*tag= a
FT sig_peptide 958..1017 /*tag= b
FT mat_peptide 1018..3216 /*tag= b
XX WO9848051-A2.
XX PD 29-OCT-1998.
XX PF 17-APR-1998; 98WO-US07714.
XX PR 10-OCT-1997; 97US-0062017.
XX PA 18-APR-1997; 97US-0044746.
XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX Holtzman D, McCarthy SA;
XX WPI; 1999-024021/02.
XX P-PSDB; AAW83927.

New isolated human FTHMA-070 and T85 proteins - used to develop products for the diagnosis and therapy of disorders involving cellular processes, e.g. neuronal development.

Claim 24; Fig 3; 127pp; English.

This claimed cDNA sequence, the coding region of which is also claimed, codes for novel human T85 (see AAW83927), also referred to as FMHB-6D4 and FMHB-SD4. The cDNA was identified in a human foetal brain cDNA library using a screen designed to identify genes encoding proteins having a functional signal sequence. T85 nucleic acids and polypeptides of the invention are useful as modulating agents in regulating a variety of cellular processes. They can be used for identifying compounds which bind to or modulate the activity of the polypeptides (claimed). They can also be used in screening assays, detection assays (e.g. chromosomal mapping, tissue typing, forensic biology), predictive medicine (e.g. diagnostic assays, prognostic assays, monitoring clinical trials, and pharmacogenomics), and methods of treatment (e.g. therapeutic and prophylactic) e.g. for neurological disorders.

Sequence 4291 BP; 1154 A; 1011 C; 1045 G; 1081 T; 0 other;

Alignment Scores:
Pred. No.: 4.87e-21 Length: 4291
Score: 446.50 Matches: 91

Percent Similarity: 55.96% Conservative: 31
 Best Local Similarity: 41.74% Mismatches: 87
 Query Match: 30.27% Indels: 9
 DB: 20 Gaps: 2

US-10-047-021-86_COPY_28_303 (1-276) x AA69278 (1-4291)

QY 1 GlnAspSerProProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGly 20
 DB 1030 GAAGATTTCACCTCGCATTTGTAACACCCCTTCAGACCTGATGTTCTCAAAAGAGAA 1089
 QY 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTrpLeuLeu 40
 DB 1090 COTGCAACTTTGAAGTGAAGCTGAAGCGCCGCCACACCCATTAATGATGGTACAAA 1149
 QY 41 AsnGlyGlnProLeuSerMetValProProAspProHisHis-----LeuLeuPro 57
 DB 1150 GGGGAGAGAGAGTGGACACACAAAGATGACCTCGCTCACCCGATGTTGTGCGG 1209
 QY 58 AspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAla 77
 DB 1210 AGTGGATCTTTATTTTCTTACGT-----ATAGTACATGGACGGAAA 1251
 QY 78 LeuSerThrAspLeuGlyValTyThrCysGluAlaSerAsnArgLeuGlyThrAlaVal 97
 DB 1252 AGTAGACCTGATGAAGAGGCTCTATGCTGTGTAGCAAGGAATTAACCTTGGAGAGCGTGTG 1311
 QY 98 SerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArg 117
 DB 1312 AGCCCAATGATCGCTGGAAGTACCATATCTTCGGGATGACTTCAGACAAACCCCTTCG 1371
 QY 118 AspMetValAlaValGlyGlnPheThrLeuGluCysGlyProProTrpGlyHis 137
 DB 1372 GATGTCATGTTGAGTAGGAGCGCTGCAGTAATGGAATGCCAATCCACCTCCACGAGCCAT 1431
 QY 138 ProGluProThrValSerTrpTrpAspGlyHisProLeuAlaLeuGlnProGlyArg 157
 DB 1432 CCTGAGCCCACTTTCATGGAAGAAAGATGGCTCTCCACTGGATGATAAGATGAAAGA 1491
 QY 158 HisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu***Thr 177
 DB 1492 ATAACATATACGAGGAGGAAAGCTCATGATCACTTACACCCGCTAAAGTGCAGCGCTGGCAA 1551
 QY 178 TyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSer 197
 DB 1552 TATGTTTGTGTTGGTACCAATATGTTGGGAACTGAGAGTGAAGTAGCCGAGCTGACT 1611
 QY 198 IleGlnGluProGlnAspTrpThrGluProValGluLeuLeuAlaValArgIle 215
 DB 1612 GTCTTAGAGAGACCATCATTTGTGAAGAGACCCAGTAACTTGGCAGTAACCTGTG 1665

RESULT 15

AA55770
 ID AA55770 standard; cDNA; 4956 BP.

AC AA55770;

DT 30-JUL-1999 (first entry)

XX Human Robo 1 polypeptide encoding cDNA.

DE Comm polypeptide; Robo polypeptide; commissureless; roundabout;

KW modulation; nerve cell function; ds.

XX Homo sapiens.

OS Homo sapiens.

XX WO925833-A1.

PN 27-MAY-1999.

XX 13-NOV-1998; 98WO-US24327.

XX 14-NOV-1997; 97US-0065543.

XX (REGC) UNIV CALIFORNIA.

XX Goodman C, Kid T, Mitchell KJ, Russell C, Tear G;

XX WPI; 1999-338008/28.

XX P-PSDB; AA113566.

XX Modulation of Robo-Comm polypeptide interactions

XX Disclosure; Page 42-44; 56pp; English.

XX The invention relates to a method for modulating the amount of Comm

XX (commissureless) polypeptide in contact with a cell expressing active

XX Robo (roundabout) on its surface. The method comprises modulating the

XX effective amount of Comm polypeptide in contact with the cell, where the

XX amount of expressed active Robo is specifically modulated inversely with

XX the modulation of the effective amount of Comm in contact with the cell.

XX The method is used to modulate the amount of active Robo expressed on a

XX cell. The method can be used to screen for agents that modulate Robo:Comm

XX interactions. This is particularly useful for modulating nerve cell

XX function.

XX Sequence 4956 BP; 1480 A; 1230 C; 1186 G; 1060 T; 0 other;

XX Alignment Scores:

Pred. No.: 5,67e-21 Length: 4956

Score: 446.50 Matches: 91

Percent Similarity: 55.96% Conservatives: 31

Best Local Similarity: 41.74% Mismatches: 87

Query Match: 30.27% Indels: 9

DB: 20 Gaps: 2

US-10-047-021-86_COPY_28_303 (1-276) x AA55770 (1-4956)

QY 1 GlnAspSerProProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGly 20

DB 190 GAAGATTTCACCTCGCATTTGTAACACCCCTTCAGACCTGATGTTCTCAAAAGAGAA 249

QY 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTrpLeuLeu 40

DB 250 CCTGCACTTTGAAGTGAAGCTGAAGCGCCGCCACACCCATTAATGATGGTACAAA 309

QY 41 AsnGlyGlnProLeuSerMetValProProAspProHisHis-----LeuLeuPro 57

DB 310 GGGGAGAGAGTGGACACACAGATGACCTCGCTCACACCGAATGTTGTGCGG 369

QY 58 AspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAla 77

DB 370 AGTGGATCTTTATTTTCTTACGT-----ATAGTACATGGACGGAAA 411

QY 78 LeuSerThrAspLeuGlyValTyThrCysGluAlaSerAsnArgLeuGlyThrAlaVal 97

DB 412 AGTAGACCTGATGAAGAGGCTCTATGCTGTGTAGCAAGGAATTAACCTTGGAGAGCGTGTG 471

QY 98 SerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArg 117

DB 472 AGCCCAATGATCGCTGGAAGTACCATATCTTCGGGATGACTTCAGACAAACCCCTTCG 531

QY 118 AspMetValAlaValGlyGlnPheThrLeuGluCysGlyProProTrpGlyHis 137

DB 532 GATGTCATGTTGCAAGTAGGAGAGCTGCAGTAATGGAATGCCAATCCACCTCCACGAGCCAT 591

QY 138 ProGluProThrValSerTrpTrpAspGlyHisProLeuAlaLeuGlnProGlyArg 157

DB 592 CCTGAGCCCACTTTCATGGAAGAAAGATGGCTCTCCACTGGATGATAAGATGAAAGA 651

QY 158 HisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu***Thr 177

DB 652 ATAACATATACGAGGAGGAAAGCTCATGATCACTTACACCCGCTAAAGTGCAGCGCTGGCAA 711

QY 178 TyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSer 197

Db 712 TATGTTTGTGTTGTTACCAATATGTTGGGGAACGTGAGAGTGAAGTAGCCGAGCTGACT 771
Qy 198 IleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIle 215
Db 772 GTCTTAGAGAGACCATCATTTTGTGAAGAGAGACCCAGTAACTTGGCAGTAACTGTG 825

Search completed: January 31, 2004, 12:48:19
Job time : 231.228 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 31, 2004, 12:35:25 ; Search time 60.5389 Seconds
(without alignments)
2012.290 Million cell updates/sec

Title: US-10-047-021-86_COPY_28_303

Perfect score: 1475

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
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Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	218.5	14.8	5690	2	Sequence 66, Appli
3	218.5	14.8	5690	2	Sequence 2, Appli
4	206.5	14.0	4078	4	US-09-016-434-1132
5	206.5	14.0	6000	1	Sequence 1132, Ap
6	206.5	14.0	6000	2	US-08-348-006B-6
7	206.5	14.0	6000	3	Sequence 6, Appli
8	206.5	14.0	6000	3	US-08-800-825A-6
9	206	14.0	6000	5	Sequence 6, Appli
10	206	14.0	3888	4	PCT-US94-10166-6
11	206	14.0	4608	3	Sequence 13, Appli
12	199	13.5	1426	4	US-08-506-296B-13
					Sequence 24, Appli
					Sequence 1, Appli
					Sequence 2, Appli

13	198	13.4	1042	2	US-08-427-497E-6	Sequence 6, Appli
14	198	13.4	3774	2	US-08-341-843B-1	Sequence 1, Appli
15	198	13.4	3774	2	US-08-427-497E-1	Sequence 1, Appli
16	198	13.4	3774	2	US-08-427-497E-2	Sequence 2, Appli
17	194.5	13.2	3943	4	US-08-506-296B-27	Sequence 27, Appli
18	192	13.0	3189	2	US-08-427-497E-3	Sequence 3, Appli
19	191.5	13.0	4078	4	US-09-016-434-1120	Sequence 1120, Ap
20	191	12.9	3783	4	US-08-506-296B-20	Sequence 20, Appli
21	189	12.8	3398	5	PCT-US95-08493-12	Sequence 12, Appli
22	189	12.8	4843	3	US-08-986-485-1	Sequence 1, Appli
23	185.5	12.6	1391	4	US-09-638-649-4	Sequence 4, Appli
24	182.5	12.4	5824	4	US-08-620-312D-72	Sequence 72, Appli
25	177.5	12.0	3551	4	US-09-620-312D-760	Sequence 760, App
26	176	11.9	3991	4	US-08-506-296B-3	Sequence 3, Appli
27	175.5	11.9	1493	2	US-08-752-307B-6	Sequence 6, Appli
28	175.5	11.9	1493	4	US-09-707-802-6	Sequence 6, Appli
29	175.5	11.9	1493	4	US-09-991-326-6	Sequence 6, Appli
30	172	11.7	957	2	US-08-633-148-3	Sequence 3, Appli
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33	170.5	11.6	3360	1	US-08-408-420A-5	Sequence 5, Appli
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35	170.5	11.6	3360	3	US-08-040-741-5	Sequence 5, Appli
36	165.5	11.2	2610	1	US-08-374-834-17	Sequence 17, Appli
37	165.5	11.2	2610	1	US-08-644-271-28	Sequence 28, Appli
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41	165	11.2	2869	4	US-09-077-955-2	Sequence 2, Appli
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ALIGNMENTS

RESULT 1

US-09-484-970B-66
; Sequence 66, Application US/09484970B
; Patent No. 6426186
; GENERAL INFORMATION:
; APPLICANT: Jones, Karen A.
; APPLICANT: Volkmut, Wayne
; APPLICANT: Walker, Michael G.
; TITLE OF INVENTION: BONE REMODELING GENES
; FILE REFERENCE: PB-0014 US
; CURRENT APPLICATION NUMBER: US/09/484,970B
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PERL Program
; SEQ ID NO 66
; LENGTH: 6814
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6426186 199882.3
; NAME/KEY: unsure
; LOCATION: 1838, 5528
; OTHER INFORMATION: a, t, c, g, or other
US-09-484-970B-66

Alignment Scores:			
Pred. No.:	1.4e-13	Length:	6814
Score:	276.50	Matches:	93
Percent Similarity:	38.80%	Conservative:	30
Best Local Similarity:	29.34%	Mismatches:	125
Query Match:	18.75%	Indels:	69
DB:	4	Gaps:	11

US-10-047-021-86_COPY_28_303 (1-276) x US-09-484-970B-66 (1-6814)

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850 ACCTGCAGACGGAAGGCAACCCCAAGCCTGAGATCATCTGCTGCGAAACAATAATGAG 909
Oy 45 LeuSerMetValProProAspProHisHisIleLeuLeuProAspGlyThrLeuLeuLeuLeu 64
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910 CTGAGCATGAAGACAGATTCCTCGCTAACTTGTGGACATGGAGCCCTGATATC--- 966
Oy 65 GlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThrAspLeuGlyVal 84
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967 -----CAGAACACACAGGAGACAGACCGGATATC 996
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997 TACCAGTCATGGCAAGACAGTGGCGGAGAGGTGAAGACGCAAGAGGTGACCTCAGG 1056
Oy 105 Val-----AlaValLeuArgGluAspPheGlnIleGlnProArgAspMetValAlaVal 122
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1057 TACTTCGGGTCTCCAGCTGACCCACTTTTGTATCCAGCCACAGATACAGAGGTGCTG 1116
Oy 123 ValGlyGluGlnPheThrLeuGluCysGlyProProProThrGlyHisProGluProThrVal 142
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1117 GTTGGGAGAGGTCACGCTGAGGTGACGCCCA---GGCCACCCCGCCCGGATC 1173
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1174 TCCTGGACGAGGTTGACCGCACACCTTGCAGTTGACCGCGGGTGAACATCACCGCT 1233
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1234 TCTGCGGGCTTTACATACAGAAGCTGTCAGAGGGGGACAGCGGAGAGATGTCGTCT 1293
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1294 GCGACCAACATGACAGGTCATCCACCGCTTTCATCATCTGCTCCAGGCTCTCTCT 1353
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Db |||:|||||
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1462 GGGAGCCAGCTCTCGTGGACCGGCGGACCTGCTCTGTCATCGGNAACACTTAGATC 1521
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1618 AGAGTCAACCCAGTGTGTCAGCAGNTTCCAGCGGACACACAGTGGGA 1664
RESULT 2
US-08-447-464-2
; Sequence 2, Application US/08447464
; Patent No. 5840842
; GENERAL INFORMATION:
; APPLICANT: Schlössinger, Joseph
; APPLICANT: Yan, Hai
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PROTEIN
; TITLE OF INVENTION: PHOSPHOTYROSINE PHOSPHATASE-SIGMA
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; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,464
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/130,570
; FILING DATE: 01-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7683-043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5690 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 833..5338
; US-08-447-464-2
Alignment Scores:
Pred. No.: 7,98e-09 Length: 5690
Score: 218.50 Matches: 67
Percent Similarity: 47.93% Conservative: 37
Best Local Similarity: 30.88% Mismatches: 74
Query Match: 14.81% Indels: 39
DB: 2 Gaps: 11
US-10-047-021-86_COPY_28_303 (1-276) x US-08-447-464-2 (1-5690)
Oy 2 AspSerProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGlyPro 21
Db |||:|||||
920 GAAGAGCCACCCAGATTTATCAGAGAGCCCAAGATCAGATTGTTGTGTCAGGAGCGGTG 979
Oy 22 AlaArgMetSerCysArgAlaSerGlyGlnProProProThrThrLeuArgTrp----- 38
Db |||:|||||
980 GCCTCTCTCTGTCGCCAGGCCACAGGTGACCTTAAGCCACGGGTGACCTGGACACAGAG 1039
Oy 39 -----LeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeu 56
Db |||:|||||
1040 GGCAAGAAAGTGAACATCAGACGCTTTGAGACCATTCATCTTGACGAG----- 1087
Oy 57 ProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGln 76
Db |||:|||||
1088 AGCTCGGGGCGCGTGTGAGGATCCAGCCA----- 1117
Oy 77 AlaLeuSerThr-----AspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGly 94
Db |||:|||||
1118 ---CTTCGGACACCCCGGATGAGACGTGTACAGTGTGTGGCCCAAGACTCGTGGGG 1174
Oy 95 ThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIle 114
Db |||:|||||
1175 ---GAGATCAGATTTCATGCGAAGCTCACC-----GTCCTCGAGAGGAC---CAGCTG 1222
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Qy	115	GlnProArgAspMetValAlaValValGlyGluGlnPhe-----	127
Db	1223	CCTCTGGCTTCCCCAACATTGACATGAGCGCCCGCCAGTTGAAGTTGTAGAGCGCACACGC	1282
Qy	128	-----ThrLeuGluCysGlyProProTrrPglYHisProGluProThrValSerTrpTrr	145
Db	1283	ACAGCCACCATTGCTCTGTCTGTCGCAGC--GGAACCCCTGACCTGAGATCATCTGGTTC	1339
Qy	146	LYAAspGlyLysProLeu-----AlaLeuGlnProGlyArg--HisThrValSerGly	162
Db	1340	AAGGACTCTCGCTGTGGACCCCGAGTCGCCAGCAATGGCGCGATCAAGCAGCTTCGGTCA	1399
Qy	163	GlySerLeuLeuMetalaaArgAlaGluLysSerAspGlu***ThrTyrMetCysValAla	182
Db	1400	GGTGGCCCTCGAGATTGAGACGACGAGGACAGACACCGAGGCGAAGTACGAGTGTGTGGCC	1459
Qy	183	ThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGln	199
Db	1460	ACCAACAGCGCTGGGGTGGCGTACTCATCACTGCGCAACTCTACGTGGCGCA	1510

RESULT 3

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US-08-716-679-2
; Sequence 2, Application US/08716679
; Patent No. 5846800
; GENERAL INFORMATION:
; APPLICANT: Schlessinger, Joseph
; APPLICANT: Yan, Hai
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PROTEIN
; TITLE OF INVENTION: PHOSPHOTYROSINE PHOSPHATASE-SIGMA
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/716.679

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Alignment Scores:		
Pred. No.:	7,98e-09	Length: 5690
Score:	218.50	Matches: 67

Percent Similarity:	47.93%	Conservative:	37
Best Local Similarity:	30.88%	Mismatches:	74
Query Match:	14.81%	Indels:	39
DB:	2	Gaps:	11

US-10-047-021-86_COPY_28_303 (1-276) x US-08-716-679-2 (1-5690)

QY	2	AppSerProProGlnIleuValHisProGlnAaspGlnLeuPheGlnGlyProGlyPro	21
DB	920	GAAGAGCCACCCAGCATTTTACAGAGAGCCCAAGGATCAGATTGGTGTGTGCAGAGGCGGTG	979
QY	22	AlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTrp	38
DB	980	GCCTCCTTCGTGTCAGAGCCACAGGTGACCTTAAGCCACGGGTGACCTGGAAACAAGAG	1039
QY	39	-----LeuLeuAsnGlyGlnProLeuSerMetValProProAaspProHisLeuLeu	56
DB	1040	GGCAGAAAAGTGAATCACAAGCGCTTTTGAGACCAITTGACTTTGACGAG	1087
QY	57	ProAaspGlyThrLeuLeuLeuLeuGlnProProAlaAlaArgGlyHisAlaHisaspGlyGln	76
DB	1088	AGTCGGGGCGCGTGTGAGGATCAGACCA	1117
QY	77	AlaLeuSerThr-----AspLeuGlyValThrCysGluAlaSerAsnArgLeuGly	94
DB	1118	---CTTCGACACCCCGGATGAGAACGTGTACGAGTGTGTGCCCAGAACTCGGTGGGG	1174
QY	95	ThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIle	114
DB	1175	--GAGATCACAGTTTCATGCGAAGCTCAC--GTCTCTGAGAGGAC--CAGCTG	1222
QY	115	GlnProArgAspMetValAlaValValGlyGluGlnPhe	127
DB	1223	CCTCTCGGCTTCCCCAACATTGACATGGGCCCCCAGTGAAGTTGTAGAGGCGCACGC	1282
QY	128	-----ThrLeuGluCysGlyProProTrpGlyHisProGluProThrValSerTrpTrp	145
DB	1283	ACAGCCACCATGCTCTGTCTGCCAGC---GGAAACCTTGACCTGAGATCACTCGTTTC	1339
QY	146	LysAspGlyLysProLeu-----AlaLeuGlnProGlyArg---HisThrValSerGly	162
DB	1340	AAGGACTTCCTGCTGTGAGACCCCAAGTGCACCAATGGCGCGATTCAAGCAGCTTCGGTCA	1399
QY	163	GlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu**ThrTyrMetCysValAla	182
DB	1400	GGTGCCTCGATTGAGAGCAGCGAGGAGACAGACCGAGCCAGGCAAGTACAGAGTGTGTGGCC	1459
QY	183	ThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGln	199
DB	1460	ACCAACAGCGCTGGGTGGGTGCTACTCATCACTCGCCAACTCTACGTGCGA	1510

RESULT 4

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US-09-016-434-1132
; Sequence 1132, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhammer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1132:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4078 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1407624
; US-09-016-434-1132

Alignment Scores:
Pred. No.: 5,3e-08 Length: 4078
Score: 206.50 Matches: 83
Percent Similarity: 42.36% Conservativity: 39
Best Local Similarity: 28.82% Mismatches: 94
Query Match: 14.00% Indels: 74
DB: 4 Gaps: 16

US-10-047-021-86_COPY_28_303 (1-276) x US-09-016-434-1132 (1-4078)

Qy 2 AspSerProGlnIleuValHisProGlnAspGlnLeuPheGlnGlyProGlyPro 21
Db 110 GAAGAGCCCCCAGGTTTATCAAGAACCCAGGACGAGTCGGCGTCTCGGGCGGTG 169
Qy 22 AlaArgMetSerCysArgAlaSerGlyGlnProProProThrIleArgTyr 38
Db 170 GCCTCTTTCGTGTGTGAGCCAGCGGTGACCCAGCCAGCCAGCCAGCCAGCCAG 229
Qy 39 -----LeuLeuAspGlyGlnProLeuSerMetValProProAspProHisLeuLeu 56
Db 230 GGCAGAGAGGTCACCTCTCAGCGCTTTCAGACGATTGAGTTTGTATGAG----- 277
Qy 57 ProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGln 76
Db 278 AGTCAGGGGAGTGTCTGAGGATCCAGCCG----- 307
Qy 77 AlaLeuSerThr-----AspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGly 94
Db 308 ---CTGAGGACACCCCGGATGMAAACGTGTACGAGTGTGTGGCCAGCACTCGTGGG 364
Qy 95 ThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAsp----- 111
Db 365 ---GAGATCACAGTCCATGCGCAAGCTTACT-----GTCCTCCGAGAGGACCACTGCC 415
Qy 112 -----PheGlnIleGlnProArgAspMetValAlaValAlaValGlyGluGln 126
Db 416 TCTGCTTCCCAACATCGATGGCCCGCAGTTGAGGTGTGGAGCGGACAGGACA 475
Qy 127 PheThrLeuGluCysGlyProProProThrGlyHisProGluProThrValSerTyrTrp 146
Db 476 GCCACCATGCTCTGTGACCCAGC---GGCAACCCCTGACCTGAGATCACCTGTTCAAG 532
Qy 147 AspGlyLysProLeu-----AlaLeuGlnProGlyArg-----HisThrValSerGlyGly 163
Db 533 GACTTCTCGCTGTGGATCTCTGAGCCAGCAATGAGCGCATCAACACAGCTCGCATCAGA 592
Qy 164 SerLeuLeuMetAlaArgAlaGluLysSerAspGlu***ThrTyrMetCysValAlaThr 183

; US-08-348-006B-6
; Sequence 6, Application US/08348006B
; Patent No. 5658756
; GENERAL INFORMATION:
; APPLICANT: RODAN, GIDEON A.
; APPLICANT: SCHMIDT, AZRIEL
; APPLICANT: RUTLEDGE, SU JANE
; TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
; TITLE OF INVENTION: TYROSINE PHOSPHATASE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: J. MARK HAND
; STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/348,006B
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/122,032
; FILING DATE: 14-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: HAND, J., MARK
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: 189921A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-594-3905
; TELEFAX: 908-594-4720
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6000 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-08-348-006B-6

Alignment Scores:
Pred. No.: 8.63e-08 Length: 6000
Score: 206.50 Matches: 83
Percent Similarity: 42.36% Conservativity: 39
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Best Local Similarity: 28.82% Mismatches: 94
Query Match: 14.00% Indels: 74
DB: 1 Gaps: 16

US-10-047-021-86_COPY_28_303 (1-276) x US-08-348-006B-6 (1-6000)

QY 2 AspSerProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGlyPro 21
DB 110 GAAGAGCCCCCAGGTTTATCAAGAACCACGAGGACGATCGGGGTGTGCGGGGGTGTG 169
QY 22 AlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTrp----- 38
DB 170 GCCTCTTCGTGTGTCAGGCCAGGTGACCCCAAGCCAGGACCTGGAAACAGAG 229
QY 39 -----LeuLeuAsnGlyGlnProLeuSerMetValProAspProHisHisLeuLeu 56
DB 230 GCACAAGAGTCACTCTCAGCGCTTGAGACGATTGAGTTGATGAG----- 277
QY 57 ProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGln 76
DB 278 AGTGCGAGGGCGAGTGTGAGGATCCAGCG----- 307
QY 77 AlaLeuSerThr-----AspLeuGlyValThrCysGluAlaSerAsnArgLeuGly 94
DB 308 ---CTGAGGACACCGCGGATGAAACCTGACGAGTGTGTGCGCCACGAACTCGGTGG 364
QY 95 ThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAsp----- 111
DB 365 ---GAGATCACAGCTCATGCCCAAGTTACT-----GTCTCCGAGAGGACCACTGGCC 415
QY 112 -----PheGlnIleGlnProArgAspMetValAlaValIleGlyGln 126
DB 416 TCTGCTTCCCAACATCGACATGGGCCACAGTTGAAGGTGTGAGGCGGACGACGACA 475

Alignment Scores:
Pred. No.: 8,63e-08 Length: 6000
Score: 206.50 Matches: 83
Percent Similarity: 42.36% Conservative: 39
Best Local Similarity: 28.82% Mismatches: 74
Query Match: 14.00% Indels: 94
DB: 2 Gaps: 16

US-10-047-021-86_COPY_28_303 (1-276) x US-08-800-825A-6 (1-6000)

QY 2 AspSerProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGlyPro 21
DB 110 GAAGAGCCCCCAGGTTTATCAAGAACCACGAGGACGATCGGGGTGTGCGGGGGTGTG 169
QY 22 AlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTrp----- 38
DB 170 GCCTCTTCGTGTGTCAGGCCAGGTGACCCCAAGCCAGGACCTGGAAACAGAG 229
QY 39 -----LeuLeuAsnGlyGlnProLeuSerMetValProAspProHisHisLeuLeu 56
DB 230 GCACAAGAGTCACTCTCAGCGCTTGAGACGATTGAGTTGATGAG----- 277
QY 57 ProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGln 76
DB 278 AGTGCGAGGGCGAGTGTGAGGATCCAGCG----- 307
QY 77 AlaLeuSerThr-----AspLeuGlyValThrCysGluAlaSerAsnArgLeuGly 94
DB 308 ---CTGAGGACACCGCGGATGAAACCTGACGAGTGTGTGCGCCACGAACTCGGTGG 364
QY 95 ThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAsp----- 111
DB 365 ---GAGATCACAGCTCATGCCCAAGTTACT-----GTCTCCGAGAGGACCACTGGCC 415
QY 112 -----PheGlnIleGlnProArgAspMetValAlaValIleGlyGln 126
DB 416 TCTGCTTCCCAACATCGACATGGGCCACAGTTGAAGGTGTGAGGCGGACGACGACA 475

US-08-800-825A-6
Alignment Scores:
Pred. No.: 8,63e-08 Length: 6000
Score: 206.50 Matches: 83
Percent Similarity: 42.36% Conservative: 39
Best Local Similarity: 28.82% Mismatches: 74
Query Match: 14.00% Indels: 94
DB: 2 Gaps: 16

US-10-047-021-86_COPY_28_303 (1-276) x US-08-800-825A-6 (1-6000)

QY 2 AspSerProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGlyPro 21
DB 110 GAAGAGCCCCCAGGTTTATCAAGAACCACGAGGACGATCGGGGTGTGCGGGGGTGTG 169
QY 22 AlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTrp----- 38
DB 170 GCCTCTTCGTGTGTCAGGCCAGGTGACCCCAAGCCAGGACCTGGAAACAGAG 229
QY 39 -----LeuLeuAsnGlyGlnProLeuSerMetValProAspProHisHisLeuLeu 56
DB 230 GCACAAGAGTCACTCTCAGCGCTTGAGACGATTGAGTTGATGAG----- 277
QY 57 ProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGln 76
DB 278 AGTGCGAGGGCGAGTGTGAGGATCCAGCG----- 307
QY 77 AlaLeuSerThr-----AspLeuGlyValThrCysGluAlaSerAsnArgLeuGly 94
DB 308 ---CTGAGGACACCGCGGATGAAACCTGACGAGTGTGTGCGCCACGAACTCGGTGG 364
QY 95 ThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAsp----- 111
DB 365 ---GAGATCACAGCTCATGCCCAAGTTACT-----GTCTCCGAGAGGACCACTGGCC 415
QY 112 -----PheGlnIleGlnProArgAspMetValAlaValIleGlyGln 126
DB 416 TCTGCTTCCCAACATCGACATGGGCCACAGTTGAAGGTGTGAGGCGGACGACGACA 475

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RESULT 6

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US-08-800-825A-6
; Sequence 6, Application US/08800825A
; Patent No. 5866397
; GENERAL INFORMATION:
; APPLICANT: RODAN, GIDEON A.
; APPLICANT: SCHMIDT, AZRIEL

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Qy 127 PheThrLeuGluCysGlyProProTrpGlyHisProGluProThrValSerThrTrpTyr 146
Db 476 GCCACCATGCTGTGCAGCCAGC---GGCAACCTGACCTGAGATCACCCTGTTCAAG 532
Qy 147 AspGlyLysProLeu-----AlaLeuGlnProGlyArg---HisThrValSerGlyGly 163
Db 533 GACTTCCTGCTGTGGATCCTAGTGCCAGCAATGGAGCATCAACAGCTCGCATCAGGA 592
Qy 164 SerLeuLeuMetAlaArgAlaGluLysSerAspGlu***ThrTyrMetCysValAlaThr 183
Db 593 GCCCTGCAGATTGAAGCAGTGCAGGAACACCGACCGGCAATATGAGTGTGTGGCCACC 652
Qy 184 AsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGluProGlnAsp 203
Db 653 AACAGCGCCGCGTGGC----- 670
Qy 204 TyrThrGluProValGluLeuAlaValArgIleGlnLeuGluAsnValThrLeuLeu 223
Db 671 TACTCTCACCTGCCAACCTCTAC---GTGGAGTCCGCGC---CGTGGCCCGCGCTTCTC 726
Qy 224 AsnPro-----AspProAlaGluGlyProLysProArgProAlaValTrp 238
Db 727 CATCTGCTCCATGAGCCAGCATCATGCCAGGGGGCAACGTGAACATCA---CTGCGCTGG 785
Qy 239 Leu***TrpLysValSerGlyPro***ArgLeuProAsnLeuThrArgProCys----- 256
Db 786 ---CCGTGG-----GCTCGCCCATGCCATCAG 809

RESULT 7
US-09-158-657-6
; Sequence 6, Application US/09158657
; Patent No. 6214564
; GENERAL INFORMATION:
; APPLICANT: RODAN, GIDEON A.
; APPLICANT: SCHMIDT, AZRIEL
; APPLICANT: RUTLEDGE, SU JANE
; TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
; TITLE OF INVENTION: TYROSINE PHOSPHATASE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: J. MARK HAND - MERCK & CO., INC.
; STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/158,657
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/800,825
; FILING DATE: 14-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: HAND, J. MARK
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: 18992DA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-3905
; TELEFAX: 732-594-4720
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6000 base pairs
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-158-657-6

Alignment Scores:
Pred. No.: 8,63e-08 Length: 6000
Score: 206.50 Matches: 83
Percent Similarity: 42.36% Conservatives: 39
Best Local Similarity: 28.82% Mismatches: 94
Query Match: 14.00% Indels: 74
DB: 3 Gaps: 16

US-10-047-021-86_COPY_28_303 (1-276) x US-09-158-657-6 (1-6000)
Qy 2 AspSerProProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGlyPro 21
Db 110 GAAGAGCCCCCAGGTTTATCAAGAAACCCAGGACGATCGCGGTGTCGGGCGGTG 169
Qy 22 AlaArgMetSerCysArgAlaSerGlyGlnProProProThrIleArgTrp----- 38
Db 170 GCCTCTTTCGTGTGTGAGCCCGGTGACCCCAAGCCAGAGTGCCTGGAAACAAGAAG 229
Qy 39 -----LeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeu 56
Db 230 GGCAAGAGGTCACTCTCAGCGCTTGACACGATTGAGTTTGATGAG----- 277
Qy 57 ProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGln 76
Db 278 AGTGCAGGGGCGAGTGTGAGGATCCAGCCG----- 307
Qy 77 AlaLeuSerThr-----AspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGly 94
Db 308 ---CTGAGGACACCGCGGATGAAAGCTAGAGTGTGTGCCCAAGACTCGTGTGG 364
Qy 95 ThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAsp----- 111
Db 365 ---GAGATCACAGTCCATGCGCAAGCTTACT-----GTCTCCGAGAGGACGAGTGC 415
Qy 112 -----PheGlnIleGlnProArgAspMetValAlaValValGlyGluGln 126
Db 416 TCTGGCTTCCCAACATCGACATGGGCCACAGTTGAAGGTGTGGAGCGGACACGACGA 475
Qy 127 PheThrLeuGluCysGlyProProTrpGlyHisProGluProThrValSerTrpTyr 146
Db 476 GCCACCATGCTGTGTGCAGCCAGC---GGCAACCTGACCTGAGATCACCCTGTTCAAG 532
Qy 147 AspGlyLysProLeu-----AlaLeuGlnProGlyArg---HisThrValSerGlyGly 163
Db 533 GACTTCCTGCTGTGGATCCTAGTGCCAGCAATGGAGCATCAACAGCTCGCATCAGGA 592
Qy 164 SerLeuLeuMetAlaArgAlaGluLysSerAspGlu***ThrTyrMetCysValAlaThr 183
Db 593 GCCCTGCAGATTGAAGCAGTGCAGGAACACCGACCGGCAATATGAGTGTGTGGCCACC 652
Qy 184 AsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGluProGlnAsp 203
Db 653 AACAGCGCCGCGTGGC----- 670
Qy 204 TyrThrGluProValGluLeuAlaValArgIleGlnLeuGluAsnValThrLeuLeu 223
Db 671 TACTCTCACCTGCCAACCTCTAC---GTGGAGTCCGCGC---CGTGGCCCGCGCTTCTC 726
Qy 224 AsnPro-----AspProAlaGluGlyProLysProArgProAlaValTrp 238
Db 727 CATCTGCTCCATGAGCCAGCATCATGCCAGGGGGCAACGTGAACATCA---CTGCGCTGG 785
Qy 239 Leu***TrpLysValSerGlyPro***ArgLeuProAsnLeuThrArgProCys----- 256
Db 786 ---CCGTGG-----GCTCGCCCATGCCATCAG 809
Qy 257 ---SerGlyProArgLeuProArg 263
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Db      810 TGAAGTGGATGCAGGGGCGCGAGG 833
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PCT-US94-10166-6
; Sequence 6, Application PC/TUS9410166
; GENERAL INFORMATION:
; APPLICANT: RODAN, GIDEON A
; APPLICANT: RODAN, GIDEON A
; APPLICANT: SCHMIDT, AZRIEL
; APPLICANT: RUTLEDGE, SU JANE
; TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
; TITLE OF INVENTION: TYROSINE PHOSPHATASE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESS: JOHN W. WALLEN III
; STREET: P.O. BOX 2000, 126 E. LINCOLN AVE.
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10166
; FILING DATE: 09-SEPT-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; FILING DATE: US 08/122,032
; FILING DATE: 14-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WALLEN, JOHN W III
; REGISTRATION NUMBER: 35403
; REFERENCE/DOCKET NUMBER: 18992
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-594-3905
; TELEFAX: 908-594-4720
; TELEX: 138825
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6000 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
PCT-US94-10166-6
Alignment Scores:
Pred. No.:      8 63e-08      Length:      6000
Score:          206.50      Matches:      83
Percent Similarity: 42.36%      Conservative: 39
Best Local Similarity: 28.82%      Mismatches: 94
Query Match:      5         Indels:      74
DB:              16         Gaps:      16
US-10-047-021-86_COPY_28_303 (1-276) x PCT-US94-10166-6 (1-6000)
Qy      2 AspSerProGlnLeuValHisProGlnAspGlnLeuPheGlnGlyProGlyPro 21
||||| ||| |||||
Db      110 GAAGAGCCCCCAGGTTTATCAAGAACCCCAAGGACCATGCGGTGTCGGGGCGGTG 169
||||| ||| |||||
Qy      22 AlaArgMetSerCysArgAlaSerGlyGlnProProProThrIleArgTrp----- 38
||||| ||| |||||
Db      170 GCCTCTTTCGTGTGTGACGCCACGGGTGACCCCAAGCCACGAGTGACCTGGAAACAAGAG 229
||||| ||| |||||
Qy      39 -----LeuLeuAsnGlyGlnProLeuSerMetValProAspProHisHisLeuLeu 56
||||| ||| |||||
Db      230 GCAAGAAGGTCAACTCTCAGCGCTTTGAGACGATGAGTTGATGAG----- 277
||||| ||| |||||
Qy      57 ProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGln 76
||||| ||| |||||
```

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Db      278 AGTCAGGGGCGAGTGTGAGGATCCAGCCG----- 307
Qy      77 AlaLeuSerThr-----AspLeuGlyValThrCysGluAlaSerAsnArgLeuGly 94
||||| ||| |||||
Db      308 ---CTGAGGACACCGCGGATGAAACGTTACGAGTGTGTGGCCAGAACTCGTTGGG 364
||||| ||| |||||
Qy      95 ThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAsp----- 111
||||| ||| |||||
Db      365 ---GAGATCACAGTCCATGCCAAGCTTACT-----GTCTCCGAGAGGACCGCTGCC 415
||||| ||| |||||
Qy      112 -----PheGlnIleGlnProArgAspMetValAlaValAlaValGlyGln 126
||||| ||| |||||
Db      416 TCTGGCTTCCCAACATCGACATGGGCCCAAGTGAAGGTGGTGGAGCCGACACGGACA 475
||||| ||| |||||
Qy      127 PheThrLeuGluCysGlyProProThrGlyHisProGluProThrValSerTrpTrpLys 146
||||| ||| |||||
Db      476 GCCACCATGCTCTGTGCAGCCAGC---GGCAACCTTGACCTGAGATCACCTGGTTCAAG 532
||||| ||| |||||
Qy      147 AspGlyLysProLeu-----AlaLeuGlnProGlyArg---HisThrValSerGlyGly 163
||||| ||| |||||
Db      533 GACTTCTGCTGTGGATCTCTAGTCCAGCAATGAGCGCATCAACACAGCTGCGATCAGGA 592
||||| ||| |||||
Qy      164 SerLeuLeuMetAlaArgAlaGluLysSerAspGlu***ThrTyrMetCysValAlaThr 183
||||| ||| |||||
Db      593 GCCCTGCAGATTGAAGCAGTGGAGAAACCCAGCCAGGCAAAATATGAGTGTGTGGCCACC 652
||||| ||| |||||
Qy      184 AsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGluProGlnAsp 203
||||| ||| |||||
Db      653 AACAGCGCGCGGTGCGC----- 670
Qy      204 TyrThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluAsnValThrLeuLeu 223
||||| ||| |||||
Db      671 TACTCTCCTCAGCTGCCAACCTCTAC---GTGCGAGTCCGCGC---GTGGGCGCGCTTCTC 726
||||| ||| |||||
Qy      224 AsnPro-----AspProAlaGluGlyProLysProArgProAlaValTrp 238
||||| ||| |||||
Db      727 CATCTGCCCCATGAGCCACGAGATCATGCCAGGGGGCAACGTGAACATCA-CCTCGGTGG 785
||||| ||| |||||
Qy      239 Leu***TrpLysValSerGlyPro***ArgLeuProAsnLeuThrArgProCys----- 256
||||| ||| |||||
Db      786 ---CCGTGG-----GCTCGCCCATGCCATACG 809
||||| ||| |||||
Qy      257 ---SerGlyProArgLeuProArg 263
||||| ||| |||||
Db      810 TGAAGTGGATGCAGGGGCGCGAGG 833
||||| ||| |||||
RESULT 9
US-08-506-296B-13
; Sequence 13, Application US/08506296B
; Patent No. 6313265
; GENERAL INFORMATION:
; APPLICANT: Phillips, Greg
; APPLICANT: Cunningham, Bruce A.
; APPLICANT: Crossin, Kathryn L.
; TITLE OF INVENTION: NEURITE OUTGROWTH-PROMOTING POLYPEPTIDES
; TITLE OF INVENTION: CONTAINING FIBRONECTIN TYPE III REPEATS AND METHODS OF USE
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute
; STREET: 10550 No. 6313265th Torrey Pines Road, TPC-8
; CITY: La Jolla
; STATE: California
; COUNTRY: U.S.
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/506,296B
; FILING DATE: 24-JUL-1995
; CLASSIFICATION: 514
```

ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 488.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 554-2937
TELEFAX: (619) 554-6312
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 3888 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 12..3773
US-08-506-296B-13

Alignment Scores:
Pred. No.: 5,498-08 Length: 3888
Score: 206.00 Matches: 87
Percent Similarity: 37.42% Conservative: 35
Best Local Similarity: 26.69% Mismatches: 106
Query Match: 13.97% Indels: 98
Gaps: 4

US-10-047-021-86_COPY_28_303 (1-276) x US-08-506-296B-13 (1-3888)

QY 1 GlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGly 20
Db 126 GAACAGTCTCCACGGCGCTGGTGTCTTCCACAGATGATC----- 170
QY 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProProThrIleArgTrpLeuLeu 40
Db 171 -----AGCCTCAAGTGTGAGCGCAGTGGCAAGCCGGAAGTGCAGTTCGCTGGACGAGG 224
QY 41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60
Db 225 GATGTGTGTC-----CACTCAACCCCAAGGAAGAG 254
QY 61 Leu-----LeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeu 78
Db 255 CTGGTGTGACCGTGTACAGTCGCGC-----CACTCTGGCTCTTCCACC 299
QY 79 SerThrAsp-----LeuGlyValTyrThrCysGluAla 89
Db 300 ATCACGGGCAACACAGCAACTTTGCTCAGAGTTCCAGGGCATCTACCGTGTCTTGGCC 359
QY 90 SerAsnArgLeuGlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArg 109
Db 360 AGCATATAGCTGGGACCGCCGATGCTCCATGATGCCGCTC-----ATGCC 407
QY 110 GlnAspPheGlnIleGlnProArgAspMetValAlaValVal-----GlyGlu 125
Db 408 GAGGTGCGCCCAAGTGGCCAAAGGACAGACAGTGAAGCCCGTGGAGGTGGAGAGGGGAG 467
QY 126 GlnPheThrLeuGluCysGlyProProTrpGlyHisProGluProThrValSerTrpTrp 145
Db 468 TCAGTGGTTCCTGCTTGAACCTCC-----CCAAAGTCAGAGCGCTCTCCGATCTACTGG 524
QY 146 LysAspGlyLysProLeuAlaGlnProGlyArgHisThrValSerGly-----Gly 163
Db 525 ATGACACCAAGATCTTCAATGAGCAGGACGAGCGGGTGCAGTGGGCCAAGCGGC 584
QY 164 SerLeuLeuMetAlaArgAlaGluLysSerAspGlu***Thr---TyrMetCysValAla 182
Db 585 AACCTCTACTTGGCAATGTCTCACCTCCCAACCACTCAGACTACATCTGC----- 638
QY 183 ThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGluProGln 202
Db 183 ThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGluProGln 202

639 -----CACGCCCACTTCCAGGCCACAGGACCATCATTCAGAAG----- 677
QY 203 AspTyrThrGluProValGluLeuAlaValAlaValArgIleGlnLeuGluAsnValThrLeu 222
Db 678 -----GAACCCATTGACCTC-----CGGGTCAAGGCCACCAAC---AGCATG 716
QY 223 LeuAsnProAspPro-AlaGluGlyProLysProArgProAlaVal-----Trp-Leu* 240
Db 717 ATTACAGAGGAGCGCGCTCTTCCCCACCACTCCAGCAGCCACCTGTGGCTTTG 776
QY 240 **TrpLysValSerGlyPro***----- 247
Db 777 CAGGGCAGCCATTGGTCTGGAGTGCATCCGAGGCTTTCCAGCCGCCCATCAAA 836
QY 248 -----ArgLeuProAsnLeuThrArgProCysSerGlyPro----- 259
Db 837 TGGCTGCGCCCGCAGTGGCCCCATCCAGCGGACCGTGTCTACCTACCAAGAACCAACAAG 896
QY 260 -----ArgLeuProArgGluAlaArgG 267
Db 897 ACCCTGCAGCTGTGAAAGTGGCGAGGAGGATGATGGCGAGTACCGCTGCTGGCCGAG 956

RESULT 10
US-09-041-886-24
Sequence 24, Application US/09041886
Patent No. 6235872
GENERAL INFORMATION:
APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharoz
TITLE OF INVENTION: Proapoptotic Peptides, Dependence
TITLE OF INVENTION: Polypeptides and Methods of Use
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2626
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 4608 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..4342
US-09-041-886-24

Alignment Scores:
Pred. No.: 6,818-08 Length: 4608

Score: 206.00 Matches: 68
Percent Similarity: 42.80% Conservative: 36
Best Local Similarity: 27.98% Mismatches: 97
Query Match: 13.97% Indels: 42
DB: 3 Gaps: 11

US-10-047-021-86_COPY_28_303 (1-276) x US-09-041-886-24 (1-4608)

QY 24 MetSerCysArgAlaSerGlyGlnProProThrThrLeuLeuAsnGlyGln 43
DB 475 CTCAGTGTGAAGTCAATGGGAGGCCATGCCAACATCCATGCGAGAACCAACAA 534

QY 44 ProLeuSerMetValProAspProHis---HisLeuLeuProAspGlyThrLeuLeu 62
DB 535 GACCTGACTCCCAATCCAGGTGACTCCCGAGTGGTGTCTTGCCTCTGGAGCATTCGAG 594

QY 63 Leu-----LeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80
DB 595 ATCAGCCGACTCCCAACCG-----GGG 615

QY 81 AspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArg--- 99
DB 616 GACATTGGAATTTACGATGCTCAGCTCGAAT-----CCAGCCAGCTCAGAACAA 666

QY 100 GlyAlaArgLeuSerValAlaValLeuArgGluAsp-----Phe 112
DB 667 GAAATGAAGCAGAGTCAAGATTTTATCAGATCCAGGACTGCATAGACAGCTGTATTTT 726

QY 113 GlnIleGlnProArgAspMetValAlaValGlyGluGlnPheThrLeuGluCysGly 132
DB 727 CTCGAAAGACCAATCAATGTAGTAGCCATTGAAGGAAAAGATGCTGTCTCGAATGTTGT 786

QY 133 ProProTyrGlyHisProGluProThrValSerTyrTyrLysAspGlyLysProLeuAla 152
DB 787 GTTCTC---GGTATCCTCCACCAAGTTTACTGTGTACGAGGCGGAGGAGTCAACAA 843

QY 153 LeuGlnProGlyArgHisThrValSerGlyGlySer---LeuLeuMetAlaArgAlaGlu 171
DB 844 CTCAGGTCTAAAAGATTTCTTTATTGGTGGTGAAGCAACTTGTCTTCAATGTGACA 903

QY 172 LysSerAspGlu---ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSer 191
DB 904 GATGATGACAGTGGGAATGTATACCTGTGTGTGCACATATATAAATGAGAATATTAGTGC 963

QY 192 ArgAlaAlaArgValSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeu 211
DB 964 TCTGACAGCTCACAGTCTTGTGTTCGCGCATGGTTTTTAATCATCTCTTCAACCTGTAT 1023

QY 212 Ala-----ValArgIleGlnLeuGluAsnValThrLeuLeuAsnProAspProAla 228
DB 1024 GCCTATGAAGCATGGATATTGAGTTTGAATGTACAGTC-----1062

QY 229 GluGlyProLysProArgProAlaValTyrLeu---TyrLysValSerGlyPro---Arg 248
DB 1063 ---CTGGAAGCCTGTGCCCATCTGTG-----AATTGGATGAAGATGAGATGTGTC 1113

QY 249 LeuProAsn 251
DB 1114 ATTCCTAGT 1122

RESULT 11

PCT-US94-05277-1

; Sequence 1, Application PC/TUS9405277

; GENERAL INFORMATION:

; APPLICANT: Bruskin, Arthur

; APPLICANT: Jarosz, David E.

; APPLICANT: Johnson, Karen

; APPLICANT: Kinzler, Kenneth W.

; APPLICANT: Vogelstein, Bert

; APPLICANT: Zabrecky, James R.

; TITLE OF INVENTION: Antibodies Specific for DCC Gene Product

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05277
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/POCKET NUMBER: 01107.42709
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202.508.9100
TELEFAX: 202.508.9299
TELEX: 197430 BBNB UT
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4608 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 18q21
FEATURE:
NAME/KEY: CDS
LOCATION: 1..4342
PCT-US94-05277-1

Alignment Scores:

Pred. No.: 6.81e-08 Length: 4608
Score: 206.00 Matches: 68
Percent Similarity: 42.80% Conservative: 36
Best Local Similarity: 27.98% Mismatches: 97
Query Match: 13.97% Indels: 42
DB: 5 Gaps: 11

US-10-047-021-86_COPY_28_303 (1-276) x PCT-US94-05277-1 (1-4608)

QY 24 MetSerCysArgAlaSerGlyGlnProProThrThrLeuLeuAsnGlyGln 43
DB 475 CTCAGTGTGAAGTCAATGGGAGGCCATGCCAACATCCATGCGAGAACCAACAA 534

QY 44 ProLeuSerMetValProAspProHis---HisLeuLeuProAspGlyThrLeuLeu 62
DB 535 GACCTGACTCCCAATCCAGGTGACTCCCGAGTGGTGTCTTGCCTCTGGAGCATTCGAG 594

QY 63 Leu-----LeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80
DB 595 ATCAGCCGACTCCCAACCG-----GGG 615

QY 81 AspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArg--- 99
DB 616 GACATTGGAATTTACGATGCTCAGCTCGAAT-----CCAGCCAGCTCAGAACAA 666

QY 100 GlyAlaArgLeuSerValAlaValLeuArgGluAsp-----Phe 112
DB 667 GAAATGAAGCAGAGTCAAGATTTTATCAGATCCAGGACTGCATAGACAGCTGTATTTT 726

QY 113 GlnIleGlnProArgAspMetValAlaValGlyGluGlnPheThrLeuGluCysGly 132
DB 727 CTCGAAAGACCAATCAATGTAGTAGCCATTGAAGGAAAAGATGCTGTCTCGAATGTTGT 786

Db 727 CTGCAAGACCAATCAATGTAGTAGCATTGAAGGAAAGATGCTGCTCGAATGTGT 786
Qy 133 ProProTrrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAla 152
Db 787 GTTCTCT---GGCTATCTCCACCAAGTTTACCTGGTTACGAGCGGAGAGTCAATCAA 843
Qy 153 LeuGlnProGlyArgHisThrValSerGlyGlySer---LeuLeuMetAlaArgAlaGlu 171
Db 844 CTCAGGTCATAAAGATTCTTTATTGGTGGAGACCACTTGCTTAATCTCAATGTGACA 903
Qy 172 LysSerAspGlu***ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSer 191
Db 904 GATGATCAGACAGTGAATGATATACCTGTCTGTCTCATATATAAATAATGAAATATTAGTCC 963
Qy 192 ArgAlaAlaArgValSerIleGlnGluProGlnAspTyrThrGluProValGluLeu 211
Db 964 TCTGAGAGCTCAGACTCTGGTTCGCGCCATGGTTTAAATCATCTCTTCCAACTGTAT 1023
Qy 212 Ala-----ValArgIleGlnLeuGluAsnValThrLeuLeuAsnProAspProAla 228
Db 1024 GCCTATGAACATGGATATTGAGTTTGATGTACAGTC-----1062
Qy 229 GluGlyProLysProArgProAlaValTrpLeu***TrpLysValSerGlyPro***Arg 248
Db 1063 ---TCTGAAAGCCTGTGCCACTGTG-----AATTGGATGAAGAATGGAGATGTGTC 1113
Qy 249 LeuProAsn 251
Db 1114 ATTCTTAGT 1122

RESULT 12

US-09-638-649-2
; Sequence 2, Application US/09638649
; Patent No. 6563015
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Yan, Shi Du
; TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED
; TITLE OF INVENTION: GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 0575/62175
; CURRENT APPLICATION NUMBER: US/09/638,649
; CURRENT FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1426
; TYPE: DNA
; ORGANISM: Bos Taurus
US-09-638-649-2

Alignment Scores:

Pred. No.:	5,96e-08	Length:	1426
Score:	199.00	Matches:	89
Percent Similarity:	38.63%	Conservative:	35
Best Local Similarity:	27.73%	Mismatches:	122
Query Match:	13.49%	Indels:	76
DB:	4	Gaps:	17

US-10-047-021-86_COPY_28_303 (1-276) x US-09-638-649-2 (1-1426)

Qy 5 ProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGly---ProGlyProAlaArg 23
Db 376 CCAGAAAT---GTTGATCGCTCTGAATCATGCTGTGTGTCCTCCCAATAAGGTGGG 432
Qy 24 MetSerCysArgAlaSerGlyGlnProProThrIleArgTrpLeuLeuAsnGlyGln 43
Db 433 ACATGTGTGTCGAGGGGGGTACCTCGAGGGACTCTTAATCTGCTCTTGATGGGAAA 492
Qy 44 ProLeuSerMetValProProAspProHisIleLeuLeuProAspGlyThrLeuLeu 63
Db 493 ACT-----CTGATTCCTGATGTGCAAGAGGATGTCA 522

Qy 64 LeuGlnProProAlaArgGlyHisAlaHisAspGlyGln---AlaLeuSerThrAspLeu 82
Db 523 GTNAGGAAGAGACCAAGACACACCCAAAGACAGGGGCTTTTCAGCTCCATTCGGAGCTG 582
Qy 83 GlyVal-----TyrThrCysGluAlaSer---90
Db 583 ATGCTGACCCACAGCTCGGGGAGGAGCTCTCACCCACCTCTCTCTAGCTTCAACCCCT 642
Qy 91 -----AsnArgLeuGlyThrAlaVal-----97
Db 643 GGCTTTCCCGCGCCGAGCCCTGCACAGCGCCCAATCCAGTCCAGGCTCGAGGTCTGAGTGAG 702
Qy 98 -----SerArgGlyAlaArgLeuSerValAlaValLeuArgGlu---AspPheGln 113
Db 703 CACGAGGTGGGAGGGCCCAACAGTGGAGCGCTGTGCCACTGAAGAGTCCAGTTCGTGTG 762
Qy 114 IleGlnProArgAspMetValAlaValIleGlnPheThrLeuGluCysGlyPro 133
Db 763 GTAGAGCCAGAGGGGAGCAGTAGCTCTCTGGTGTACTGTGACCTTGACCTGTGAAGCC 822
Qy 134 ProTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeu 153
Db 823 CCC---GCCAGAGCCCACTCAATCCACTGATCAAGATGCGAGCGCCCTGCCCTT 879
Qy 154 GlnProGlyArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSer 173
Db 880 CCCCT-----GGCCCATGCTGCTCTCCAGAGTAGGCGCTGAG 921
Qy 174 AspGlu***ThrTyrMetCysValAlaThrAsn---SerAlaGlyHisArgGluSerArg 192
Db 922 -GACCAAGGAACTACAGTTGTGTGGCCACCATCCAGCCATGGGCCCCAGGAGCGCT 981
Qy 193 AlaAlaArgValSerIleGlnGluProGlnAspTyrThrGluProValGluLeuAla 212
Db 982 GCTGTACGCTCAGATCATCGAA-----ACAGCGAGGAGGGGACGACTGCA 1029
Qy 213 ValArgIleGlnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLys 232
Db 1030 GGCTCTGTGAAGGGCGGGCTGGAAACCTAGC-CTGACCTCTGGGATCTCTGGGAGG 1088
Qy 233 Pro-----ArgProAlaValTrp-----Leu***TrpLysValSer-----244
Db 1089 CCTGGGACAGTCGCGCTGCTCATTTGGGTGTCGTGTGCATCGAAGCGGCAACGCAA 1148
Qy 245 -----GlyPro***ArgLeu-----ProAsnLeuThr 253
Db 1149 AGCACAGGAGGAGGAGGTCCTCCGAAACACAGGAGGAGGAGGAGGAGGAGCGAACT 1208
Qy 254 ArgProCysSerGlyProArgLeuProArgGlu-----AlaArgGluLeuArgGlyGln 271
Db 1209 GAACCAAGCAGAGAGCCCGAGCGGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1268
Qy 272 Arg 272
Db 1269 CGG 1271

RESULT 13

US-08-427-497E-6
; Sequence 6, Application US/08427497E
; Patent No. 5969124
; GENERAL INFORMATION:
; APPLICANT: Lemmon, Vance
; TITLE OF INVENTION: A Method for Characterizing the
; TITLE OF INVENTION: Nucleotide Sequence of LICAM and
; Patent No. 5969124
; TITLE OF INVENTION: the Nucleotide Sequence
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fay, Sharpe, Beall, Fagan,
; ADDRESSEE: Minnich & McKee
; STREET: 1100 Superior Avenue

STREET: Suite 700
CITY: Cleveland
STATE: Ohio
COUNTRY: U.S.A.
ZIP: 44114-2518
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
MEDIUM TYPE: Storable
COMPUTER: Compaq Prolinea 5100e
OPERATING SYSTEM: DOS 5.0
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/427,497E
FILING DATE: April 24, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/904,991
FILING DATE: June 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Minnich, Richard J.
REGISTRATION NUMBER: 24,175
REFERENCE/DOCKET NUMBER: CWR 2 149-3-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 861-5582
TELEFAX: (216) 241-1666
TELEX: (216) 980162
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1042
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: nucleic acids
HYPOTHETICAL: irrelevant
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: homo sapiens
INDIVIDUAL ISOLATE: 17-18 week fetus
IMMEDIATE SOURCE:
LIBRARY: Stratagene CDNA Library 936206
CLONE: C2
PUBLICATION INFORMATION:
AUTHORS: Hlavin, Mary Louise
AUTHORS: Lemmon, Vance
TITLE: Molecular structure and functional testing of
TITLE: human LiCAM: an interspecies comparison.
JOURNAL: GENOMICS
VOLUME: 11
ISSUE:
PAGES: 416-423
DATE: 1991
RELEVANT RESIDUES IN SEQ ID NO: -26 to 1016
US-08-427-497E-6

Alignment Scores:
Pred. No.: 4,86E-08 Length: 1042
Score: 198.00 Matches: 88
Percent Similarity: 36.59% Conservative: 32
Best Local Similarity: 26.83% Mismatches: 106
Query Match: 13.42% Indels: 102
DB: 2 Gaps: 19

US-10-047-021-86_COPY_28_303 (1-276) x US-08-427-497E-6 (1-1042)

QY 1 GlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGly 20
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141 GAACAGTCTCCACGGCGCTGTGTCTTCCCAAGATGACATC----- 185

QY 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTrpLeuLeu 40
::: ||||| ::::::::::: ||||| :::
186 -----AGCTTCAAGTGTGAGGCCAGTGGCAAGCCGAGTGCAGTTCGCTGGACGAGG 239

QY 41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60
::: ||||| ::::::::::: ||||| :::

NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fay, Sharpe, Beall, Pagan,
ADDRESSEE: Minnich & McKee
STREET: 1100 Superior Avenue
STREET: Suite 700
CITY: Cleveland
STATE: Ohio
COUNTRY: U.S.A.
ZIP: 44114-2518
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
MEDIUM TYPE: scorable
COMPUTER: Compaq Prolinea 5100e
OPERATING SYSTEM: DOS 5.0
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/427,497E
FILING DATE: April 24, 1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/904,991
FILING DATE: June 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Minnich, Richard J.
REGISTRATION NUMBER: 24,175
REFERENCE/DOCKET NUMBER: CWR 2 149-3-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 861-5582
TELEFAX: (216) 241-1666
TELEX: (216) 980162
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3774
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: nucleic acids
HYPOTHETICAL: irrelevant
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Homo Sapiens
INDIVIDUAL ISOLATE: 17-18 week fetus
IMMEDIATE SOURCE:
LIBRARY: Stratagene cDNA Library 936206
CLONE: synthesis of 4 clones
PUBLICATION INFORMATION:
AUTHORS: Hlavin, Mary Louise
AUTHORS: Lemmon, Vance
TITLE: Molecular structure and functional
TITLE: testing of human LiCAM: an
TITLE: interspecies comparison.
JOURNAL: GENOMICS
VOLUME: 11
ISSUE:
PAGES: 416-423
DATE: 1991
RELEVANT RESIDUES IN SEQ ID NO: 1 to 3774

Alignment Scores:
Pred. No.: 2,47e-07 Length: 3774
Score: 198.00 Matches: 88
Percent Similarity: 36.59% Conservative: 32
Best Local Similarity: 26.83% Mismatches: 106
Query Match: 13.42% Indels: 102
DB: 2 Gaps: 19

US-10-047-021-86_COPY_28_303 (1-276) x US-08-427-497E-1 (1-3774)

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Qy 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTrpLeuLeu 40
Db 160 -----AGCCTCAAGTGTGAGCCAGTGGCAAGCCGGAAGTGCAGTTCGCTCGGACGAGG 213
Qy 41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60
Db 214 GATGGTGTCT-----CACTTCAAAACCAAGGAAGAG 243
Qy 61 Leu-----LeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeu 78
Db 244 CTGGGTGTGACCGGTGTACCACTGCGCC-----CACTCTGGGTCTCTTACC 288
Qy 79 SerThrAsp-----LeuGlyValTyrThrCysGluAla 89
Db 289 ATCAGGGGCAACAACAGCAACTTTGCTCAGAGGTTCCAGGGCATCTACCGCTGCTTTGCC 348
Qy 90 SerAsnArgLeuGlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArg 109
Db 349 AGCAATAGCTGGGCACCGCCATGTCCCATGAGATCCGGCTC-----ATGGCC 396
Qy 110 GluAspPheGlnIleGlnProArgAspMetValAlaValVal-----GlyGlu 125
Db 397 GAGGTGTCCTCCAAAGTGGCCAAAGAGACAGACAGTGAAGCCCGTGGAGTGGAGGAAGGGAG 456
Qy 126 GlnPheThrLeuGluCysGlyProProTrpGlyHisProGluProThrValSerTrpTrp 145
Db 457 TCAGTGGTTCCTGCTTGGCAACCTCCC-----CCAAGTGCAGAGCTCTCCGGATCTACTGG 513
Qy 146 LysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrValSerGly-----Gly 163
Db 514 ATGAACAGCAAGATCTTGCACATCAAGCAGACGAGCGGTGACGATGGGCAGAACGCG 573
Qy 164 SerLeuLeuMetAlaArgAlaGluLysSerAspGlu***Thr---TyrMetCysValAla 182
Db 574 AACCTCTACTTTGCCAATGTGCTCCTCCGACAAACCACTCAGACTACTCTG----- 627
Qy 183 ThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGluProGln 202
Db 628 -----CAGGCCCACTTCCAGGCACCGAGGACCATCATTCAGAAG----- 666
Qy 203 AspTyrThrGluProValGluLeuAlaValArgIleGlnLeuGluAsnValThrLeu 222
Db 667 -----GAACCCATTGACCTC-----CGGTCAAGGCCCAAC---AGCATG 705
Qy 223 LeuAsnProAspPro-AlaGluGlyProLysProArgProAlaVal----- 237
Db 706 ATTGACAGGAAGCGCGCTCTGCTCTTCCCAACCACTCCAGCAGCCACTGTGGTGGCCTTG 765
Qy 238 -----TrpLeu***TrpLysValSerGlyPro***ArgLeuPro----- 250
Db 766 CAGGGGACGACCATGG---TCCTGGAGTGCATCG---CCGAGGGCTTTCCACAGCCACC 819
Qy 251 -----AsnLeu 252
Db 820 ATCAATATGGTGTGCGCCCGCAGTGGCCCATGCCAGTGCACCTGTACCTACCAAGAACAC 879
Qy 252 uThrArgProCysSer-GlyPro-----ArgLeuProArgGluA 265
Db 880 AACCAAGACCTTCAGCTGCTGAAAGTGGCGAGGAGGATGATGGCGAGTACCGTGCCTG 939
Qy 265 LaArgGluLeuArgGlyGln 271
Db 940 GCCGAGAACTCACTGGGCGAG 959

Search completed: January 31, 2004, 15:30:59
Job time : 74.5389 secs

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; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: US 60/058,974
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: US 60/058,973
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: US 60/058,666
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: US 60/090,112
; PRIOR FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 1346
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (637)..(637)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (850)..(850)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-047-021-31
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Pred. No.: 2,59e-131 Length: 1346
Score: 1469.00 Matches: 276
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.59% Indels: 0
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US-10-047-021-86_COPY_28_303 (1-276) x US-10-047-021-31 (1-1346)
Qy 1 GlnAspSerProGlnLeuValHisProGlnAspGlnLeuPheGlnGlyProGly 20
Db 112 CAGGACTCCCGCCCGCCAGATCTTAGTCCACCCCGAGGACAGCTGTTCCAGGGCCCTGGC 171
Qy 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProProThrIleArgTrpLeuLeu 40
Db 172 CCTGCGAGGATGAGCTGCGAGCCTCAGGCGAGCCACCTCCACCATCCGCTGGTGTG 231
Qy 41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60
Db 232 AATGGGACGCCCTGAGCATGGTGGCCCGGAGCATGCCACACACCTCCCTCGCTGATGGGACC 291
Qy 61 LeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80
Db 292 CTCTGCTGTACAGCCCGCTGCGCGGGAGCATGCCACGATGGCCAGGCCCTGTCACCA 351
Qy 81 AspLeuGlyValThrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100
Db 352 GACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCAGCGAGTCAGCAGAGGC 411
Qy 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal 120
Db 412 GCTCGGCTGTCTGTGGCTGTCTCTCGGAGGATTTCCAGATCCAGCCCTCGGGACATGGTG 471
Qy 121 AlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluPro 140
Db 472 GCTGTGGTGGTGAGCAGTTTACTCTGAATGTGGCGCGCCCTCCAGCCCGGAGCCAGGCC 531
Qy 141 ThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrVal 160
Db 532 ACAGTCTCATGTGGAAGATGGGAACCCCTGGCCCTCCAGCCCGGAGGCACACAGTG 591
Qy 161 SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu***ThrTrpMetCys 180
Db 592 TCCGGGGGTCCCTGCTGATGCGAAGACAGAGAGAGTGCAGANGACCTACATGTGT 651
Qy 181 ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu 200
Db 651
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652 GTGGCCACCAACAGCGCAGGACACAGGGAGAGCGCGCGCGGGTTTCCATCCAGGAG 711
201 ProGlnAspTyThrGluProValGluLeuAlaValArgIleGlnLeuGluAsnVal 220
712 CCCAGGACTACACGAGCGCTGTGGAGCTTCTGGCTGTGGCAATTACGCTGGAAATGTG 771
221 ThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAlaValTrpLeu*** 240
772 AACTCTGAACCGGATCTCTGCAGARGGCCCCAGCCTAGACCGGGGTGTGGCTCARG 831
241 TrpLysValSerGlyPro***ArgLeuProAsnLeuThrArgProCysSerGlyProArg 260
832 TGAARGTCAGTGGCCCTNTGCGCTGCCCCAATCTTACACGGGCTTGTTCAGGACCCAGA 891
261 LeuProArgGluAlaArgGluLeuArgGlyGlnArgArgAsnThrGly 276
892 CTGCCCCGGGAGGCCAGGGAGCTCCGTGGCGCAGGAGGAGGAGGAGGAGGAGGAGGAG 939
RESULT 2
US-10-411-224-31
; Sequence 31, Application US/10411224
; Publication No. US20030186906A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 50 Human Secreted Proteins
; FILE REFERENCE: P2016P1
; CURRENT APPLICATION NUMBER: US/10/411,224
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: US/09/722,329
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/262,109
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: 60/057,626
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/057,663
; PRIOR FILING DATE: 1997-09-05
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; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/058,666
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/090,112
; PRIOR FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 1346
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (637)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (850)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-411-224-31
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Pred. No.: 2,59e-131 Length: 1346
Score: 1469.00 Matches: 276
Percent Similarity: 100.00% Conservative: 0
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Query Match: 99.59% Indels: 0
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US-10-047-021-86_COPY_28_303 (1-276) x US-10-411-224-31 (1-1346)
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Qy	1	GlnAspSerProProGlnIleLeuValHisProGlnInAspGlnInLeuPheGlnGlyProGly	20
Db	112	CAGGACTCCCGCCCGCAGATCTTAGTCACCCCCAGGACAGAGCTGTTTCCAGGCGCCCTGGC	171
Qy	21	ProAlaArgMetSerCysArgAlaSerGlyGlnProProProThrIleArgTTrpLeuLeu	40
Db	172	CCTGCCAGGATGAGTGGCCGAGCCTCAGSCCAGCCACTCCACCATCCGCTGGTGGCTG	231
Qy	41	AsnGlyGlnProLeuSerMetValProProAspProHisIleLeuLeuProAspGlyThr	60
Db	232	AATGGCAGCCCTGAGCATGTGTGCCCCCAGACCCACACCACTCTCTCCGCTGATGGGACC	291
Qy	61	LeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr	80
Db	292	CTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCACGATGGCCAGGCGCTGTCCACA	351
Qy	81	AppLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly	100
Db	352	GACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCACGGCAGTCAGCAGAGGC	411
Qy	101	AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal	120
Db	412	GCTCGGCTGTCTGTGGCTGTCTCCGGAGAGATTCCAGATCCAGCCTCGGGACATGGTG	471
Qy	121	AlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluPro	140
Db	472	GCTGTGCTGGGTGAGCAGTTTACTCTGGAATGTGGGCGCCCTGGGGGCCACCCAGAGCCG	531
Qy	141	ThrValSerTrpTrpLeuAspGlyValProLeuAlaLeuGlnProGlyArgHisThrVal	160
Db	532	ACAGTCTCATGTGTGAAGATGGGAACCCCTGGCCCTCCAGCCCGGAAGGCACACAGTG	591
Qy	161	SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu***ThrTrpMetCys	180
Db	592	TCCGGGGGTCTCCTGTATGTCAGAGACAGAGAAGAGTGACGAAGAGCACTCATGTGT	651
Qy	181	ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu	200
Db	652	GTGGCCACCAACAGCGCAGGACACAGGAGAGCCGCGCAGCCGGGTTCCTATCCAGAGAG	711
Qy	201	ProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluAsnVal	220
Db	712	CCCCAGGACTACACGGAGCCTGTGGAGCTTCTGGCTGTGCGAATTCAGCTGGAAATGTG	771
Qy	221	ThrLeuLeuAsnProAspProAlaGluGlyProIlysProArgProAlaValTrpLeu***	240
Db	772	ACACTCTGAACCCGGATCTCTGCAGARGGCCCAAGCCTAGACCCGCGGTGTGGCTCARC	831
Qy	241	TrpLysValSerGlyPro***ArgLeuProAsnLeuThrArgProCysSerGlyProArg	260
Db	832	TGGAAAGTCTAGTGGCCCTTGGCCCTGCCCAATCTTTCACGGCCCTGTGTTCAGACCAGA	891
Qy	261	LeuProArgGluAlaArgGluLeuArgGlyGlnArgArgAsnThrGly	276
Db	892	CTGCCCGGGAGCCAGAGAGCTCGTGGCAGAGGAGGACACAGAGA	939

RESULT 3

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US-09-378-295A-210
; Sequence 210, Application US/09978295A
; Patent No. US2002015606A1
; GENERAL INFORMATION:
; APPLICANT: Aekhenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Botstein, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Pilyarovoff, Ellen
; APPLICANT: Pong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.

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; PRIOR FILING DATE:	1998-05-05
; PRIOR APPLICATION NUMBER:	60/084414
; PRIOR FILING DATE:	1998-05-06
; PRIOR APPLICATION NUMBER:	60/084441
; PRIOR FILING DATE:	1998-05-06
; PRIOR APPLICATION NUMBER:	60/084637
; PRIOR FILING DATE:	1998-05-07
; PRIOR APPLICATION NUMBER:	60/084639
; PRIOR FILING DATE:	1998-05-07
; PRIOR APPLICATION NUMBER:	60/084640
; PRIOR FILING DATE:	1998-05-07
; PRIOR APPLICATION NUMBER:	60/084637
; PRIOR FILING DATE:	1998-05-07
; PRIOR APPLICATION NUMBER:	60/084598
; PRIOR FILING DATE:	1998-05-07
; PRIOR APPLICATION NUMBER:	60/084600
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; PRIOR FILING DATE:	1998-05-15
; PRIOR APPLICATION NUMBER:	60/085704
; PRIOR FILING DATE:	1998-05-15
; PRIOR APPLICATION NUMBER:	60/085697

Alignment Scores:

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Score:	1432.00	Matches:	268
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Query Match:	97.08%	Indels:	1
DB:	10	Gaps:	0

US-10-047-021-86_COPY_28_303 (1-276) x US-09-978-295A-210 (1-3716)

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Qy	21	ProAlaArgMetSerCyAtgAlaSerGlyGlnProProThrIleArgTrpLeuLeu	40
Db	133	CTTGCCAGGATGAGCTGCCAGCCTCAGCCAGCCACCTCCACCATTCCGCTGGTTGCTG	192
Qy	41	AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr	60
Db	193	AATGGCAGCCCTTGAGCATGTCCTCCCCCACACCACACCTCTCTGCTGATGGACC	252
Qy	61	LeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr	80
Db	253	CTTCTGTGCTACAGCCCTTCGCCGGGGAATGCCACGATGGCCCTGTGCCACA	312
Qy	81	AspLeuGlyValTyThrCysGluAlaSerAnArgLeuGlyThrAlaValSerArgGly	100
Db	313	GACCTGGTGTCATACATGTAGGCCCAAGAACCGCTTGGCACGGCAGTCAGCAGAGGC	372
Qy	101	AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal	120


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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:
Pred. No.: 2,72e-127 Length: 3716
Score: 1432.00 Matches: 268
Percent Similarity: 98.53% Conservatives: 1
Best Local Similarity: 98.17% Mismatches: 3
Query Match: 97.08% Indels: 1
DB: 10 Gaps: 0

US-10-047-021-86_COPY_28_303 (1-276) x US-09-978-697-210 (1-3716)

Qy 1 GlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGly 20
Db 73 CAGGACTCCCGCCGCCAGATCCTAGTCCACCCCGAGGACGCTGTTCCAGGGCCCTGGC 132
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Db 133 CTTGCCAGAGTAGCTGCCAAGCTCAGGCCAGCCACCTCCACCATTCCGCTGGTGTG 192
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Db 253 CTTCTGCTGTACAGCCCTGCGGGGAGCATGCCACCATGGCCAGGCGCTGTCCACA 312
Qy 81 AspLeuGlyValTrrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100
Db 313 GACCTGGGTGTCTACATGTGAGGCCAGCAACCGGTTGGCCAGGAGTCAGCAGAGGC 372
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Db 553 TCCGGGGGGTCCCTGCTGTATGGCAAGAGAGAGAGAGTGCACGAAGGACCTACATGTGT 612
Qy 181 ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu 200
Db 613 GTGGCCACCAACAGCGCAGACATAGGGAGAGCGCGCCCGGGTTCATCCAGAGAG 672
Qy 201 ProGlnAspTrrThrGluProValGluLeuAlaValArgIleGlnLeuGluAsnVal 220
Db 673 CCCAGGAGCTACAGGAGCCTGTGGAGCTTCTGGCTGTGGATTCAGCTGGAAAAATGTG 732
Qy 221 ThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAlaValTrrLeu*** 240
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QY 260 gleuProArgGluAlaArgLeuArgGlyGlnArg 272
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; Patent No. US20020177553A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C9
; CURRENT APPLICATION NUMBER: US/09/978,192A
; CURRENT FILING DATE: 2001-10-15
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;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

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Best Local Similarity: 98.17% Mismatches: 3

Query Match: 97.08% Indels: 1
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Qy 121 AlaValValGlyGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluPro 140
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; Sequence 210, Application US/09999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman
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APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
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APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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CURRENT FILING DATE: 2001-10-24
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RESULT 7

US-09-978-189-210

; Sequence 210, Application US/09978189

; Publication No. US20030004102A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: KJavin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James;

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2630P1C7

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;; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

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DB:	11	Gaps:	0

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Db	133	CTGCCAGGATGAGCTGCAGAGCTCAGGCGAGCCACCTCCACCATCCGCTGGTGTG	192
Qy	41	AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr	60
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Qy	61	LeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr	80
Db	253	CTTCTGTGTCTAGTACGCTCCCGGGGAGATGCCACGATGGCCAGCCCTGTCCACA	312
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Db	313	GACCTGGGTGTCTACACATGTAGGCCCGAGCAACCGGCTTGCCAGCGCATCAGCAGGC	372
Qy	101	AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal	120
Db	373	GCTCGGTGTCTGTGGCTGTCTCCCGGAGGATTTCCAGATCCAGCTCCGGACATGGTG	432
Qy	121	AlaValValGlyGluGlnPheThrLeuGlnCysGlyProProTrpGlyHisProGluPro	140
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Qy	141	ThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrVal	160
Db	493	ACAGTCTCATGTGGGAAGATGGGAACCTCTGGCCCTCCAGCCCGGAGGACACACAGTG	552
Qy	161	SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu***ThrTyMetCys	180
Db	553	TCCGGGGGTCCCTGCTGATGGCAGAGCAGAGAAGAGTGACGAAGGACCTACATGTGT	612
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Db	613	GTGGCCACCAACGCGCAGGACATAGGAGAGCGCGCAGCCCGGGTTTCCATCCAGAG	672
Qy	201	ProGlnAspTyThrGluProValGluLeuAlaValArgIleGlnLeuGluAsnVal	220

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Qy	221	ThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAlaValTrpLeu***	240
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Qy	241	TrpLysValSerGlyPro***-ArgLeuProAsnLeuThrArgProCysSerGlyProAr	260
Db	793	TGGAAGTCTAGTGGCCCTGTCTGGCTTGCCTTCCCAATCTTACACGGCTTGTTCAGGACCAG	852
Qy	260	gLeuProArgGluAlaArgGluLeuArgGlyGlnArg	272
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RESULT 8

US-09-978-608A-210
; Sequence 210, Application US/09978608A
; Publication No. US20030045462A1

GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi
;; APPLICANT: Baker Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan
;; APPLICANT: Ferrara, Napoleon
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gao, Wei-Qiang
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gottard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Hillan, Kenneth J.
;; APPLICANT: Kijavlin, Ivar J.
;; APPLICANT: Kuo, Sophia S.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James;
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Shelton, David L.
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tamas, Daniel
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2630P1C22
;; CURRENT APPLICATION NUMBER: US/09/978,608A
;; CURRENT FILING DATE: 2001-10-16
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;; ORGANISM: Homo sapiens
US-09-978-608A-210

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Pred. No.:	2,72e-127	Length:	3716
Score:	1432.00	Matches:	268
Percent Similarity:	98.53%	Conservative:	1
Best Local Similarity:	98.17%	Mismatches:	3
Query Match:	97.08%	Indels:	1
DB:	11	Gaps:	0

US-10-047-021-86_COPY_28_303 (1-276) x US-09-978-608A-210 (1-3716)

Qy	1	GlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGly	20
Db	73	CAGGACTCCCGCCCCAGATCTAGTCCACCCCGAGGACCATCTCCAGGCGCCCTGGC	132

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; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
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; APPLICANT: Shelton, David L.
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; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C15
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; CURRENT FILING DATE: 2001-10-16
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Db 193 AATGGCAGCCCTGAGCATGTGGTCCCGCAGACCCACACCATCTCTGCTGATGGAGC 252
QY 61 LeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80
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; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15

; PRIOR APPLICATION NUMBER: 60/085697
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Best Local Similarity: 98.17% Mismatches: 3
Query Match: 97.08% Indels: 1
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Db 133 CCTGCCAGGATGAGCTGCCAAGCCTCAGGCCAGCCATCCACCATCCGCTGTGTGCTG 192
QY 41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60
Db 193 AATGGCAGCCCTTGAGCATGTGTCCTCCACACCCAGCCACCTCTCTCCCTGATGGGACC 252
QY 61 LeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80
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QY 81 AspLeuGlyValThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100
Db 313 GACCTGGGTGTCTACATGTGAGCCAGCAACCGGTGTGGCAGCGCAGTCAGCAGAGGC 372
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Db 553 TCCGGGGGTCCCTGCTGTGTGGAAGACAGAGAGAGTGACGAAGGACCTTACATGTGT 612
QY 181 ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu 200
Db 613 GTGGCCACCAACAGCCAGGAGACATAGGAGAGCGCGCAGCCCGGGTTTCCATCCAGGAG 672
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; Sequence 210, Application US/09978403A
; Publication No. US20030050240A1
; GENERAL INFORMATION:
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APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
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APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C17
CURRENT APPLICATION NUMBER: US/09/978,403A
CURRENT FILING DATE: 2002-03-19
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/ PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:
Pred. No.: 2,72e-127 Length: 3716
Score: 1432.00 Matches: 268
Percent Similarity: 98.53% Conservative: 1
Best Local Similarity: 98.17% Mismatches: 3
Query Match: 97.08% Indels: 1
DB: 11 Gaps: 0

US-10-047-021-86_COPY_28_303 (1-276) x US-09-978-403A-210 (1-3716)

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QY 41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60
Db 193 AATGGGCAGCCCTGAGCATGGTGGCCCGCCAGACCCACACCATCTCTGCTGATGGGACC 252
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RESULT 12
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; Sequence 210, Application US/09978564A
; Publication No. US20030050241A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
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; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC25
CURRENT APPLICATION NUMBER: US/09/978,564A
CURRENT FILING DATE: 2001-10-16
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Alignment Scores:

Pred. No.: 2,728-127 Length: 3716
Score: 1432.00 Matches: 268
Percent Similarity: 98.53% Conservativity: 1
Best Local Similarity: 98.17% Mismatches: 3
Query Match: 97.08% Indels: 1
DB: 11 Gaps: 0

US-10-047-021-86_COPY_28_303 (1-276) x US-09-978-564A-210 (1-3716)

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Qy 61 LeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80
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Db 313 GACCTGGGTGTACACATGTAGAGCCAGCAACCGGCTTGGCAGCGCAGTACAGAGGC 372
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Db 853 ACTGCCCGGAGGCGCAGGAGCTCCGTGGGCGAGAG 889

RESULT 13

US-09-999-833A-210
; Sequence 210, Application US/09999833A
; Publication No. US20030054405A1
; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C65
; CURRENT APPLICATION NUMBER: US/09/999,833A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11

;	PRIOR FILING DATE:	1998-04-21	
;	PRIOR APPLICATION NUMBER:	60/0823669	
;	PRIOR FILING DATE:	1998-04-21	
;	PRIOR APPLICATION NUMBER:	60/0827004	
;	PRIOR FILING DATE:	1998-04-22	
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;	PRIOR FILING DATE:	1998-04-22	
;	PRIOR APPLICATION NUMBER:	60/0827000	
;	PRIOR FILING DATE:	1998-04-22	
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;	PRIOR FILING DATE:	1998-04-22	
;	PRIOR APPLICATION NUMBER:	60/082796	
;	PRIOR FILING DATE:	1998-04-23	
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;	PRIOR FILING DATE:	1998-04-27	
;	PRIOR APPLICATION NUMBER:	60/083322	
;	PRIOR FILING DATE:	1998-04-28	
;	PRIOR APPLICATION NUMBER:	60/083392	
;	PRIOR FILING DATE:	1998-04-29	
;	PRIOR APPLICATION NUMBER:	60/083495	
;	PRIOR FILING DATE:	1998-04-29	
;	PRIOR APPLICATION NUMBER:	60/083496	
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;	PRIOR APPLICATION NUMBER:	60/083499	
;	PRIOR FILING DATE:	1998-04-29	
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;	PRIOR APPLICATION NUMBER:	60/083500	
;	PRIOR FILING DATE:	1998-04-29	
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;	PRIOR FILING DATE:	1998-04-30	
;	PRIOR APPLICATION NUMBER:	60/084366	
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;	PRIOR APPLICATION NUMBER:	60/084414	
;	PRIOR FILING DATE:	1998-05-06	
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;	PRIOR FILING DATE:	1998-05-07	
;	PRIOR APPLICATION NUMBER:	60/085339	
;	PRIOR FILING DATE:	1998-05-13	
;	PRIOR APPLICATION NUMBER:	60/085338	
;	PRIOR FILING DATE:	1998-05-13	
;	PRIOR APPLICATION NUMBER:	60/085323	
;	PRIOR FILING DATE:	1998-05-13	
;	PRIOR APPLICATION NUMBER:	60/085582	
;	PRIOR FILING DATE:	1998-05-15	
;	PRIOR APPLICATION NUMBER:	60/085700	
;	PRIOR FILING DATE:	1998-05-15	
;	PRIOR APPLICATION NUMBER:	60/085689	
;	PRIOR FILING DATE:	1998-05-15	
;	PRIOR APPLICATION NUMBER:	60/085579	
;	PRIOR FILING DATE:	1998-05-15	
;	PRIOR APPLICATION NUMBER:	60/085580	
;	PRIOR FILING DATE:	1998-05-15	

;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.: 2, 72e-127 Length: 3716
Score: 1432.00 Matches: 268
Percent Similarity: 98.53% Conservative: 1
Best Local Similarity: 98.17% Mismatches: 3
Query Match: 97.08% Indels: 1
DB: 11 Gaps: 0

US-10-047-021-86_COPY_28_303 (1-276) x US-09-999-833A-210 (1-3716)

QY 1 GlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGly 20
DB 73 CAGGACTCCCGCCCGCAGATCTAGTCCACCCCGCAGGACCACTGTTCCAGGGCCCTGGC 132
QY 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTrpLeuLeu 40
DB 133 CCTGCCAGATGAGTGTGCAAGCCTCAGGCCAGCACTCCACCACTCGCTGGTGTG 192
QY 41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60
DB 193 AATGGCAGCCCTCAGCATGTGTGCCCCCAGACCCACACCACTCCTCGCTGATGGACC 252
QY 61 LeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80
DB 253 CTTCTGCTGTACAGCCCTCCCGGGGACATGCCCCAGATGGCCAGGCCCCCTGTCCACA 312
QY 81 AspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100
DB 313 GACCTGGGTGTCTACACATGTAGGCCAGCAACCGGCTTGGCAGCGCAGTACAGAGGC 372
QY 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal 120
DB 373 GCTCGGCTGTCTGTGTGCTCTCGGGAGGATTTCCAGATCCAGCCTCGGGACATGTG 432
QY 121 AlaValValGlyGlnGlnPheThrLeuGluCysGlyProProTrpTrpGlyHisProGluPro 140
DB 433 GCTGTGGTGGGTGACAGCTTACTCTGAATGTGGGCCGCCCTGGGGCCACCCAGAGCCC 492
QY 141 ThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrVal 160
DB 493 ACAGTCTCATGTGTGAAGATGGGAACCCCTGGCCCTCCAGCCCGGAGGCACACAGTG 552
QY 161 SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu***ThrTyrMetCys 180
DB 553 TCCGGGGGTCCTCTGCTGATGCAAGACAGACAGAGAGTGCAGAGGACCTACATGTGT 612
QY 181 ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu 200
DB 613 GTGGCCACCAACAGCCGAGCATAGGAGAGCCGCGAGCCGCGGTTTCCATCCAGGAG 672
QY 201 ProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluAsnVal 220
DB 673 CCCCAGGACTACAGGAGCCTGTGAGCTTCTGGCTGTGCGAATTCAGCTGGAAAATGTG 732
QY 221 ThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAlaValTrpLeu*** 240
DB 733 ACACGTCTGAACCCGGATCTGCAGAGGGCCCCCAGCCTTAGNCCCGCGGTGTGGCTCAGC 792
QY 241 TrpLysValSerGlyPro***ArgLeuProAsnLeuThrArgProCysSerGlyProAr 260
DB 793 TGGAAAGGTCACTGGGCGCTGTGCGCTGTGCCAATCTTACAGCGCTTGTTCAGGACCCAG 852
QY 260 GlnProArgGluAlaArgGluLeuArgGlyClnArg 272
DB 853 ACTGCCCGGGAGGCCAGGAGCTCCGTGGGCAGAGG 889

RESULT 14

US-09-981-915A-210
;; Sequence 210, Application US/09981915A
;; Publication No. US20030054986A1
;; GENERAL INFORMATION:
;; APPLICANT: Ashkenazi, Avi
;; APPLICANT: Baker Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan
;; APPLICANT: Ferrara, Napoleon
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Fong, Sherman
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;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Shelton, David L.
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; TITLE OF INVENTION: Acids Encoding the Same
;; FILE REFERENCE: P2630F1C12
;; CURRENT APPLICATION NUMBER: US/09/981.915A
;; CURRENT FILING DATE: 2001-10-16
;; PRIOR APPLICATION NUMBER: 09/918585
;; PRIOR FILING DATE: 2001-07-30
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/064249
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 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085704
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.:	2.72e-127	Length:	3716
Score:	1432.00	Matches:	268
Percent Similarity:	98.53%	Conservative:	1
Best Local Similarity:	98.17%	Mismatches:	3
Query Match:	97.08%	Indels:	1
DB:	11	Gaps:	0

US-10-047-021-86_COPY_28_303 (1-276) x US-09-981-915A-210 (1-3716)

Qy	1	GlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGly	20
Db	73	CAGGACTCCCGCCCGCCAGATCTTAGTCCACCCAGGACCCAGCTGTTCCAGGCGCCCTGC	132
Qy	21	ProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTrpLeu	40
Db	133	CCTGCCAGGATGAGCTGCCAAGCCTCAGGCGCAGCCACCTCCCATCGCTGTTGCTG	192

QY 41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60
Db AATGGCAGCCCTGAGCATGTGCCCCCAGACCCACACCACTCTCTGCTGATGGAGCC 252
QY 61 LeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80
Db CTTCTGCTGTACTACAGCCCTGCTGCGGGGACATGCGCCAGTGGCGAGCCCTGTCCACA 312
QY 81 AspLeuGlyValTyrThrCysGluAlaSerAnArgLeuGlyThrAlaValSerArgGly 100
Db GACCTGGGTGTCTACATGTGAGCGCCAGCAACCGCTTGGCAGCGCATGACAGAGCC 372
QY 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal 120
Db GCTGGGTGTCTGTGCTGCTCGGGAGGATTTCCAGATCCAGCCCTCGGGACATGTG 432
QY 121 AlaValValGlyGlnGlnPheThrLeuGluCysGlyProProTyrGlyHisProGluPro 140
Db GCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCGCCCTGGGGCCACCCAGAGCCC 492
QY 141 ThrValSerTyrTyrLeuAspGlyLysProLeuAlaLeuGlnProGlyValHisThrVal 160
Db ACAGTCTCATGTGGAAGATGGGAACCCCTGGCCCTCCAGCCCGGAGGACCACTACATGTG 552
QY 161 SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu***ThrTyrMetCys 180
Db TCCGGGGGTCTCTGCTGATGSCAAGACAGAGAGAGTGAGAGGAGGACCTACATGTG 612
QY 181 ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu 200
Db GTGGCCACCAACAGCGGAGGACATAGGGAGAGCGCGAGCGCGCGGTTCATCCAGGAG 672
QY 201 ProGlnAspTyrThrGluProValGluLeuAlaValArgIleGlnLeuGluAsnVal 220
Db CCCCAGGACTACAGGAGCCTGTGAGCTTCTGGCTGTGCGAATTCAGCTGGAAATGTG 732
QY 221 ThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAlaValTyrLeu*** 240
Db ACATCTGTGACCCCGGATCTGCAGAGGGCCCCAGAGCTAGACCCGGGTGTGGTTCAGC 792
QY 241 TrpLysValSerGlyPro***ArgLeuProAsnLeuThrArgProCysSerGlyProAr 260
Db TGGAGGTGAGTGGGCTGCTGCGCTGCGCCATCTTACAGCGCTTGTTCAGGAGCCAG 852
QY 260 GluProArgGluAlaArgGluLeuArgGlyGlnArg 272
Db ACTGCCCCGGGAGCGGAGCTCCGTGGGAGAGG 889

RESULT 15

US-09-978-824-210
; Sequence 210, Application US/09978824
; Publication No. US20030055216A1

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C14
; CURRENT APPLICATION NUMBER: US/09/978,824
; CURRENT FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR FILING DATE: 1998-04-01

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; PRIOR APPLICATION NUMBER: 60/080333
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; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081049
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; PRIOR APPLICATION NUMBER: 60/083500
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083742
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; PRIOR APPLICATION NUMBER: 60/084414
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; PRIOR APPLICATION NUMBER: 60/084441
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; PRIOR APPLICATION NUMBER: 60/084637
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084639

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; PRIOR APPLICATION NUMBER: 60/084640
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; PRIOR APPLICATION NUMBER: 60/084598
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; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
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; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.: 2,72e-127 Length: 3716
Score: 1432.00 Matches: 268
Percent Similarity: 98.53% Conservative: 1
Best Local Similarity: 98.17% Mismatches: 3
Query Match: 97.08% Indels: 1
DB: 11 Gaps: 0

US-10-047-021-86_COPY_28_303 (1-276) x US-09-978-824-210 (1-3716)

Qy 1 GlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGly 20
Db 73 CAGACTCCCGCCCGCCAGATCTTAGTCCACCCAGGACGAGTGTTCAGGGCCCTGGC 132
Qy 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProProThrIleArgTrpLeuLeu 40
Db 133 CTTGCCAGGATGAGTGCCTGCAAGCCTCAGGCCAGCCACCTCCACCATCCGCTGCTGCTG 192
Qy 41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60
Db 193 AATGGGCAGCCCTGAGCATGTGCCCCCAGACCCACACACCTCTCTGCTGATGGGACC 252
Qy 61 LeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80
Db 253 CTTCTGCTGTACAGCCCCCTGCCGGGACATGCCCATGGCCAGGCCCTGTCCACA 312
Qy 81 AspLeuGlyValTrpThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100
Db 313 GACCTGGGTGCTACACATGTGAGGCCAGCAACCGGCTTGGCAGCGGAGTCAGCAGAGGC 372
Qy 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal 120
Db 373 GCTCGGCTGTCTGTGGTGTCTCCGGGAGGATTTCCAGATCCAGCCTCGGAGCATGGTG 432
Qy 121 AlaValValGlyGlnGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluPro 140
Db 433 GCTGTGGTGGTGAGCAGATTACTCTGGAATGTGGCCCGCCCTGGGGCCACCCAGAGCCC 492
Qy 141 ThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrVal 160

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Db 493 ACAGTCTCATGTGGGAAGATGGGAACCCCTGGGCCCTCCAGCCCGGAAGGCACACAGTG 552
Qy 161 SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu**ThrTyrMetCys 180
Db 553 TCCGGGGGGTCCCTGCTGATGGCAAGAGCAGAGAGAGTGACGAAGGGACCTACATGTGT 612
Qy 181 ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu 200
Db 613 GTGGCCACCACACAGCGCAGGACATAGGGAGAGCCGCGAGCCCGGGTTTCCATCCAGGAG 672
Qy 201 ProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluAsnVal 220
Db 673 CCCCAAGGACTACACGAGCCTGTGGAGCTTCTGGCTGTGCGAATTTCAGCTGGAAAATGTG 732
Qy 221 ThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAlaValTriLeu** 240
Db 733 ACACTGCTGAACCCGGATCCTGCAGAGGGCCCCAAGCCTAGACCCGGCGGTGTGGCTCAGC 792
Qy 241 TrpLysValSerGlyPro***-ArgLeuProAsnLeuThrArgProCysSerGlyProAr 260
Db 793 TGGAAAGGTCAGTGGGCCCTGCTGGGCTGCCCCAATCTTACACGGCCTTGTTCAGGACCCAG 852
Qy 260 GluProArgGluAlaArgGluLeuArgGlyGlnArg 272
Db 853 ACTGCCCCGGAGGCCAGGGAGCTCCGTGGGCAGAGG 889
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Search completed: January 31, 2004, 17:18:27
Job time : 314.648 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 30, 2004, 15:52:09 ; Search time 13.3472 Seconds
(without alignments)
1988.631 Million cell updates/sec

Title: US-10-047-021-86_COPY_28_303
Perfect score: 1475
Sequence: 1 QDSPQILVHFQDQLFQFG.....SGPRLPREARLQRRNTG 276

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: Pir1:*
2: Pir2:*
3: Pir3:*
4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	448.5	30.4	1651	T14160	transmembrane rece
2	445.5	30.2	1512	T30805	duttl protein - mo
3	414.5	28.1	1344	T14316	rig-1 protein - mo
4	354.5	24.0	423	T29549	hypothetical prote
5	354.5	24.0	1273	T42405	sax-3 protein - Ca
6	253	17.2	1535	S46224	peroxidasin - frui
7	251	17.0	1272	S26180	neurofascin - chic
8	245	16.6	1427	I51669	tumor suppressor -
9	234.5	15.9	1898	S46216	leukocyte antigen-
10	232.5	15.8	1897	1TDHUK	leukocyte antigen-
11	230.5	15.6	1040	A34695	axonal glycoprotei
12	228	15.5	1040	A49156	transient axonal g
13	228	15.5	5175	T20992	hypothetical prote
14	228	15.5	5198	T43290	hemocentin precurs
15	225	15.3	3707	S18252	heparan sulfate pr
16	222	15.1	1912	T56178	protein-tyrosine-p
17	222	15.1	2029	1TDFLK	protein-tyrosine-p
18	220.5	14.9	1894	C54689	protein-tyrosine-p
19	219.5	14.9	1028	A53449	plasmacytoma-assoc
20	219	14.8	1028	I58164	BIG-1 protein - ra
21	218.5	14.8	1501	I58148	protein-tyrosine-p
22	218.5	14.8	1863	S46217	protein-tyrosine-p
23	218.5	14.8	1907	S50893	protein-tyrosine-p
24	215.5	14.6	1443	I50600	neogenin - chicken
25	213.5	14.5	1036	S22383	axonin 1 precursor
26	212.5	14.4	1070	JC4593	protein-tyrosine k
27	209	14.2	267	T43844	probable tumor su
28	208.5	14.1	1262	1B48758	protein-tyrosine-p
29	208.5	14.1	1496	1A48758	protein-tyrosine-p

30	208	14.1	1239	1	A32579	neuroglian - fruit
31	206	14.0	1447	2	A54100	tumor suppressor p
32	205	13.9	1328	2	T23007	hypothetical prote
33	204.5	13.9	1499	2	I50212	protein-tyrosine-p
34	203.5	13.8	4391	2	A38096	perlecan precursor
35	201	13.6	1277	2	T30532	neural cell adhesi
36	195.5	13.3	1880	2	T18531	tractin - medicina
37	195.5	13.3	6642	2	T29757	protein UNC-89 - C
38	195	13.2	7962	2	I38346	elastin - hu
39	194.5	13.2	1259	2	A43425	Bravo/Nr-CAM cell
40	194.5	13.2	1268	1	A39640	neural cell adhesi
41	192	13.0	1091	2	A58532	glial cell membran
42	191.5	13.0	1091	1	IUCHNL	neural cell adhesi
43	191	12.9	1260	1	S05479	neural cell adhesi
44	191	12.9	1375	2	T13822	frazzled gene prot
45	189	12.8	946	1	A47299	ror-related recept

ALIGNMENTS

RESULT 1

T14160

transmembrane receptor protein Robol - rat
C:Species: Rattus norvegicus (Norway rat)

C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:Accession: T14160

R:Kidd, T.; Brose, K.; Mitchell, K.J.; Fetter, R.D.; Tessier-Lavigne, M.; Goodman, C.S.;

Cell 92, 205-215, 1998

A:Title: Roundabout controls axon crossing of the CNS midline and defines a novel subfam

A:Reference number: 217897; PMID:9458045

A:Accession: T14160

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1651 <KID>

A:Cross-references: EMBL:AF041082; NID:g2811215; PID:g2811216; PIDN:AAC39960.1

C:Function:

A:Description: appears to function as the gatekeeper controlling midline crossing

C:Keywords: transmembrane protein

Query Match 30.4%; Score 448.5; DB 2; Length 1651;

Best Local Similarity 42.2%; Pred. No. 1.9e-26;

Matches 92; Conservative 31; Mismatches 86; Indels 9; Gaps 2;

Qy	1	QDSPQILVHFQDQLFQSGPGARMSCRASGQPPPTIRWLLNGOPLSMVPPPHH---	L1P 57
Db	64	EDFPRIVEHPSDLIVSKGEPATLNCXKAGRPPTIIEWYKGERVETDKDPRSHRMLLP	123
Qy	58	DGTLILLQPPARGHAHDQALSTDLGVVTCASNRLGTAVSGRGLSVAVLRDFQIQPR	117
Db	124	SGSLPFLR-----IVHGKSRPDEGVYICVARNYLGEAVSHNASLEVALRDDPRQNP	177
Qy	118	DMVAVGEGQFTLECGPPWGHPEPTVSWWKKPKALQGRHTVSGGSLMARAEKSDXT	177
Db	178	DMVAVGEPVAVMECPGRGHEPTISWKKGSPLDKDERTIRGKLMITVTRKSDAGK	237
Qy	178	YMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRI	215
Db	238	YVCVGTNMVGRSKVADVTVLERPSFVKRPSNLAVTV	275

RESULT 2

T30805

duttl protein - mouse

N:Alternate names: Transmembrane receptor protein Robol homolog

C:Species: Mus musculus (house mouse)

C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999

C:Accession: T30805

R:Wu, M.C.; Lowe, N.; Fordham, R.; Rabbitts, P.

submitted to the EMBL Data Library, July 1998

A:Description: The mouse homologue of human DUTTL/H-robol gene: protein sequence and chr

A:Reference number: 220879

A:Accession: T30805

A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-1612 <YU>
A:Cross-references: EMBL:Y17793; NID:el329712; PID:el329713; PIDN:CAA7680.1
A:Experimental source: brain
C:Genetics:
A:Gene: dutt1
A:Map position: 16

Query Match 30.2%; Score 445.5; DB 2; Length 1612;
Best Local Similarity 41.7%; Pred. No. 3.2e-26;
Matches 91; Conservative 31; Mismatches 87; Indels 9; Gaps 2;

Qy 1 QDSPPQILVHPDQLFQCGPGPARMSCRASGPPPTIRWLLNGQPLSMVPPDPHH---LLP 57
Db 25 EDFPRPIVEHSDDLVSGBEATLNCAGRTPTIWKYKGERVETDKDPRSHRMLLP 84
Qy 58 DGTLLLOPPARGHAHDQALSTDLGVYTCASNRLGTAVSRGARSLSVAVLRDFQIQPR 117
Db 85 SGLSFLFLR-----IVHGKSRPDGVIICVARNVILGEAVSHNASLEVAIILRDDFRQNP 138
Qy 118 DMVAVVGQFTLECGPPHGHPEPTVSWWKGKPLAQGRHTVSGGSLLMARAKSDEXT 177
Db 139 DMVAVGEPVAMECQPPRGHPEPTISWKGKSPDLDDKDERITIRGGKLMITYTRKSDAG 198
Qy 178 YMCVATNSAGHRESRAARVSIQEPDYTEPVELLAVRI 215
Db 199 YVCVTNVMGERSEVAELTVLERSFVKRPSNLAVTV 236

RESULT 3
T14316
zig-1 protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T14316
R:Yuan, S.S.F.; Cox, L.A.; Dasika, G.K.; Lee, E.Y.H.P.
submitted to the EMBL Data Library, April 1998
A:Reference number: Z17975
A:Accession: T14316
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-1344 <YUA>
A:Cross-references: EMBL:AF060570; NID:g4206385; PID:g4206386; PIDN:AAD11628.1

Query Match 28.1%; Score 414.5; DB 2; Length 1344;
Best Local Similarity 39.9%; Pred. No. 6.4e-24;
Matches 101; Conservative 27; Mismatches 94; Indels 31; Gaps 8;

Qy 1 QDSPPQILVHPDQLFQCGPGPARMSCRASGPPPTIRWLLNGQPLSMVPPDP--HH-I-LP 57
Db 38 EDAMPRIVEQPDLLVSSGEGEATLPCRAEGRPRIEYKNGARVATAREDPRAHRLLLP 97
Qy 58 DGTLLLOPPARGHAHDQALSTDLGVYTCASNRLGTAVSRGARSLSVAVLRDFQIQPR 117
Db 98 SGALEFF---PRIVH---GRRSRPDGVIICVARNVILGAAASRNASLEVAIILRDDFRQSPG 151
Qy 118 DMVAVVGQFTLECGPPHGHPEPTVSWWKGKPLAQGRHTVSGGSLLMARAKSDEXT 177
Db 152 NVVAVGEPVAMECQPPRGHPEPTVWKGKIKLKEEGRITIRGGKLMGSHSTFKSDAGM 211
Qy 178 YMCVATNSAGHRESRAAR-VSIQEPDYTEPVELLAVRIQLENTVLLNPDPAE----- 229
Db 212 YMCVASNWAGRESGAELVLERPSFLRRPI-----NQVLADAPVNFCEVQG 261
Qy 230 GPKRPAPVWLXWK 242
Db 262 DPQPN----LHW 270

RESULT 4
T29549
hypothetical protein ZK377.3 - Caenorhabditis elegans

A:Status: preliminary; translated from GB/EMBL/DBDJ
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T29549
R:Nhan, M.; Hawkins, J.
submitted to the EMBL Data Library, February 1997
A:Description: The sequence of C. elegans cosmid ZK377.
A:Reference number: Z20639
A:Accession: T29549
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-423 <NHA>
A:Cross-references: EMBL:U88183; PIDN:AAB52658.1; GSPDB:GN00028; CESP:ZK377.3
A:Experimental source: strain Bristol N2; clone ZK377
C:Genetics:
A:Gene: CESP:ZK377.3
A:Map position: X
A:Introns: 24/1; 142/3; 229/3; 284/2; 408/3

Query Match 24.0%; Score 354.5; DB 2; Length 423;
Best Local Similarity 34.0%; Pred. No. 7.2e-20;
Matches 96; Conservative 44; Mismatches 101; Indels 41; Gaps 11;

Qy 5 PQILVHPDQLFQCGPGPARMSCRASGPPPT--IRWLLNGQPL--SMVPPDPHLLPD-G 59
Db 30 PVIIEHPIDVVVSRGSPATLNC---GAKPSTAKITWKDGPVITNKEQVNSHRIVLDTG 86
Qy 60 TLLLOPPARGHAHDQALSTDLGVYTCASNRLGTAVSRGARSLSVAVLRDFQIQPRDM 119
Db 87 SLFLKYNKNGKND-----SDAGAYVCASNEHGEVKSNEGSLKLAHLRDFRVRPTV 141
Qy 120 VAVVGEQFTLECGPPHGHPEPTVSWWKGKPLAQ--GRHTV--SGGSLLMARAKSDEXT 177
Db 142 QALGEMAVLECSPPRCFPFVSVWRKDKELRIQDMPRYTLHSDGNLIIDPVDSDSGT 201
Qy 178 YMCVATNSAGHRESRAARVSI-----QBPQDYTEPVELLAVRIQLENTVLLNPDPAEG 230
Db 202 YQCVANNMVGERSVNPAPLSVFEKPKPEQPKDMT-----VDVGAALVFCRVTDG 252
Qy 231 PKRPPAVWLXWKVSGPXELPNLTPCSGPRLPREARELRQR 272
Db 253 PQPO-----ITWK-----RKNEPMFVTRAYIAKDNRLRIER 284

RESULT 5
T42405
sax-3 protein - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C:Accession: T42405
R:Zallen, J.A.; Yi, B.A.; Bargmann, C.I.
Cell 92, 217-227, 1998
A:Title: The conserved immunoglobulin superfamily member SAX-3/Robo directs multiple asp
A:Reference number: Z22160; MUID:98117250; PMID:9458046
A:Accession: T42405
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-1273 <ZAL>
A:Cross-references: EMBL:AF041053; NID:g2804779; PIDN:AAC38848.1; PID:g2804780
C:Genetics:
A:Note: sax-3
C:Function:
A:Description: sax-3 function is required at the time of axon guidance

Query Match 24.0%; Score 354.5; DB 2; Length 1273;
Best Local Similarity 34.0%; Pred. No. 2.4e-19;
Matches 96; Conservative 44; Mismatches 101; Indels 41; Gaps 11;

Qy 5 PQILVHPDQLFQCGPGPARMSCRASGPPPT--IRWLLNGQPL--SMVPPDPHLLPD-G 59
Db 31 PVIIEHPIDVVVSRGSPATLNC---GAKPSTAKITWKDGPVITNKEQVNSHRIVLDTG 87
Qy 60 TLLLOPPARGHAHDQALSTDLGVYTCASNRLGTAVSRGARSLSVAVLRDFQIQPRDM 119

Db 88 SLFLKLVNKGKND-----SDAGAYCYVASNEHGEVSKNBSGLKLA MLREDFRVRPTV 142
Qy 120 VAVVGEQFTLECGPPWGHPEPTVSWWKGKPLALOP-GRHTV-SGSLMARAESKSDXT 177
Db 143 QALGEMAVLECSPPRGPEPVPVSWRKDKELRIQDMRYTLHSDGNLIIDPVRSDSGT 202
Qy 178 YNCVATNSAGHRESRAARVSI-----QEPDYTEPVELLAVRIQLENVTLLNPDPAEG 230
Db 203 YQCVANNMVGERVSNPABLSVPEKPKFEQPKDMT-----VDVGAAVLFDRCRVTGD 253
Qy 231 PKPRPAVVLXWVSGPXLNLTRECSGPRLPREARELRGQR 272
Db 254 FQPOQ-----ITWK-----RKNEFMPVTRAYIAKONRGLRIER 285

RESULT 6
S46224
peroxidasein - fruit fly (*Drosophila* sp.)
C:Species: *Drosophila* sp.
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Oct-2000
C:Accession: S46224
R:Neelson, R.E.; Fessler, L.I.; Takagi, Y.; Blumberg, B.; Keene, D.R.; Olson, P.F.; Parker, E.M.B. J. Biol. Chem. 263:3438-3447, 1989
A:Title: Peroxidasein: a novel enzyme-matrix protein of *Drosophila* development.
A:Reference number: S46224; MUID:94341255; PMID:8062820
A:Accession: S46224
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1535 <NE>
A:Cross-references: G8:U1052; NID:G531384; PIDN:AAA61568.1; PID:G531385
C:Superfamily: peroxidasein; myeloperoxidase homology; proteoglycan amino-terminal homology
F:19-44/Domain: proteoglycan amino-terminal homology <PAH4>
F:661-1350/Domain: myeloperoxidase homology <MPX>

Query Match 17.2%; Score 253; DB 2; Length 1535;
Best Local Similarity 30.3%; Pred. No. 1.9e-11;
Matches 80; Conservative 33; Mismatches 109; Indels 42; Gaps 13;

Qy 3 SPPQILVHPDQL--FQGGPARGMCRASGPPPTIRWLLNGQPLSMVPPDPHLLPDGT 60
Db 367 SPPHTHPPDQIVAHSSGHVLLDCAASGPPQDIPFVNGRQLQSTPS-LQIQANGS 425
Qy 61 LLLQPPARGHAHQDQALSTDLGVYTCEASNRGLGTAVSRGARLSVAVLRDFQIQPRDMV 120
Db 456 LLLQPP-----NQLSA--GTYRCEARNSLG-SVQATARIELKELPE-ILTPAQSGT 472
Qy 121 AVVGEQFTLECGPPWGHPEPTVSWWKGKPLALOPG-----RHTVSGSLMARAESKSD 175
Db 473 IKLGKAFVLECDAD-GNPLPTIDMQLNGVPL---FGNTPDLQLENENTELVVGARQSHA 528
Qy 176 XYTCMVATNSAGHRESRAARVSIQ8-----PDYTEPVELLAV---RIQLENVTLLNPDPA 228
Db 529 GYVRCATNENG-ETSVETATIKVRSQSPQLAIEPSNLVAITGTITEL-----PC 578
Qy 229 EGPKPRPAVVLXWVSGPXPRLPNL 252
Db 579 QADQPEDGLQISWRHGRDLIDPNV 602

RESULT 7
S26180
neurofascin - chicken
C:Species: *Gallus gallus* (chicken)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C:Accession: S26180
R:Volkmann, H.; Hassel, B.; Wolff, J.M.; Frank, R.; Rathjen, F.G.
J. Cell Biol. 118, 149-161, 1992
A:Title: Structure of the axonal surface recognition molecule neurofascin and its relative
A:Reference number: S26180; MUID:92317154; PMID:1377696
A:Accession: S26180
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1272 <VOL>

A:Cross-references: EMBL:X65224; NID:G63659; PIDN:CAA46330.1; PID:G63660
C:Superfamily: neural cell adhesion molecule L1; fibronectin type III repeat homology;
F:275-336/Domain: immunoglobulin homology <IMW>

Query Match 17.0%; Score 251; DB 2; Length 1272;
Best Local Similarity 34.5%; Pred. No. 2.2e-11;
Matches 71; Conservative 34; Mismatches 71; Indels 30; Gaps 11;

Qy 5 POILVHPDQLFQGGP-PAARMSCRASGPPPTIRWLLNGQPLSMVPPDPHLLPDGTLL 63
Db 355 PYWLDEFQNL-LILAPGEDGRVLCRANGPKRSIQWLVNGEFIEGSPNPSREVAGDTIVF 413
Qy 64 LOPPARGHAHQDQALSTDLGVYTCEASNRGLGTAVSRGARLSVAVLRDFQIQPR----- 117
Db 414 -----RDTQIGSS--AVYQCNVSNHGHYLL---ANAFVSVL-----DVPRLILAPRN 455
Qy 118 DMVAVVGEQFT-LECGPPWGHPEPTVSWWKGKPLALOPGRHTV-SGSLMARAESKSD 175
Db 456 QLIKVIQVNRTRLDG-PFFGSPITLRFNKGQGNMLDGGNYKAHENGSLMSMARKEDQ 514
Qy 176 XYTCMVATNSAGHRESRAARVSIQEP 201
Db 515 GIYTCVATNLGKVEAQ-VRLVEKDP 539

RESULT 8
S46216
tumor suppressor - African clawed frog
C:Species: *Xenopus laevis* (African clawed frog)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: S46216
R:Pierce, W.E.; Reale, M.A.; Candia, A.F.; Wright, C.V.; Cho, K.R.; Fearon, E.R.
Dev. Biol. 166, 654-665, 1994
A:Title: Expression of a homologue of the deleted in colorectal cancer (DCC) gene in the
A:Reference number: S46216; MUID:95113183; PMID:7813784
A:Accession: S46216
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1427 <PIE>
A:Cross-references: EMBL:U10986; NID:G606873; PIDN:AAA70168.1; PID:G606874
C:Genetics:
A:Gene: XDCCA

Query Match 16.6%; Score 245; DB 2; Length 1427;
Best Local Similarity 31.0%; Pred. No. 7.1e-11;
Matches 75; Conservative 32; Mismatches 99; Indels 36; Gaps 10;

Qy 22 ARMSCRASGPPPTIRWLLNGQPLSMVPPDPHLL-LPDGTLLLLQPPARGHAHQDQALST 80
Db 157 ALLRCBITGEMPTISWQKNEEDLKVTPGDPRLVLPSTGLQI-----SRLQADG----- 207
Qy 81 DLGVYTCEASNRGLGTAVSRGARLSVAVLRD-----FQIQPRDMVAVVGEQFTLECGP 133
Db 208 --GYVRCATNENG-SARVNGEAEEL--RILSESGLHQQVFLQPRSNVVAIEGQDAVLECAV 263
Qy 134 PWGHPEPTVSWWKGKPLALOPGRHTVSGGS-LLMARAESKSDXYTCMVATNSAGHRESR 192
Db 264 S-GYPTTIWVGQDEPVPITRKYVGLGSNLLISNVITDDAGAYTCVATYKNTSFS 322
Qy 193 AARVSIQEPDYTEPVELLA---VRIQLENVTLLNPDPAEGPKPRPAVVLXWVSGPXPRL 249
Db 323 ADLTVMVPPQPLNHPANLYAVESMDIEFE-----CAVSGKPSPTV--KWTNKGVEVI 372
Qy 250 PN 251
Db 373 PS 374

RESULT 9
S46216
leukocyte antigen-related protein precursor - rat
N:Alternate names: leukocyte common antigen homolog
N:Contains: protein-tyrosine-phosphatase (EC 3.1.3.48)

C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Feb-1995 #sequence revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S46216; S23252; A41032; A33154
R;Zhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, B.J.
Biochem. J. 302, 39-47, 1994
A;Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine-phosphatase from rat liver
A;Reference number: S46216; MUID:94347119; PMID:8068021
A;Accession: S46216
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1898 <ZHA>
A;Cross-references: EMBL:L11586; NID:9205132; PIDN:AAC37655.1; PID:9205133
R;Hashimoto, N.; Zhang, W.R.; Goldstein, B.J.
Biochem. J. 284, 569-576, 1992
A;Title: Insulin receptor and epidermal growth factor receptor dephosphorylation by three different protein-tyrosine phosphatases
A;Reference number: S23252
A;Accession: S23252
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1361-1604;1649-1898 <HAS>
R;Pot, D.A.; Woodford, T.A.; Remboutsika, E.; Haun, R.S.; Dixon, J.E.
J. Biol. Chem. 266, 19688-19696, 1991
A;Title: Cloning, bacterial expression, purification, and characterization of the cytoplasmic region of the insulin receptor
A;Reference number: A41032; MUID:92011772; PMID:1918076
A;Accession: A41032
A;Molecule type: mRNA
A;Residues: 1035-1072, 'S', 1074-1433, 'T', 1435-1638, 'N', 1640-1642, 'HT', 1645-1898 <POT>
A;Cross-references: GB:M0103; NID:9205130; PIDN:AAM41510.1; PID:9205131
R;Pot, D.A.; Woodford, T.A.; Remboutsika, E.; Haun, R.S.; Dixon, J.E.
Submitted to the Protein Sequence Database, December 1990
A;Reference number: A33154
A;Accession: A33154
A;Molecule type: mRNA
A;Residues: 1035-1072, 'S', 1074-1433, 'T', 1435-1638, 'N', 1640-1642, 'HT', 1645-1898 <POT>
C;Comment: Only the first of the two domains homologous with protein-tyrosine-phosphatase
C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology; glycoprotein; glycoprotein; phosphoprotein; phosphoric monoester hydrolase; tyrosine phosphatase
C;Keywords: duplication; signal sequence #status predicted <SIG>
F;1-27/Domain: (or 1-26) signal sequence #status predicted <SIG>
F;28-1898/Product: (or 27-1898) leukocyte antigen-related protein #status predicted <MAT>
F;128-1251/Domain: (or 27-1251) extracellular #status predicted <EXT>
F;147-109/Domain: immunoglobulin homology <IMM1>
F;149-209/Domain: immunoglobulin homology <IMM2>
F;246-300/Domain: immunoglobulin homology <IMM3>
F;318-400/Domain: fibronectin type III repeat homology <FN3A>
F;413-499/Domain: fibronectin type III repeat homology <FN3B>
F;511-593/Domain: fibronectin type III repeat homology <FN3C>
F;606-695/Domain: fibronectin type III repeat homology <FN3D>
F;708-799/Domain: fibronectin type III repeat homology <FN3E>
F;811-895/Domain: fibronectin type III repeat homology <FN3F>
F;906-990/Domain: fibronectin type III repeat homology <FN3G>
F;1002-1079/Domain: fibronectin type III repeat homology <FN3H>
F;1252-1275/Domain: (or 1259-1275) transmembrane #status predicted <TM>
F;1276-1898/Domain: intracellular #status predicted <INT>
F;1286-1898/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F;1366-1587/Domain: protein-tyrosine-phosphatase homology <PTP1>
F;1655-1878/Domain: protein-tyrosine-phosphatase homology <PTP2>
F;154-207, 253-298/Disulfide bonds: #status predicted
F;117, 250, 295, 721, 957/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;1539/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1545/Binding site: substrate phosphate (Arg) #status predicted
F;1830/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1836/Binding site: substrate phosphate (Arg) #status predicted

Db 86 GAGSVLRIQP-----LRVQDEAIYEECTATNSIG-EINTSAKLK--VLEEDQLPSG 133
QY 112 ---FQIQPRDMVAVGVEQFTLECGPWGHPPEPTVSWKQCKPL--ALQPCR-HTVSGSL 165
Db 134 FPTIDMGPKVVEKARTATMLCA-AGNPDPIBSWFKDFLPVDPASSNGRIKQLRSGAL 192
QY 166 LMAAEKSDXTYMCVATNSAGHRESRAARVSQ 199
Db 193 QIESSESDDGKYECVATNSAGTRYSSAPANLYVR 226
RESULT 10
TDHULK
leukocyte antigen-related protein precursor - human
N;Alternate names: leukocyte common antigen homology
N;Contains: protein-tyrosine-phosphatase (EC 3.1.3.48)
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 22-Jun-1999
C;Accession: S03841; JL0051
R;Streuli, M.; Krueger, N.X.; Hall, L.R.; Schlossman, S.F.; Saito, H.
J. Exp. Med. 168, 1523-1530, 1988
A;Title: A new member of the immunoglobulin superfamily that has a cytoplasmic region homologous to the leukocyte antigen-related protein; fibronectin type III repeat homology;
A;Reference number: JL0051; MUID:89035978; PMID:2972792
A;Accession: S03841
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1897 <STR>
A;Cross-references: EMBL:Y00815; NID:934266; PIDN:CAA68754.1; PID:g34267
C;Genetics:
A;Gene: GDB:PTPRF; LAR
A;Cross-references: GDB:120138; OMIM:179590
A;Map position: lp34-lp34
C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
C;Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-1897/Product: leukocyte antigen-related protein #status predicted <MAT>
F;17-1250/Domain: extracellular #status predicted <EXT>
F;37-99/Domain: immunoglobulin homology <IMM1>
F;139-199/Domain: immunoglobulin homology <IMM2>
F;236-290/Domain: immunoglobulin homology <IMM3>
F;308-390/Domain: fibronectin type III repeat homology <FN3A>
F;403-489/Domain: fibronectin type III repeat homology <FN3B>
F;501-583/Domain: fibronectin type III repeat homology <FN3C>
F;586-585/Domain: fibronectin type III repeat homology <FN3D>
F;698-798/Domain: fibronectin type III repeat homology <FN3E>
F;810-893/Domain: fibronectin type III repeat homology <FN3F>
F;905-989/Domain: fibronectin type III repeat homology <FN3G>
F;1001-1078/Domain: fibronectin type III repeat homology <FN3H>
F;1251-1274/Domain: transmembrane #status predicted <TM>
F;1275-1897/Domain: intracellular #status predicted <INT>
F;1365-1897/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F;1365-1586/Domain: protein-tyrosine-phosphatase homology <PTP1>
F;1654-1877/Domain: protein-tyrosine-phosphatase homology <PTP2>
F;44-97, 146-197, 243-288/Disulfide bonds: #status predicted
F;107, 240, 285, 711, 956/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;1538/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1544/Binding site: substrate phosphate (Arg) #status predicted
F;1829/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1835/Binding site: substrate phosphate (Arg) #status predicted
Query Match 15.8%; Score 232.5; DB 1; Length 1897;
Best Local Similarity 31.6%; Pred. No. 8.9e-10;
Matches 68; Conservative 37; Mismatches 75; Indels 35; Gaps 9;
QY 2 DSPPQILVHPQDQLFQGGPARMSCRASGQPPPTIRWLLNGQPLS-----MVPDPHLL 56
Db 20 DSKPVFKVPEQDQGLSGGVASFVQCQATGEPKPRITWMKGGKVSQRFVEIEDD---- 75
QY 57 PDGTLILLQPPARGHAHDGQALSTDLGVYTCESASRLGTVASRGARLSVAVLRDFQIQP 116
Db 76 GAGSVLRIQP-----LRVQDEAIYEECTATNSIG-EINTSAKLKSVL---BEEQLPP 122

A-Molecule type: mRNA
A:Residues: 1-296, 'T', 298-1040 <HA2>
A:Cross-references: EMBL:X68274
R:Tsotra, P.C.; Kariogooes, D.; Theodorakis, K.; Michaelidis, T.M.; Modi, W.S.; Furley, J.
Genomics 18, 562-567, 1993
A:A:Title: Isolation of the cDNA and chromosomal localization of the gene (TAX1) encoding
A:Reference number: A49356; MUID:94140354; PMID:8307567
A:Accession: A49356
A:Molecule type: mRNA
A:Residues: 1-1001, 'G', 1003-1040 <TSI>
A:Cross-references: GB:X67734
C:Genetics:
A:Gene: GDB:TAX; TAX1
A:Cross-references: GDB:138782
A:Map position: lg32-1q32
C:Superfamily: contactin; fibronectin type III repeat homology; immunoglobulin homology
C:Keywords: cell adhesion; glycoprotein
F:1-28/Domain: signal sequence; status predicted <SIG>
F:29-1040/Product: axonal glycoprotein TAG-1; status predicted <MAT>
F:254-308/Domain: immunoglobulin homology <IMM1>
F:341-397/Domain: immunoglobulin homology <IMM2>
F:76,198,204,461,477,498,525,775,830,904,918,940/Binding site: carbohydrate (Asn) (cova)

Query Match 15.5%; Score 228; DB 2; Length 1040;
Best Local Similarity 29.5%; Pred. No. 1e-09;
Matches 79; Conservative 38; Mismatches 99; Indels 52; Gaps 13;

QY 1 QDSPQILVHPQDLFQGGPARMSCRAGQPPTIRLLNGQLSPVPPDPHLLPDGT 60
DDB 40 EDQPLSVL-FPESTEE---QVLLACRASPATYRWKMGTEMKLEPGSRHQLV-GGN 94
QY 61 LLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSGCARLSVAVLREDFOIQPRDMV 120
DDB 95 LVINP-----TKAQDAGVYQCLASNPVGTVVSREAILRFGFLOE-FSKEERDPV 143
QY 121 AVVGEQFTLECGPWGHEPTVSNWCKGLAL-QPGRHTVS--CGSLLMARAEKSDX 176
DDB 144 KAHEGCGWMLPCNPAPHPGLSYRLNLEFPNIPITDGRHFVSQTTGNLYIARTNASDLG 203
QY 177 TYMCVATNSAGHRE-----SRAARVSIQ-----EPQDYTEPVELLAVRIQLE 218
DDB 204 NYSLCATS---HWDSTKSVFSKFAQLNLAEDTRLFAPSIKARFPAETVALVGQVTVLE 260
QY 219 NYTLNPPDAEGPKPRPAVWLXW-KVSG 245
DDB 261 CFAFGNPVPR-----IKWRKVDG 278

RESULT 13
T20992
hypothetical protein F15G9.4a - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T20992; T24733
R:Sulston, J.
submitted to the EMBL Data Library, December 1994
A:Reference number: Z19355
A:Accession: T20992
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-5175 <W1>
A:Cross-references: EMBL:Z47068; PIDN:CAA87335.1; GSPDB:GN00028; CESP:F15G9.4a
A:Experimental source: clone F15G9
R:Kershaw, J.
submitted to the EMBL Data Library, December 1994
A:Reference number: Z19929
A:Accession: T24733
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-5175 <W12>
A:Cross-references: EMBL:Z47070; PIDN:CAA87344.1; GSPDB:GN00028; CESP:F15G9.4a
A:Experimental source: clone T09B9
C:Genetics:

Query Match 15.5%; Score 228; DB 2; Length 5198;
Best Local Similarity 28.6%; Pred. No. 6.1e-09;

Query Match	15.3%	Score	225;	DB 2;	Length	3707;			
Best Local Similarity	27.6%;	Pred. No.	7.1e-09;						
Matches	72;	Conservative	37;	Mismatches	86;	Indels	66;	Gaps	13;

QY	4	PROILVHPQDLQFGGCPARM-----SCRASGQPPPTIRWLNGOPLSMVP-----PDP 52
DB	2433	PPTVSVLP-----EGPVHVKMGKDIITLCTSSGEPSSPRWTRLGIPVKLEPRMFLGMMNS 2487
QY	53	HLLLPDCTLLLLLOPPARGHAHDGQALSTDLGVVTCBASNRLGTA-----VSRGARLSV 105
DB	2488	HAML-----KTASVXP-----SDAGTVVCAQNALGTAQKVELIVDTG---TV 2528
QY	106	AVLREDFOIQPRDMVAVVGEOFTLECGPPMGHPPEPTVSMWKDGKPIALOPGRHTVSGSL 165
DB	2529	APCTPQVQVESELTLGAGHTATLHCSAT-GNFPPTIHMSKLAPL---PWQHRIEGNTL 2584
QY	166	LMARAEKSDEXTVMCVATNSAGHRESRAARVSTQEPQDYT-----BPVELLAVRIQL 217
DB	2585	VIPRAVQDSGGQVCINATNSAGHTATV-LHVESPPYATIIPEHTSAQPGNL---VOL 2639
QY	218	ENVTLINPDPAEGPKPRPAVV 238
DB	2640	QCL-----AHGTPPLTYQW 2653

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Job time : 14.3472 secs

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DR SMART; SM00200; SEA; 1.
DR PROSITE; PS00022; EGF 1; 9.
DR PROSITE; PS01186; EGF 2; 6.
DR PROSITE; PS08835; IG_LIKE; 22.
DR PROSITE; PS00025; LAM_G DOMAIN; 3.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 11.
DR PROSITE; PS01209; LDLRA 1; 4.
DR PROSITE; PS00068; LDLRA 2; 4.
DR PROSITE; PS00024; SEA; 1.
KW Signal; Basement membrane; Proteoglycan; Repeat; Glycoprotein;
KW Heparan sulfate; Laminin EGF-like domain; Immunoglobulin domain;
KW Extracellular matrix; EGF-like domain; Disease mutation.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 4391 BASEMENT MEMBRANE-SPECIFIC HEPARAN
FT FT Sulfate proteoglycan core protein.
FT FT SEA.
FT DOMAIN 80 194 LDL-RECEPTOR CLASS A 1.
FT DOMAIN 198 235 LDL-RECEPTOR CLASS A 2.
FT DOMAIN 284 320 LDL-RECEPTOR CLASS A 3.
FT DOMAIN 324 360 LDL-RECEPTOR CLASS A 4.
FT DOMAIN 367 404 IG-LIKE C2-TYPE 1.
FT DOMAIN 405 504 LAMININ EGF-LIKE 1 (N-TERMINAL).
FT DOMAIN 521 530 LAMININ DOMAIN IV 1 (DOMAIN III A).
FT DOMAIN 531 730 LAMININ EGF-LIKE 1 (C-TERMINAL).
FT DOMAIN 731 763 LAMININ EGF-LIKE 2.
FT DOMAIN 764 813 LAMININ EGF-LIKE 3.
FT DOMAIN 814 871 LAMININ EGF-LIKE 4 (INCOMPLETE).
FT DOMAIN 879 923 LAMININ EGF-LIKE 5 (N-TERMINAL).
FT DOMAIN 924 933 LAMININ EGF-LIKE 6.
FT DOMAIN 934 1125 LAMININ EGF-LIKE 7.
FT DOMAIN 1126 1158 LAMININ EGF-LIKE 8.
FT DOMAIN 1159 1208 LAMININ EGF-LIKE 9 (N-TERMINAL).
FT DOMAIN 1209 1265 LAMININ EGF-LIKE 10.
FT DOMAIN 1275 1324 LAMININ EGF-LIKE 11.
FT DOMAIN 1325 1334 LAMININ EGF-LIKE 12.
FT DOMAIN 1335 1329 LAMININ EGF-LIKE 13.
FT DOMAIN 1330 1562 LAMININ EGF-LIKE 14.
FT DOMAIN 1563 1612 LAMININ EGF-LIKE 15.
FT DOMAIN 1613 1670 LAMININ EGF-LIKE 16.
FT DOMAIN 1677 1771 LAMININ EGF-LIKE 17.
FT DOMAIN 1772 1865 IG-LIKE C2-TYPE 2.
FT DOMAIN 1866 1955 IG-LIKE C2-TYPE 3.
FT DOMAIN 1956 2051 IG-LIKE C2-TYPE 4.
FT DOMAIN 2052 2151 IG-LIKE C2-TYPE 5.
FT DOMAIN 2152 2244 IG-LIKE C2-TYPE 6.
FT DOMAIN 2245 2340 IG-LIKE C2-TYPE 7.
FT DOMAIN 2341 2436 IG-LIKE C2-TYPE 8.
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FT DOMAIN 3022 3112 IG-LIKE C2-TYPE 15.
FT DOMAIN 3113 3211 IG-LIKE C2-TYPE 16.
FT DOMAIN 3212 3311 IG-LIKE C2-TYPE 17.

Db 3274 GQICNATSPAGHAETII-LHVESPPYATTVPBHASVQAGETVQLQCL-----AHGT 3325
Qy 232 KPRPAVWLXWKVSGPKR 248
Db 3326 PPLTFQMSRVGSSLPGR 3342
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Best Local Similarity 26.5%; Pred. No. 9.4e-08;
Matches 68; Conservative 38; Mismatches 114; Indels 37; Gaps 9;
Qy 4 PPQILVHPDQLFQSGGPA-RMSCRAGQPPPTIRWLNGQPLSMVPPDPHLLPDGTL 62
Db 3111 PPTVSVLPEGPVWVKVKAIVLECVSAGEPRSSARWTRISSTPAKLEQRTYGLMDSHAVL 3170
Qy 63 LQPPARGHNDGQALSTDLGVYTCASNRLGTA-----VSRCARLSVAVLREDFOIQ 115
Db 3171 QI-----SSAKPSDAGTYVCLAQNALQKQVEVIVDTGA---MAPGAPQVQAE 3217
Qy 116 PRDMVAVVGEQFTLECGPPGWPBPEPTVSWKDGKPLALQPGRHTVSGGSLLMARAEKSD 175
Db 3218 EAEITVEAGHTATLECSAT-GSPATIIHWSKLRSL---PWQHRLEGDTLIIIPVAQODS 3273
Qy 176 XYTMCVATNSAGHRESRAARVSIQEPDYTEPVELLAVR-----IQLENVTLLNPDPAEGP 231

PGSM_HUMAN STANDARD; PRT; 4391 AA.
P98160; Q16287; Q9H3V5;
01-OCT-1996 (Rel. 34, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
DE Basement membrane-specific heparan sulfate proteoglycan core
DE protein precursor (HSPG) (Perlecan) (PLC).
GN HSPG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=92112994; PubMed=1730768;
RA Kallunki P., Tryggvason K.;
RT "Human basement membrane heparan sulfate proteoglycan core protein: a
RT 467-kD protein containing multiple domains resembling elements of the
RT low density lipoprotein receptor, laminin, neural cell adhesion
RT molecules, and epidermal growth factor.";
RL J. Cell Biol. 116:559-571(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon, and Skin;
RX MEDLINE=92235084; PubMed=1569102;
RA Murdoch A.D., Dodge G.R., Cohen I., Tuan R.S., Iozzo R.V.;
RT "Primary structure of the human heparan sulfate proteoglycan from
RT basement membrane (HSPG2/perlecan). A chimeric molecule with multiple
RT domains homologous to the low density lipoprotein receptor, laminin,
RT neural cell adhesion molecules, and epidermal growth factor.";
RL J. Biol. Chem. 267:8544-8557(1992).
RN [3]
RP SEQUENCE OF 22-4391 FROM N.A. AND VARIANT SJS1 TYR-1532.
RX MEDLINE=20553141; PubMed=1101850;
RA Nicole S., Davoine C.-S., Topaloglu H., Cattolico L., Barral D.,
RA Beighton P., Ben-Hamida C., Hammouda H., Cruaud C., White P.S.,
RA Samson D., Urtizberea J.A., Lehmann-Horn F., Weissenbach J.,
RA Hentati F., Fontaine B.;
RT "Perlecan, the major proteoglycan of basement membranes, is altered in
RT patients with Schwartz-Jampel syndrome (Chondrodysplastic myotonia).";
RL Nat. Genet. 26:480-483(2000).
RN [4]
RP SEQUENCE OF 1016-1470 FROM N.A.
RC TISSUE=Colon;
RX MEDLINE=91365376; PubMed=1679749;
RA Dodge G.R., Kovalszky I., Chu M.L., Hassell J.R., McBride O.W.,
RA Yi H.F., Iozzo R.V.;
RT "Heparan sulfate proteoglycan of human colon: partial molecular
RT cloning, cellular expression, and mapping of the gene (HSPG2) to the
RT short arm of human chromosome 1.";
RL Genomics 10:673-680(1991).
RN [5]
RP SEQUENCE OF 890-1396 FROM N.A.
RC TISSUE=Fibroarcoma;
RX MEDLINE=92120660; PubMed=1685141;
RA Kallunki P., Eddy R.L., Byers M.G., Kestila M., Shows T.B.,
RA Tryggvason K.;
RT "Cloning of human heparan sulfate proteoglycan core protein,
RT assignment of the gene (HSPG2) to lp36.1--p35 and identification of
RT a BamHI restriction fragment length polymorphism.";
RL Genomics 11:389-396(1991).
RN [6]
RP SEQUENCE OF 1-21 FROM N.A.
RX MEDLINE=94052171; PubMed=8234307;
RA Cohen I.R., Graessel S., Murdoch A.D., Iozzo R.V.;
RT "Structural characterization of the complete human perlecan gene and
RT its promoter.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:10404-10408(1993).
CC -!- FUNCTION: This protein is an integral component of basement
CC membranes. It is responsible for the fixed negative electrostatic
CC charge and is involved in the charge-selective ultrafiltration
CC properties. It serves as an attachment substrate for cells.
CC -!- SUBUNIT: Purified perlecan has a strong tendency to aggregate in

dimers or stellate structures. It interacts with other basement
membrane components such as laminin, prolargin and collagen type
IV.
-!- SUBCELLULAR LOCATION: Extracellular.
-!- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES.
-!- PTM: CONTAINS THREE HEPARAN SULFATE CHAINS AS WELL AS N-LINKED
AND O-LINKED OLIGOSACCHARIDES.
-!- DISEASE: Defects in HSPG2 are the cause of Schwartz-Jampel
syndrome (SJS1) [MIM:255800]; a rare autosomal recessive disorder
characterized by permanent myotonia (prolonged failure of muscle
relaxation) and skeletal dysplasia, resulting in reduced stature,
kyphoscoliosis, bowing of the diaphyses and irregular epiphyses.
-!- SIMILARITY: Contains 4 LDL-receptor class A domains.
-!- SIMILARITY: Contains 11 laminin EGF-like domains.
-!- SIMILARITY: Contains 3 laminin IV domains.
-!- SIMILARITY: Contains 22 immunoglobulin-like C2-type domains.
-!- SIMILARITY: Contains 3 laminin G-like domains.
-!- SIMILARITY: Contains 4 EGF-like domains.
-!- SIMILARITY: Contains 1 SEA domain.

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EMBL; X62515; CAA44373.1; -;
DR EMBL; M85289; AAA52700.1; -;
DR EMBL; AL445795; CAC18534.1; -;
DR EMBL; M64283; AAA52699.1; -;
DR EMBL; S76436; AAB21121.2; -;
DR EMBL; L22078; -; NOT_ANNOTATED_CDS.
DR PIR; A38096; A38096.
DR HSPG; P00740; 1EDM.
DR Sienna-2DPAGE; P98160; -;
DR Genew; HGNC:5273; HSPG2.
DR MIM; 142461; -;
DR MIM; 255800; -;
DR GO; GO:0005206; F:heparin sulfate proteoglycan; TAS.
DR InterPro; IPR00742; EGF_2.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR006210; EGF.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003598; Ig_C2.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR InterPro; IPR000034; Laminin_B.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR002172; LDL_receptor_A.
DR InterPro; IPR000082; SEA_domain.
DR Pfam; PF00008; EGF_4.
DR Pfam; PF00047; Ig_22.
DR Pfam; PF00052; laminin_B; 3.
DR Pfam; PF00053; laminin_EGF; 7.
DR Pfam; PF00054; laminin_G; 3.
DR Pfam; PF00057; ldl_recept_a; 4.
DR Pfam; PF01390; SEA_1.
DR PRINTS; PR00010; EGFBLD.
DR PRINTS; PR00261; LDLRECEPTOR.
DR ProDom; PD003031; Laminin_B; 3.
DR SMART; SM00181; EGF; 15.
DR SMART; SM00180; EGF_Lam; 12.
DR SMART; SM00409; IG_22.
DR SMART; SM00408; IGC2; 21.
DR SMART; SM00406; IGV; 7.
DR SMART; SM00281; LamB; 3.
DR SMART; SM00282; LamG; 3.
DR SMART; SM00192; LDLa; 4.

RC TISSUE=Brain;
RX MEDLINE=97407661; PubMed=9264410;
RA Keeling S.L., Gad J.M., Cooper H.M.;
RT "Mouse neogenin, a DC-like molecule, has four splice variants and is
expressed widely in the adult mouse and during embryogenesis.";
RL Oncogene 15:691-700(1997).
CC -!- FUNCTION: MAY BE INVOLVED AS A REGULATORY PROTEIN IN THE
TRANSITION OF UNDIFFERENTIATED PROLIFERATING CELLS TO THEIR
DIFFERENTIATED STATE. MAY ALSO FUNCTION AS A CELL ADHESION
MOLECULE IN A BROAD SPECTRUM OF EMBRYONIC AND ADULT TISSUES.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=5;
CC Comment=Additional isoforms seem to exist;
CC Name=1;
CC IsoId=P97798-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P97798-2; Sequence=VSP_002594;
CC Name=3;
CC IsoId=P97798-3; Sequence=VSP_002595;
CC Note=Expression developmentally regulated;
CC Name=4;
CC IsoId=P97798-4; Sequence=VSP_002596;
CC Note=Expression developmentally regulated;
CC Name=5;
CC IsoId=P97798-5; Sequence=VSP_002597;
CC Note=Expression developmentally regulated;
CC -!- TISSUE SPECIFICITY: Widely expressed.
CC -!- DEVELOPMENTAL STAGE: EXPRESSED UBQUITOUSLY THROUGHOUT THE MID TO
LATE STAGES OF GESTATION AND IN ADULT TISSUES. STRONG EXPRESSION
IS OBSERVED IN THE VENTRAL REGION OF THE VENTRICULAR ZONE OF THE
E15.5 MOUSE NEURAL TUBE. AS WELL AS IN THE VENTRICULAR ZONES OF
THE MESENCEPHALON AND RHOMBENCEPHALON. ISOFORMS 3 AND 4 ARE
EXPRESSED AT HIGHER LEVEL COMPARED TO OTHER ISOFORMS BETWEEN E11.5
AND E16.5.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. DCC
SUBFAMILY.
CC -!- SIMILARITY: Contains 4 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 6 fibronectin type III domains.
CC
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CC
CC EMBL; Y09535; CAA70727.1; -.
CC HSP; P02751; 1TTF.
DR MGD; MGI:1097159; Neol.
DR InterPro; IPR003961; FN.III.
DR InterPro; IPR003962; FniII_subd.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig C2.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00041; fn3; 6.
DR Pfam; PF00047; Ig; 4.
DR PRINTS; PR00014; FNTYPEIII.
DR SMART; SM00060; FN3; 6.
DR SMART; SM00408; IGC2; 4.
DR PROSITE; PS00835; IG LIKE; 4.
DR Cell adhesion; Repeat; Signal; Transmembrane; Immunoglobulin domain;
KW Glycoprotein; Alternative splicing.
FT SIGNAL 1 36
FT CHAIN 37 1493
FT DOMAIN 37 1136
FT TRANSMEM 1137 1157
FT DOMAIN 1158 1493
FT DOMAIN 63 158
FT DOMAIN 163 249
FT DOMAIN 254 347
FT DOMAIN 352 437

FT	DOMAIN	467	564	FIBRONECTIN TYPE-III 1.
FT	DOMAIN	567	660	FIBRONECTIN TYPE-III 2.
FT	DOMAIN	561	760	FIBRONECTIN TYPE-III 3.
FT	DOMAIN	766	860	FIBRONECTIN TYPE-III 4.
FT	DOMAIN	881	981	FIBRONECTIN TYPE-III 5.
FT	DOMAIN	982	1083	FIBRONECTIN TYPE-III 6.
FT	DOMAIN	1149	1153	POLY-VAL.
FT	DISULFID	85	140	BY SIMILARITY.
FT	DISULFID	184	232	BY SIMILARITY.
FT	DISULFID	271	331	BY SIMILARITY.
FT	DISULFID	373	421	BY SIMILARITY.
FT	CARBOHYD	84	84	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	221	221	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	337	337	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	501	501	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	520	520	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	670	670	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	746	746	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	940	940	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPLIC	442	461	Missing (in isoform 2). /FTid=VSP_002594.
FT	VARSPLIC	863	878	Missing (in isoform 3). /FTid=VSP_002595.
FT	VARSPLIC	1086	1096	Missing (in isoform 4). /FTid=VSP_002596.
FT	VARSPLIC	1279	1331	Missing (in isoform 5). /FTid=VSP_002597.
SQ	SEQUENCE	1493 AA;	163159 MW;	441DE919D5E17C0E CRC64;

Query Match 14.2%; Score 209; DB 1; Length 1493;
Beat Local Similarity 29.5%; Pred. No. 1e-08;
Matches 64; Conservative 32; Mismatches 99; Indels 22; Gaps 6;

Qy	3	SPQILVHPQDLFGQPGPARMSCRAGQPPPTIRLLNGQLSMVPPDPHLLPDGTL 62
Db	62	TPFVFLVPEVDTLSVRGSSVILNCAYSERSPNIEWKDGTFLLNLESDRRQLPDGSLF 121
Qy	63	LLQPPARGHADGQALSTDLGVYTCAS-NRLGTAVSARGARLSVAVLREDFOIQPRDVA 121
Db	122	ISNVVHSHKN-----KPDGFGYOCVATVDNLGTFIVSTAKTLVAGLPR-FTSQPEPSSV 174
Qy	122	VVGQFTLEGPPMGHPE-----PTVSWKDGKPLALQPGRHTVSGGSLMARAESDE 175
Db	175	YVGNAILNC-----EVNADLVFVRWEQNRQPLLLDDRIKVLPSGTLVISNATEGDG 227
Qy	176	XTYMCVATNSAGHRESRAARVSI-QEPQDYTEPVELL 211
Db	228	GLYRCIVESGGPPKFSDEALKVLQDPEEIVDLVFLM 264

RESULT 14
DCC_HUMAN
ID -DCC_HUMAN STANDARD; PRT; 1447 AA.
AC P43146;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tumor suppressor protein DCC precursor (Colorectal cancer suppressor).
GN DCC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95011532; PubMed=7926722;
RA Hedrick L., Cho K.R., Fearon E.R., Wu T.-C., Kinzler K.W.,
RA Vogelstein B.;
RT "The DCC gene product in cellular differentiation and colorectal
tumorigenesis";
RL Genes Dev. 8:1174-1183(1994).
RN [2]
RP SEQUENCE OF 1-750 FROM N.A.

DCC_MOUSE
ID - DCC_MOUSE STANDARD; PRT; 1447 AA.
AC P70211;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tumor suppressor protein DCC precursor.
GN DCC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBT_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS A; B AND C).
RC STRAIN=BALB/c; TISSUE=Brain;
RX MEDLINE=96112625; PubMed=8570174;
RA Cooper H.M., Ames P., Britto J., Gad J., Wilke A.F.;
RT "Cloning of the mouse homologue of the deleted in colorectal cancer
gene (mdcc) and its expression in the developing mouse embryo.";
RL Oncogene 11:2243-2254(1995).
RN [2]
RP REVISIONS.
RC STRAIN=BALB/c; TISSUE=Brain;
RA Cooper H.M.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: IMPLICATED AS A TUMOR SUPPRESSOR GENE.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=A;
CC IsoId=p70211-1; Sequence=Displayed;
CC Note=Isoform B is produced by alternative initiation at Met-85
CC of isoform A;
CC Name=C;
CC IsoId=p70211-2; Sequence=VSP_002501;
CC Comment=2 isoforms, A (shown here) and B, are produced by
CC alternative initiation at Met-1 and Met-85;
CC -!- TISSUE SPECIFICITY: IN THE EMBRYO, EXPRESSED AT HIGH LEVELS IN THE
CC DEVELOPING BRAIN AND NEURAL TUBE. IN ADULT, HIGHLY EXPRESSED IN
CC BRAIN WITH VERY LOW LEVELS FOUND IN TESTIS, HEART AND THYMUS.
CC ISOFORM C IS EXPRESSED ONLY IN THE EMBRYO.
CC -!- DEVELOPMENTAL STAGE: LOW LEVELS IN EARLY GESTATION. HIGHEST LEVELS
CC EXPRESSED DURING MID GESTATION. LEVELS DECREASE IN LATE GESTATION
CC AND REMAIN AT THIS LEVEL IN THE ADULT.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. DCC
CC SUBFAMILY.
CC -!- SIMILARITY: Contains 4 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 6 fibronectin type III domains.

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DR EMBL; X85788; CAA59786.1; -;
DR HSSP; P56276; ITUK.
DR MGD; MGI:94869; DCC.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR003962; FNIII subd.
DR InterPro; IPR007110; Ig-Like.
DR InterPro; IPR003598; Ig_C2.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00041; fn3; 6.
DR PRINTS; PR00014; FNTPYPIII.
DR SMART; SM00060; FN3; 6.
DR SMART; SM00408; IGC2; 3.
DR PROSITE; PS50835; IG_LIKE; 4.
KW Glycoprotein; Immunoglobulin domain; Transmembrane; Signal;

Repeat; Anti-oncogene; Alternative initiation; Alternative splicing.
KW SIGNAL 1 25
FT CHAIN 26 1447
FT CHAIN 85 1447
FT INIT_MET 85 85
FT DOMAIN 26 1097
FT TRANSMEM 1098 1122
FT DOMAIN 1123 1447
FT DOMAIN 36 135
FT DOMAIN 139 229
FT DOMAIN 234 326
FT DOMAIN 331 416
FT DOMAIN 426 522
FT DOMAIN 525 618
FT DOMAIN 619 716
FT DOMAIN 722 816
FT DOMAIN 840 940
FT DOMAIN 941 1042
FT DISULFID 61 117
FT DISULFID 161 212
FT DISULFID 261 310
FT DISULFID 352 400
FT CARBOHYD 60 60
FT CARBOHYD 94 94
FT CARBOHYD 299 299
FT CARBOHYD 318 318
FT CARBOHYD 478 478
FT CARBOHYD 628 628
FT CARBOHYD 702 702
FT CARBOHYD 819 838
FT VARSPLIC
SQ SEQUENCE 1447 AA; 158298 MW; ODIF1097C22DSB9F CRC64;
Query Match 14.2%; Score 209; DB 1; Length 1447;
Best Local Similarity 27.7%; Pred. No. 9.6e-09;
Matches 67; Conservative 37; Mismatches 98; Indels 40; Gaps 10;
Qy 24 MSCRASQPPPTIRWLINGQPLSMVPPDPH-HLLPDCGTL--LQPPARGAHDGQALST 80
Db 159 LKCEVIGEPPTTHWKNQDNLPLPGDSRVVLPSCALQISRLQP-----G 205
Qy 81 DLGYTCEASNRLGTAVSRCARLSAVLRD-----FQIQPDMVAVVGEQFTLEGCP 133
Db 206 DSGYRCSARN--PASIRTGNEAEVRILSDPGLHRQLYFLQRPNSVIAIEGKDAVLECCV 263
Qy 134 PWGHPPTVSWKDGKPLALQGRHTVSGGS-LLMARAESDXYTMCVATNSAGHRESR 192
Db 264 S-GYPPSPFTWLRGEEVIQSRKYSLLGGSNLLISNVTDDSGTYTCVVTYKKNISAS 322
Qy 193 AARVSIQEPQDYTEPVELLA---VRIQLENVTLINPDPAEGPKPRPAVWLXWKVSGPKRL 249
Db 323 AELTVLVPFPFLNHPNSLYAVESMDIEFE-----CAVSGKPVPTV--NMKNGDVI 372
Qy 250 PN 251
Db 373 PS 374
RESULT 13
NEOI_MOUSE
ID NEOI_MOUSE STANDARD; PRT; 1493 AA.
AC P97798;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Neogenin precursor.
GN NEOI OR NGN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBT_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon carcinoma, and Placenta;
RX MEDLINE=96074849; PubMed=7478540;
RA Mossie K., Jallal B., Alves F., Sures I., Plowman G.D., Ullrich A.;
RT "Colon carcinoma kinase-4 defines a new subclass of the receptor
RT tyrosine kinase family.";
RL Oncogene 11:2179-2184(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Fibroblast; PubMed=8882711;
RX MEDLINE=97037064; PubMed=8882711;
RA Park S.-K., Lee H.-S., Lee S.-T.;
RT "Characterization of the human full-length PTK7 cDNA encoding a
RT receptor protein tyrosine kinase-like molecule closely related to
RL chick KLG.";
RN J. Biochem. 119:235-239(1996).
RN [3]
RP SEQUENCE FROM N.A., AND REVISION TO 834.
RA Lee S.-T., Park S.-K., Lee H.-S., Ji A.R., Jung J.W.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: MAY FUNCTION AS A CELL ADHESION MOLECULE. LACKS PROBABLY
CC THE CATALYTIC ACTIVITY OF TYROSINE KINASE. MAY BE CONNECTED TO THE
CC PATHOPHYSIOLOGY OF COLON CARCINOMAS AND/OR MAY REPRESENT A TUMOR
CC PROGRESSION MARKER.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LUNG, LIVER, PANCREAS,
CC KIDNEY, PLACENTA AND MELANOCYTES. WEAKLY EXPRESSED IN THYROID
CC GLAND, OVARY, BRAIN, HEART AND SKELETAL MUSCLE. ALSO EXPRESSED IN
CC ERTHROLEUKEMIA CELLS. BUT NOT EXPRESSED IN COLON.
CC -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. INSULIN
CC RECEPTOR SUBFAMILY.
CC -!- SIMILARITY: Contains 7 immunoglobulin-like C2-type domains.
CC -----
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CC -----
DR EMBL; U33635; AA87565.1; -
DR EMBL; U40271; AAC50484.2; -
DR EMBL; AF447176; AAL39062.1; -
DR EMBL; AF447157; AAL39062.1; JOINED.
DR EMBL; AF447158; AAL39062.1; JOINED.
DR EMBL; AF447162; AAL39062.1; JOINED.
DR EMBL; AF447164; AAL39062.1; JOINED.
DR EMBL; AF447167; AAL39062.1; JOINED.
DR EMBL; AF447170; AAL39062.1; JOINED.
DR EMBL; AF447171; AAL39062.1; JOINED.
DR EMBL; AF447173; AAL39062.1; JOINED.
DR EMBL; AF447174; AAL39062.1; JOINED.
DR EMBL; AF447175; AAL39062.1; JOINED.
DR HSSP; P08631; IAD5.
DR Genew; HGNC:9618; PTK7.
DR MIM; 601830; -
DR GO; GO:0005886; C:plasma membrane; TAS.
DR GO; GO:0005888; C:proteoglycan integral to plasma membrane; TAS.
DR GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. .; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002011; RTKinaseII.
DR InterPro; IPR001245; Tyr_kinase.
PFam; PF00047; ig; 7.

DR PFam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00408; IGc2; 5.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00835; IG_LIKE; 7.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
DR PROSITE; PS00239; RECEPTOR_TYR_KIN_II; FALSE NEG.
KW Receptor; Transmembrane; Signal; Glycoprotein; Cell adhesion;
KW Immunoglobulin domain; Repeat.
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 1070 TYROSINE-PROTEIN KINASE-LIKE 7.
FT DOMAIN 31 704 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 705 725 POTENTIAL.
FT DOMAIN 726 1070 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 31 120 IG-LIKE C2-TYPE 1.
FT DOMAIN 128 218 IG-LIKE C2-TYPE 2.
FT DOMAIN 225 317 IG-LIKE C2-TYPE 3.
FT DOMAIN 309 407 IG-LIKE C2-TYPE 4.
FT DOMAIN 412 497 IG-LIKE C2-TYPE 5.
FT DOMAIN 503 586 IG-LIKE C2-TYPE 6.
FT DOMAIN 578 680 IG-LIKE C2-TYPE 7.
FT DOMAIN 796 1066 PROTEIN KINASE; INACTIVE.
FT DISULFID 53 101 BY SIMILARITY.
FT DISULFID 150 200 BY SIMILARITY.
FT DISULFID 246 301 BY SIMILARITY.
FT DISULFID 343 391 BY SIMILARITY.
FT DISULFID 433 481 BY SIMILARITY.
FT DISULFID 524 570 BY SIMILARITY.
FT DISULFID 613 664 BY SIMILARITY.
FT CARBOHYD 116 116 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 175 175 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 184 184 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 214 214 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 268 268 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 283 283 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 405 405 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 567 567 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 646 646 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 92 92 P -> R (IN REF. 2 AND 3).
FT CONFLICT 147 147 K -> T (IN REF. 2 AND 3).
FT CONFLICT 207 207 S -> G (IN REF. 2 AND 3).
FT CONFLICT 495 496 VL -> RV (IN REF. 2 AND 3).
FT CONFLICT 515 515 G -> E (IN REF. 2 AND 3).
FT CONFLICT 881 881 E -> G (IN REF. 2 AND 3).
FT CONFLICT 969 969 A -> P (IN REF. 2 AND 3).
FT CONFLICT 992 992 S -> F (IN REF. 2 AND 3).
SQ SEQUENCE 1070 AA; 118260 MW; 47CDF25B8E3698A5 CRC64;
Query Match 14.4%; Score 212.5; DB 1; Length 1070;
Best Local Similarity 29.1%; Pred. No. 3.6e-09;
Matches 62; Conservative 34; Mismatches 92; Indels 25; Gaps 7;
Qy 2 DSPQILVHPDQLFCQGGPARMSCRASGQPPPTIRLLNQ-Q-PLSMVPPDPH---HLL 56
Db 222 ESPARVVLAPQDVVVAARYEAMFHCQFSAQPPPSLQWLFEDETITNRSRPHLRATVF 281
Qy 57 PDGTLILLQPPARGHAGDQALSTDLGVYTCASNRLGTAVSRGARSVAVLREDFQIQP 116
Db 282 ANGSLLLTQVRP-----NAGIYICGQGRGPPILEATLHLAIEDMPLEP 330
Qy 117 RDMVAVVGEQFTLECGPPWGHPEPTVSWKDGKPLQPGRHVTYGGSLMARAKSDX 176
Db 331 R--VFTAGSERVTCPLPKGLPEPSV-WWEHAGVRLPTHGRVYQKGHVLVLAIESDAG 387
Qy 177 TYMCVATNSAGHRES-----RAARVS--IQSPQD 203
Db 388 VYTCHAANLAGQRQRRQDNYITVATVPSWLKKPQD 420
RESULT 12

```
FT CONFLICT 168 168 /FTid=VSP 002593.
SQ SEQUENCE 1461 AA; 159958 MW; 7AAE897E69635A21 CRC64;

Query Match 14.5%; Score 214.5; DB 1; Length 1461;
Best Local Similarity 22.7%; Pred. No. 3.6e-09;
Matches 79; Conservative 39; Mismatches 117; Indels 113; Gaps 9;

Qy 3 SPPQILVHPDQFQPGFAPKSCASQPPPTIRWLLNGQPLSMVPPDPHLLPDGTL 62
Db 51 TFFVFLVPEVDTLSVRGSSVILNAYSSEPKIEWKDGTFLLNLSDDRRQLLPDGS 110
Qy 63 LLQPPARGHAGDQALSDGLVYTCAS-NRLGTAVSRGARSVA----- 106
Db 111 ISNVVHSHKN-----KDEGYQCVAVESLGTIIISRTAKLIVAGLPRFTSQBPSSVY 164
Qy 107 -----VLRED----- 111
Db 165 AGGAILNCEVNAIDLVPVRWEQNRQPLLLDDRVIKLPGLMVLVSNATEGGGLYRCVVE 224
Qy 112 -----FOIQPRDMVAVVGEQFTLECGPPWGHGPTVSWW 145
Db 225 SGGPKPYSDVELKVLDPDEVIDLFLKQPSPLRVIGQDVLPVPCVAS-GLPTTIKMM 283
Qy 146 KDGKPLALQPGRHVTV--SGSLLMARAEKSDXTYMCVATNSAGHRESRAARVSTQEPQD 203
Db 284 KNEEALDTSESSERVLVLLAGSLISDVTEDDAGTYFCIADNGNETIEAQAELTVQAQEPF 343
Qy 204 YTEPVELLAVRIQLENVLLNPDPAAGPKPRPAVWLKWKVSGPRKLPN 251
Db 344 LKQPTNIYA----HESMDIVFECEVTG-KPTPTV--KWKNGDMVIPS 384

RESULT 10
AXOI CHICK STANDARD; PRT; 1036 AA.
AC P28685;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Contactin 2 precursor (Axonin-1).
GN CNTN2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauromorpha; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX TISSUE=Brain;
RA MEDLINE=92174898; PubMed=1311675;
RA Zuehlig R.A., Rader C., Schroeder A., Kalousek M.B.,
RA von Bohlen Und Halbach F., Osterwalder T., Inan C., Stoeckli E.T.,
RA Affolter H.-U., Fritz A., Hafen E., Sonderegger P.;
RT "The axonally secreted cell adhesion molecule, axonin-1. Primary
RT structure, immunoglobulin-like and fibronectin-type-III-like domains
RT and glycosyl-phosphatidylinositol anchorage.";
RL Eur. J. Biochem. 204:453-463(1992).
CC -!- FUNCTION: AXON-ASSOCIATED CELL ADHESION MOLECULE (AXCAM) WHICH
CC PROMOTES NEURITE OUTGROWTH BY INTERACTION WITH THE AXCAM L1 (G4)
CC OF NEURITIC MEMBRANE.
CC -!- SUBCELLULAR LOCATION: ATTACHED TO THE NEURONAL MEMBRANE BY A
CC GPI-ANCHOR.
CC -!- PTM: The N-terminus is blocked.
CC -!- SIMILARITY: Contains 6 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 4 fibronectin type III domains.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
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CC
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or send an email to license@isb-sib.ch.
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CC EMEL; X63101; CAA44815.1; -.
CC PIR; S22383; S22383.
CC PDB; 1CS6; 19-MAY-00.
CC InterPro; IPR003961; FN III.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003598; Ig_c2.
CC InterPro; IPR003006; Ig_MHC.
CC Pfam; PF00041; fn3; 3.
CC Pfam; PF00047; Ig; 6.
CC SMART; SM00408; IGG2; 5.
CC PROSITE; PS00835; IG_LIKE; 6.
KW Immunoglobulin domain; Glycoprotein; Signal; GPI-anchor;
KW Cell adhesion; Repeat; 3D-structure.
FT SIGNAL 1 23 OR 25 (POTENTIAL)..
FT CHAIN 24 ? CONTACTIN 2.
FT PROPEP ? 1036 REMOVED IN MATURE FORM.
FT DOMAIN 32 123 IG-LIKE C2-TYPE 1.
FT DOMAIN 128 223 IG-LIKE C2-TYPE 2.
FT DOMAIN 234 317 IG-LIKE C2-TYPE 3.
FT DOMAIN 322 406 IG-LIKE C2-TYPE 4.
FT DOMAIN 412 499 IG-LIKE C2-TYPE 5.
FT DOMAIN 504 598 IG-LIKE C2-TYPE 6.
FT DOMAIN 599 608 HINGE (POTENTIAL).
FT DOMAIN 601 607 GLY/PRO-RICH.
FT DOMAIN 608 709 FIBRONECTIN TYPE-III 1.
FT DOMAIN 710 811 FIBRONECTIN TYPE-III 2.
FT DOMAIN 812 912 FIBRONECTIN TYPE-III 3.
FT DOMAIN 913 1009 FIBRONECTIN TYPE-III 4.
FT CARBOHYD 71 71 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 199 199 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 456 456 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 472 472 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 493 493 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 520 520 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 770 770 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 900 900 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 914 914 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 1036 AA; 113301 MW; 08B80143BE79794 CRC64;

Query Match 14.5%; Score 213.5; DB 1; Length 1036;
Best Local Similarity 30.7%; Pred. No. 2.9e-09;
Matches 70; Conservative 31; Mismatches 96; Indels 41; Gaps 11;

Qy 24 MSCRASGQPPPTIRWLLNGQPLSMVPPDPHLLPDGTLTLLQPPARGHAGDQALSD 83
Db 54 LTCRANPPATYRWKNGTELKM-GPDSRYRLVAGDLVISNP-----VKAKDAG 102
Qy 84 VYTCEASNRLGTAVSRGARSVAVLREDFOIQPRDMVAVV---GEQFTLECGPPWGHPEP 140
Db 103 SYQCVAATNARGTVVSRASLRFGLQF-FAAEEDPVKITEGWMVFT--CSPPPHYPAL 159
Qy 141 TVSWKDKGKPLAL-QPGRHVTYS--GGSLLMARAEKSDXTYMCVATNSAGHRE----- 190
Db 160 SYRWLLNEFFNFIPADGRFVSQTTGNLYIAKTEASDLGNYSFCFATS---HIDFTTKSVF 216
Qy 191 SRAARVSI--QEPDYTEPVE-----LLAVRIQLENVTLNPD 227
Db 217 SKFSQLSLAAEDARQYAPSIKAKFPADTYALTQMTVLECFAGFNPVP 264

RESULT 11
PTK7 HUMAN
ID PTK7 HUMAN STANDARD; PRT; 1070 AA.
AC Q13308; Q13417;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tyrosine-protein kinase-like 7 precursor (Colon carcinoma kinase-4)
DE (CCK-4).
GN PTK7 OR CCK4.
```


CC IsoId=P23468-1; Sequence=Displayed;
 CC Name=2; Synonym=Kidney;
 CC IsoId=P23468-2; Sequence=VSP_005147, VSP_005148, VSP_005149;
 CC Name=3; Synonym=Fetal brain;
 CC IsoId=P23468-3; Sequence=VSP_005150;
 CC FROM THE TRANSMEMBRANE SEGMENT.
 CC -1- CLEAVAGE OCCURS THAT SEPARATES THE EXTRACELLULAR DOMAIN
 CC FROM THE TRANSMEMBRANE SEGMENT.
 CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
 CC -1- SIMILARITY: Contains 8 fibronectin type III domains.
 CC -1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; L38929; AAC41749.1; -;
 CC EMBL; X54133; CAA38068.1; -;
 CC PIR; A56178; A56178.
 CC HSP; P18052; 1YFO.
 CC Genew; HGNC:9668; PTPRD.
 CC MIM; 601598; -;
 CC GO; GO:0005887; C: integral to plasma membrane; TAS.
 CC GO; GO:0005001; P: transmembrane receptor protein tyrosine pho. . .; TAS.
 CC GO; GO:0006470; P: protein amino acid dephosphorylation; TAS.
 CC GO; GO:0007185; P: transmembrane receptor protein tyrosine pho. . .; TAS.
 CC InterPro; IPR003961; FN_III.
 CC InterPro; IPR003962; FNIII_subd.
 CC InterPro; IPR007110; IG-like.
 CC InterPro; IPR003598; IG_c2.
 CC InterPro; IPR003006; IG_MHC.
 CC InterPro; IPR000387; TYR phosphatase.
 CC InterPro; IPR000242; Tyr_PP.
 CC Pfam; PF00041; fn3; 8.
 CC Pfam; PF00047; Ig; 3.
 CC Pfam; PF00102; Y_phosphatase; 2.
 CC PRINTS; PR00014; FNTYPEIII.
 CC PRINTS; PR00700; PRTPHPTASE.
 CC SMART; SM00060; FN3; 8.
 CC SMART; SM00408; IGC2; 2.
 CC SMART; SM00194; PTPC; 2.
 CC PROSITE; PS00835; IG LIKE; 3.
 CC PROSITE; PS00383; TYR PHOSPHATASE 1; 2.
 CC PROSITE; PS00056; TYR_PHOSPHATASE_2; 2.
 CC PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 2.
 KW Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane; Repeat;
 KW Immunoglobulin domain; Alternative splicing.
 FT SIGNAL 1 20
 FT CHAIN 21 1912
 FT DOMAIN 21 1265
 FT TRANSMEM 1266 1290
 FT DOMAIN 1291 1912
 FT DOMAIN 24 114
 FT DOMAIN 126 224
 FT DOMAIN 236 318
 FT DOMAIN 320 414
 FT DOMAIN 417 513
 FT DOMAIN 516 606
 FT DOMAIN 609 708
 FT DOMAIN 711 822
 FT DOMAIN 825 916
 FT DOMAIN 918 1017
 FT DOMAIN 1020 1137
 FT DOMAIN 1375 1618
 FT DOMAIN 1619 1912
 FT ACT_SITE 1553 1553
 FT ACT_SITE 1844 1844
 FT SITE 1175 1178
 FT CARBOHYD 254 254
 FT CARBOHYD 299 299

FT CARBOHYD 724 724 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 832 832 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 181 189 Missing (in isoform 2).
 FT VARSPLIC 226 229 Missing (in isoform 2).
 FT VARSPLIC 775 783 Missing (in isoform 2).
 FT VARSPLIC 609 1137 Missing (in isoform 3).
 FT MUTAGEN 1178 1178 R->A: 2.5-FOLD REDUCTION IN CLEAVAGE.
 SQ SEQUENCE 1912 AA; 214759 MW; 3A88C8CD32182E26 CRC64;
 Query Match 15.1%; Score 222; DB 1; Length 1912;
 Best Local Similarity 32.5%; Pred. No. 1.3e-09;
 Matches 74; Conservative 37; Mismatches 67; Indels 50; Gaps 14;
 Qy 2 DSPQILVHPDQLFQCGPGPARMSCRAGQPPPTIRWLLNGQPLS-----MVPDPHLL 56
 Db 21 ETPPFRTRTPVDQTGSGVASFCQATGDPRPKIVWKKGVSNORFEVIEFDD---- 76
 Qy 57 PDGTLTLLQPPARGHAGHQAALST--DLGVYTCASNRLGTAVERGARLSVAVLRDFOI 114
 Db 77 GSGSVLRIQP-----LRTPRDEAIYECVASNNVG-EISVSTRLT--VLRED-QI 121
 Qy 115 QPRDMVAV-VGEQF-----TLECGPPWGHPEPTVSWMKGKPL--ALQPCR----- 157
 Db 122 -PRGFPIDMGPKLVKVERETATMLCAAS-GNPDPEITWFKDPLVDTSNNNGRIKQLR 179
 Qy 158 -HTVSG-----GSLMARAEKSDXTYMCVATNSAGHRESRAARVSIQE 200
 Db 180 SESGGTPIRGALQIEQESDQGYECVATNSAGTRYSPANLYVRE 227
 RESULT 6
 LAR_DROME
 ID LAR DROME STANDARD; PRT; 2029 AA.
 AC P16621;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Protein-tyrosine phosphatase lar precursor (EC 3.1.3.48) (Protein-
 DE tyrosine-phosphate phosphohydrolase) (dLAR).
 GN LAR.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90046860; PubMed=2554325;
 RA Streuli M., Krueger N.X., Tsai A.Y.M., Saito H.;
 RT "A family of receptor-linked protein tyrosine phosphatases in humans
 RT and Drosophila."
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8698-8702(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Canton-S;
 RX MEDLINE=96178473; PubMed=8598047;
 RA Krueger N.X., van Vactor D., Wan H.I., Gelbart W.M., Goodman C.S.,
 RA Saito H.;
 RT "The transmembrane tyrosine phosphatase DLAR controls motor axon
 RT guidance in Drosophila."
 RL Cell 84:611-622(1996).
 CC -1- FUNCTION: IT IS POSSIBLE THAT DLAR IS A CELL ADHESION RECEPTOR.
 CC IT POSSESSES AN INTRINSIC PROTEIN TYROSINE PHOSPHATASE ACTIVITY
 CC (PTPASE). IT CONTROLS MOTOR AXON GUIDANCE.
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
 CC tyrosine + phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: SELECTIVELY EXPRESSED IN A SUBSET OF AXONS AND
 CC PIONEER NEURONS IN THE EMBRYO.

FT	DOMAIN	924	933	LAMININ EGF-LIKE 5 (N-TERMINAL).	FT	DISULFID	1641	1650	BY SIMILARITY.
FT	DOMAIN	934	1125	LAMININ DOMAIN IV 2 (DOMAIN III B).	FT	DISULFID	1653	1668	BY SIMILARITY.
FT	DOMAIN	1126	1158	LAMININ EGF-LIKE 5 (C-TERMINAL).	FT	DISULFID	1792	1839	BY SIMILARITY.
FT	DOMAIN	1159	1208	LAMININ EGF-LIKE 6.	FT	DISULFID	1886	1932	BY SIMILARITY.
FT	DOMAIN	1209	1265	LAMININ EGF-LIKE 7.	FT	DISULFID	1976	2021	BY SIMILARITY.
FT	DOMAIN	1275	1324	LAMININ EGF-LIKE 8.	FT	DISULFID	2073	2118	BY SIMILARITY.
FT	DOMAIN	1325	1334	LAMININ EGF-LIKE 9 (N-TERMINAL).	FT	DISULFID	2170	2215	BY SIMILARITY.
FT	DOMAIN	1335	1529	LAMININ DOMAIN IV 3 (DOMAIN III C).	FT	DISULFID	2268	2313	BY SIMILARITY.
FT	DOMAIN	1530	1562	LAMININ EGF-LIKE 9 (C-TERMINAL).	FT	DISULFID	2365	2413	BY SIMILARITY.
FT	DOMAIN	1563	1612	LAMININ EGF-LIKE 10.					
FT	DOMAIN	1613	1670	LAMININ EGF-LIKE 11.					
FT	DOMAIN	1677	1771	IG-LIKE C2-TYPE 2.					
FT	DOMAIN	1772	1865	IG-LIKE C2-TYPE 3.					
FT	DOMAIN	1866	1954	IG-LIKE C2-TYPE 4.					
FT	DOMAIN	1955	2049	IG-LIKE C2-TYPE 5.					
FT	DOMAIN	2050	2148	IG-LIKE C2-TYPE 6.					
FT	DOMAIN	2149	2244	IG-LIKE C2-TYPE 7.					
FT	DOMAIN	2245	2343	IG-LIKE C2-TYPE 8.					
FT	DOMAIN	2344	2436	IG-LIKE C2-TYPE 9.					
FT	DOMAIN	2437	2532	IG-LIKE C2-TYPE 10.					
FT	DOMAIN	2533	2619	IG-LIKE C2-TYPE 11.					
FT	DOMAIN	2620	2720	IG-LIKE C2-TYPE 12.					
FT	DOMAIN	2721	2809	IG-LIKE C2-TYPE 13.					
FT	DOMAIN	2810	2895	IG-LIKE C2-TYPE 14.					
FT	DOMAIN	2896	2980	IG-LIKE C2-TYPE 15.					
FT	DOMAIN	2984	3162	LAMININ G-LIKE 1.					
FT	DOMAIN	3163	3241	EGF-LIKE.					
FT	DOMAIN	3245	3425	LAMININ G-LIKE 2.					
FT	DOMAIN	3518	3705	LAMININ G-LIKE 3.					
FT	SITE	65	67	HEPARAN SULFATE (POTENTIAL).					
FT	SITE	71	73	HEPARAN SULFATE (POTENTIAL).					
FT	SITE	76	78	HEPARAN SULFATE (POTENTIAL).					
FT	SITE	3615	3617	MEDIATES MOTOR NEURON ATTACHMENT (POTENTIAL).					
FT	DISULFID	199	212	BY SIMILARITY.					
FT	DISULFID	206	225	BY SIMILARITY.					
FT	DISULFID	219	234	BY SIMILARITY.					
FT	DISULFID	285	297	BY SIMILARITY.					
FT	DISULFID	222	310	BY SIMILARITY.					
FT	DISULFID	304	319	BY SIMILARITY.					
FT	DISULFID	325	337	BY SIMILARITY.					
FT	DISULFID	332	350	BY SIMILARITY.					
FT	DISULFID	344	359	BY SIMILARITY.					
FT	DISULFID	368	381	BY SIMILARITY.					
FT	DISULFID	375	394	BY SIMILARITY.					
FT	DISULFID	388	403	BY SIMILARITY.					
FT	DISULFID	428	479	BY SIMILARITY.					
FT	DISULFID	764	773	BY SIMILARITY.					
FT	DISULFID	766	780	BY SIMILARITY.					
FT	DISULFID	783	792	BY SIMILARITY.					
FT	DISULFID	795	811	BY SIMILARITY.					
FT	DISULFID	814	829	BY SIMILARITY.					
FT	DISULFID	816	839	BY SIMILARITY.					
FT	DISULFID	842	851	BY SIMILARITY.					
FT	DISULFID	854	869	BY SIMILARITY.					
FT	DISULFID	1159	1168	BY SIMILARITY.					
FT	DISULFID	1161	1175	BY SIMILARITY.					
FT	DISULFID	1178	1187	BY SIMILARITY.					
FT	DISULFID	1190	1206	BY SIMILARITY.					
FT	DISULFID	1209	1224	BY SIMILARITY.					
FT	DISULFID	1211	1234	BY SIMILARITY.					
FT	DISULFID	1237	1246	BY SIMILARITY.					
FT	DISULFID	1249	1263	BY SIMILARITY.					
FT	DISULFID	1277	1287	BY SIMILARITY.					
FT	DISULFID	1295	1304	BY SIMILARITY.					
FT	DISULFID	1307	1322	BY SIMILARITY.					
FT	DISULFID	1563	1572	BY SIMILARITY.					
FT	DISULFID	1565	1579	BY SIMILARITY.					
FT	DISULFID	1582	1591	BY SIMILARITY.					
FT	DISULFID	1594	1610	BY SIMILARITY.					
FT	DISULFID	1613	1628	BY SIMILARITY.					
FT	DISULFID	1615	1638	BY SIMILARITY.					

Query Match 15.3%; Score 225; DB 1; Length 3707;

Best Local Similarity 27.6%; Pred. No. 1.6e-09;

Matches 72; Conservative 37; Mismatches 86; Indels 66; Gaps 13;

QY 4 PPQILVHPQDQOLFQPGPARM-----SCRASGPPPTIRWLLNGQPLSMWP-----PDP 52

Db 2433 PPTVSVLP-----EGPVHVMGKDITLCSGSPRSPRWTRLGIPVKLEPRMGLMNS 2487

QY 53 HLLPDGTLLLPARGHAGHDGQALSTDLGVYTCESNRILGTA-----VSRGARSV 105

Db 2488 HAML---KIASVKP-----SDAGTYVCOAQNALGTAQKQVELIVDTG---TV 2528

QY 106 AVLREDFQIQPRDMVAVVGEQFTLECGPPFHPPTVSWKDGKPLALQPGRHVTSGSL 165

Db 2529 APGTPQVQVESELTLGAGHTATLHCSAT-GNPPPTIHWKLRAPL---PQHRIEGNTL 2584

QY 166 LMAAEKSDXTYMCVATNSAGHRESRAARVISIOPQDYT-----EPVELLAVRIQL 217

Db 2585 VIPVAQDQSQYICNATNSAGHTEATVV-LHVESPPYATIPEHTSAQGNL-----VOL 2639

QY 218 ENVTLLNPDPAGPKPRPAVW 238

Db 2640 QCL-----AHGTPPLTYQW 2653

RESULT 5

PTPD HUMAN

ID_PTPD HUMAN STANDARD; PRT; 1912 AA.

AC P23468;

DT 01-NOV-1991 (Rel. 20, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Protein-tyrosine phosphatase delta precursor (EC 3.1.3.48) (R-PTP-

delta).

GN PTPRD.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

[1]

RP SEQUENCE FROM N.A., AND MUTAGENESIS OF ARG-1178.

RX MEDLINE=9520468; PubMed=7896816;

RA Pulido R., Krueger N.X., Serra-Pages C., Saito H., Streuli M.;

"Molecular characterization of the human transmembrane protein-

tyrosine phosphatase delta. Evidence for tissue-specific expression of

alternative human transmembrane protein-tyrosine phosphatase delta

isoforms.";

RL J. Biol. Chem. 270:6722-6728 (1995).

[2]

RN SEQUENCE OF 390-1912 FROM N.A.

RC TISSUE=Placenta;

RX MEDLINE=91006018; PubMed=2170109;

RA Krueger N.X., Streuli M., Saito H.;

"Structural diversity and evolution of human receptor-like protein

tyrosine phosphatases.";

RL EMBO J. 9:3241-3252 (1990).

CC -|- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein

tyrosine + phosphate.

CC -|- SUBCELLULAR LOCATION: Type I membrane protein.

CC -|- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=3;

Comment=Additional isoforms seem to exist;

Name=1;

;; PRIOR APPLICATION NUMBER: 60/081838
;; PRIOR FILING DATE: 1998-04-15
;; PRIOR APPLICATION NUMBER: 60/082568
;; PRIOR FILING DATE: 1998-04-21
;; PRIOR APPLICATION NUMBER: 60/082569
;; PRIOR FILING DATE: 1998-04-21
;; PRIOR APPLICATION NUMBER: 60/082704
;; PRIOR FILING DATE: 1998-04-22
;; PRIOR APPLICATION NUMBER: 60/082804
;; PRIOR FILING DATE: 1998-04-22
;; PRIOR APPLICATION NUMBER: 60/082700
;; PRIOR FILING DATE: 1998-04-22
;; PRIOR APPLICATION NUMBER: 60/082797
;; PRIOR FILING DATE: 1998-04-22
;; PRIOR APPLICATION NUMBER: 60/082796
;; PRIOR FILING DATE: 1998-04-23
;; PRIOR APPLICATION NUMBER: 60/083336
;; PRIOR FILING DATE: 1998-04-27
;; PRIOR APPLICATION NUMBER: 60/083322
;; PRIOR FILING DATE: 1998-04-28
;; PRIOR APPLICATION NUMBER: 60/083392
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083495
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083496
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083499
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083545
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083554
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Alignment Scores:
Pred. No.: 2,9e-136 Length: 3716
Score: 1550.00 Matches: 292
Percent Similarity: 98.65% Conservative: 1
Best Local Similarity: 98.32% Mismatches: 3
Query Match: 96.39% Indels: 1
DB: 10 Gaps: 0

US-10-047-021-86 (1-303) x US-09-978-697-210 (1-3716)

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QY 24 GlyGlyMetAlaGlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPhe 43
Db 61 GGAGGCATGGCTCAGGACTCCCGCCCGATCCTAGTCCACCCCGAGGACCGAGCTGTTTC 120

QY 44 GlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProProProThrIle 63
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QY 64 ArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisLeuLeu 83
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Db 241 CCTGATGGAGCCCTCTCTGCTACAGCCCTGCGGGGACATGCCCGATGGCCAG 300

QY 104 AlaLeuSerThrAspLeuGlyValTyThrCysGluAlaSerAsnArgLeuGlyThra 123
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QY 124 ValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnPro 143
Db 361 GTCAGCAGAGCGCTCGGCTGTCTGTGCTGTCTCCGGGAGGATTTCCAGATCCAGCT 420

QY 144 ArgAspMetValAlaValValGlyGlnPheThrLeuGluCysGlyProProTrpGly 163
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QY 164 HisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGly 183
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QY 244 LeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAla 263
Db 721 CTGGAATAATGTGACACTCTGAACCCGGATCCTCGAGAGGGCCCCCAACCTAGACCGGG 780

QY 264 ValTrpLeu***TrpLysValSerGlyPro***ArgLeuProAsnLeuThrArgProCy 283

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Oy 283 sSerClyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArg 299
Db 841 TTCAGGACCCAGACTGCCCGGAGGCCAGGAGCTCCGTGGGCAGAGG 889

RESULT 6
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; Sequence 210, Application US/09978192A
; Patent No. US2002017753A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary B.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavir, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC9
; CURRENT APPLICATION NUMBER: US/09/978,192A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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;; PRIOR APPLICATION NUMBER: 60/085697

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Query Match: 96.39% Indels: 1
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US-10-047-021-86 (1-303) x US-09-978-192A-210 (1-3716)

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QY 124 ValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnileGlnPro 143
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; Publication No. US20020192706A1
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; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman


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; PRIOR APPLICATION NUMBER: 60/085697

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Score:          1550.00      Matches:      292
Percent Similarity: 98.65%      Conservative: 1
Best Local Similarity: 98.32%      Mismatches: 3
Query Match:      96.39%      Indels:      1
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US-10-047-021-86 (1-303) x US-09-999-832A-210 (1-3716)

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Qy      44 GlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIle 63
Db      121 CAGGCGCTTGGCCCTGCCAGGATGAGTGCAGGCTCAGGCGCCACCTCCACCATC 180

Qy      64 ArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisLeuLeu 83
Db      181 CCTGGTGTGCTGAATGGGCGAGCCCTCTGAGCATGTGGTCCCGCCAGACCCACCATCTCTG 240

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; Publication No. US20030004102A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
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; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
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;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2630P1C7
;; CURRENT APPLICATION NUMBER: US/09/978,189
;; CURRENT FILING DATE: 2001-10-15
;; PRIOR APPLICATION NUMBER: 09/918585
;; PRIOR FILING DATE: 2001-07-30
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
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;; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.: 2,9e-136 Length: 3716
Score: 1550.00 Matches: 292
Percent Similarity: 98.65% Conservative: 1
Best Local Similarity: 98.32% Mismatches: 3
Query Match: 96.39% Indels: 1
DB: 11 Gaps: 0

US-10-047-021-86 (1-303) x US-09-978-189-210 (1-3716)

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Db 1 GGAGGAGACAGCTCTCGGGGGGAGGGTTCCTGCTCTGCTCTGCTCATATG 60
Qy 24 GlyGlyMetAlaGlnAspSerProGlnLeuValHisProGlnAspGlnLeuPhe 43
Db 61 GGAGGAGTGGCTCAGACTCTCCCGCCCGCCAGATCTAGTCCACCCAGGACCATGTC 120
Qy 44 GlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIle 63
Db 121 CAGGGCCCTGGCTGCCAGGATGAGTGCCCAAGCTCAGGCCAGCCACCTCCACCATC 180
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Db 181 CGCTGGTTGCTGAATGGGCGAGCCCTGAGCATGGTGGCCCGCCAGACCCACCATCCTG 240
Qy 84 ProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGln 103
Db 241 CCGTGAAGGAGCCCTTCTGCTGCTCAGACCCCTGCGGGGAGATGCCACGATGGCCAG 300
Qy 104 AlaLeuSerThrAspLeuGlyValTrpCysGluAlaSerAsnArgLeuGlyThrAla 123
Db 301 GCCCTGTCCACAGACTGGGTGTCTACACATGTGAGGCGAGCAACCGGCTGGCAGCGCA 360
Qy 124 ValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnPro 143
Db 361 GTCCAGCAGAGGGCGCTGGGTGTCTGTGGCTGTCTCCCGGGAGGATTTCCAGATCCAGCT 420
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Qy 164 HisProGluProThrValSerTrpTrpAspGlyLysProLeuAlaLeuGlnProGly 183
Db 481 CACCCAGAGCCACAGTCTCATGTGGAAAGATGGAAACCCCTGCGCTCCAGCCCGGA 540
Qy 184 ArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu*** 203

Db 541 AGGCACACAGTGTCTCGGGGGGTCTCCTGTGTGTATGGCAAGAGCAGAGAGTGACGAAGGG 600
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Db 721 CTGGAAATGTGACACTCTGAACCCGGATCTCTGAGAGGGCGCCCAAGCCTAGACCGGG 780
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Db 781 GTGTGGCTCAGCTGGAGGTCTGCTGGCTCTGCTGGCTCTGCTGGCTCTTACACGGCCTTG 840
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RESULT 9

US-09-978-608A-210

;; Sequence 210, Application US/09978608A
;; Publication No. US20030045462A1
;; GENERAL INFORMATION:
;; APPLICANT: Ashkenazi, Avi
;; APPLICANT: Baker Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Deenoyers, Luc
;; APPLICANT: Eaton, Dan
;; APPLICANT: Ferrara, Napoleon
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gao, Wei-Qiang
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Hillan, Kenneth J.
;; APPLICANT: Kijavini, Ivar J.
;; APPLICANT: Kuo, Sophia S.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James;
;; APPLICANT: Paoni, Nicholas P.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Shelton, David L.
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2630P1C22
;; CURRENT APPLICATION NUMBER: US/09/978,608A
;; CURRENT FILING DATE: 2001-10-16
;; NUMBER OF SEQ ID NOS: 624
;; Prior Application removed - See File Wrapper or Palm
;; SEQ ID NO 210
;; LENGTH: 3716
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-978-608A-210

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Score: 1550.00 Matches: 292
Percent Similarity: 98.65% Conservative: 1
Best Local Similarity: 98.32% Mismatches: 3
Query Match: 96.39% Indels: 1

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Db 1 GGAGGAGACAGCTCTCTGGGGGAGGGTTCCTGCTGCTGCTGCTGCTCATG 60
Qy 24 GlyGlyMetAlaGlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPhe 43
Db 61 GGAGCATGGCTCAGACTCCCGCCAGATCTCTAGTCCACCCCGAGGACAGCTGTC 120
Qy 44 GlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIle 63
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Qy 283 sSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArg 299
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
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; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 210
; LENGTH: 3716
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-978-585A-210
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Pred. No.: 2,9e-136 Length: 3716
Score: 1550.00 Matches: 292
Percent Similarity: 98.65% Conservative: 1
Best Local Similarity: 98.32% Mismatches: 3
Query Match: 96.39% Indels: 1
DB: 11 Gaps: 0
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Db 1 GGAGGAGACAGCTCTCTGGGGGAGGGTTCCTGCTGCTGCTGCTGCTCATG 60
Qy 24 GlyGlyMetAlaGlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPhe 43
Db 61 GGAGCATGGCTCAGACTCCCGCCAGATCTCTAGTCCACCCCGAGGACAGCTGTC 120
Qy 44 GlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIle 63
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Qy 283 sSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArg 299
Db 841 TTCAGGCCAGACTGCTCCCGGAGGCCAGGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 889
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; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
;
Alignment Scores:
Pred. No.: 2.9e-136 Length: 3716
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Best Local Similarity: 98.32% Mismatches: 3
Query Match: 96.39% Indels: 1
DB: 11 Gaps: 0
US-10-047-021-86 (1-303) x US-09-978-191A-210 (1-3716)
Qy 4 GlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeuLeuMet 23
Db 1 GGAGGAGACAGCCTCTGGGGGAGGGGTTCCTGCTCTGCTGCTGCTCATG 60
Qy 24 GlyGlyMetAlaGlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPhe 43
Db 61 GGAGGCATGGCTCAGGACTCCCGCCCGCCAGATCTAGTCCACCCAGGACCAGCTGTC 120
Qy 44 GlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIle 63
Db 121 CAGGGCCCTGGCCCTGCCAGGATGAGCTGCAAGCCTCAGGCAGCCACCTCCACCATC 180
Qy 64 ArgTrpLeuLeuGlnGlnProLeuSerMetValProProaspProHisHisLeuLeu 83
Db 181 CGCTGGTTGCTGAATGGGCGAGCCCTGAGCATGTGTGCCCCCAGACCACCTCCTG 240
Qy 84 ProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGln 103
Db 241 CTTGATGGGACCCCTTCTGCTGTCTACAGCCCTGCCCGGGGACATGCCCAGATGGCCAG 300
Qy 104 AlaLeuSerThrAspLeuGlyValThrCysGluAlaSerAsnArgLeuGlyThrAla 123
Db 301 GCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCAGCGCA 360
Qy 124 ValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnPro 143
Db 361 GTCAGCAGAGGCGCTCGGCTGTCTGTGGCTGTCTCCGGGAGGATTTCCAGATCCAGCCT 420
Qy 144 ArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGly 163
Db 421 CGGGACATGTGGCTGTGGTGGGTGAGCAGTTTACTCTGGATGTGGGCGCCCTGGGGC 480
Qy 164 HisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGly 183
Db 481 CACCCAGAGCCACAGTCTCATGTGTGGAAGATGGGAAACCCCTTGGGCGCTCCAGCCGGA 540
Qy 184 ArgHisThrValSerGlyGlySerLeuMetAlaArgAlaGluLysSerAspGlu*** 203
Db 541 AGGCACACAGTGTCCGGGGGTCCCTGCTGATGCCAAGAGCAGAGAGAGTGCAGAGGG 600
Qy 204 ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAArgVal 223
Db 601 ACCTACATGTGTGGCCACCAACAGCGCAGGACATAGGAGAGCGCGCAGCCCGGTT 660
Qy 224 SerIleGlnGluProGlnAspTyrThrGluProValGlnLeuAlaValArgIleGln 243

Db 661 TCATCCAGAGCCCGAGGACTACAGGAGCCTGTGGAGCTTCTGGCTCTGCGAATTCAG 720
Qy 244 LeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAla 263
Db 721 CTGGAATGTGACACTGCTGAACCGGATCTGCGAGAGGCCCCCAGGCTAGACGGCG 780
Qy 264 ValTrpLeu***TrpLysValSerGlyPro***ArgLeuProAsnLeuThrArgProCy 283
Db 781 GTGTGGCTCAGCTGGAAGGTCAGTGGCCCTGTGGCCCTGCCCAATCTTACACGGCCTTG 840
Qy 283 sSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArg 299
Db 841 TTCAGGACCAGACTGCCCCCGAGGCCAGGAGCTCCCTGGGCGAGG 889
RESULT 12
US-09-978-403A-210
; Sequence 210, Application US/09978403A
; Publication No. US20030050240A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
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; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC17
; CURRENT APPLICATION NUMBER: US/09/978,403A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:
Pred. No.:

Length:

2.9e-136

3716

Score: 1550.00 Matches: 292
Percent Similarity: 98.65% Conservative: 1
Best Local Similarity: 98.32% Mismatches: 3
Query Match: 96.39% Indels: 1
DB: 11 Gaps: 0

US-10-047-021-86 (1-303) x US-09-978-403A-210 (1-3716)

QY 4 GlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeuMet 23
DB 1 GGAGGAGACAGCCTCTGGGGGGCAGGGGTTCCTGCTCTGCTGCTCTCATG 60
QY 24 GlyGlyMetAlaGlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPhe 43
DB 61 GGAGGCATGGCTCAGGACTCCCGCCCCAGATCCTAGTCCACCCAGGACCACTGTTT 120
QY 44 GlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProProThrile 63
DB 121 CAGGGCCCTGGCCCTGCCAGGATGAGCTGCAAGCCTCAGGCCAGCACCTCCACCATC 180
QY 64 ArgTrpLeuLeuGlnProLeuSerMetValProProAspProHisLeuLeu 83
DB 181 CGCTGGTTGCTGAATGGGCAGCCCCCTGAGCATGGTCCCCCAGACCACCACTCTCTG 240
QY 84 ProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGln 103
DB 241 CCTGATGGGACCCCTTCTGCTGTACAGCCCCCTGCCCGGGGACATGCCAGATGGCAG 300
QY 104 AlaLeuSerThrAspLeuGlyValThrCysGlnAlaSerAsnArgLeuGlyThrAla 123
DB 301 GCCCTGTCCACAGACCTGGGTGTCTACATGTGAGGCCAGCAACCGGCTTGGCAGCGCA 360
QY 124 ValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnPro 143
DB 361 GTCAGCAGAGCGCTCGGCTGTCTGTGGCTGTCTCCGGGAGGATTTCCAGATCCAGCCT 420
QY 144 ArgAspMetValAlaValGlyGlnPheThrLeuGluCysGlyProProTrpGly 163
DB 421 CGGGACATGTGGCTGTGGTGGTGAGCAGTTTACTCTGGAAATGTGGCGCCCTGGGGC 480
QY 164 HisProGlnProThrValSerTrpTrpLeuAspGlyProLeuAlaLeuGlnProGly 183
DB 481 CACCCAGAGCCACAGTCTCATGTGGAAGATGGGAAACCCCTGGCCCTCCAGCCCGGA 540
QY 184 ArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu*** 203
DB 541 AGGCACACAGTGTCCGGGGGGTCCCTGCTGATGGCAAGAGCAGAGAAGAGTGACGAAGG 600
QY 204 ThrTrpMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAaArgVal 223
DB 601 ACCTACATGTGTGGCCACCAACAGCGCAGGACATAGGGAGAGCCGCGCAGCCGGGTT 660
QY 224 SerileGlnProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGln 243
DB 661 TCCATCCAGGAGCCCGCAGGACTACACGAGCCTGTGGAGCTTCTGGGTGTGCGAATTGAG 720
QY 244 LeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProAspProAla 263
DB 721 CTGGAAAATGTGACACTGCTGAACCCGGATCCTGCAGAGGGCCCCCAGACCTAGACCGGCG 780
QY 264 ValTrpLeu***TrpLysValSerGlyPro***ArgLeuProAsnLeuThrArgProCys 283
DB 781 GTGTGGCTCAGCTGGAAGGTTCAGTGGCCCTGCTGCGCTGCCCAATCTTACACGGCCTTG 840
QY 283 sSerGlyProArgLeuProArgGluAlaArgLeuLeuArgGlyGlnArg 299
DB 841 TTCAGGACCCAGACTGCCCGGGAGGCCAGGAGCTCCGTGGGCAGAGG 889

RESULT 13

US-09-978-564A-210
; Sequence 210, Application US/09978564A
; Publication No. US20030050241A1
; GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC25
CURRENT APPLICATION NUMBER: US/09/978,564A
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
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;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.: 2,9e-136 Length: 3716
Score: 1550.00 Matches: 292
Percent Similarity: 98.65% Conservative: 1
Best Local Similarity: 98.32% Mismatches: 3
Query Match: 96.39% Indels: 1
DB: 11 Gaps: 0

US-10-047-021-86 (1-303) x US-09-978-564A-210 (1-3716)

Qy 4 GlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeuMet 23
Db 1 GGAGGAGACACCCCTCTGGGGGAGGGTTCCCTGCTCTGCTGCTCTCATG 60
Qy 24 GlyGlyMetAlaGlnAspSerProGlnLeuValHisProGlnAspGlnLeuPhe 43
Db 61 GGAGGATGGCTCAGGACTCCCGCCCGCCAGATCTAGTCCACCCCGAGGACGCTGTT 120
Qy 44 GlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIle 63
Db 121 CAGGCCCCCTGGCCCTGCCAGGATGAGCTGCCAAGCCTCAGGCGCACCTCCACCATC 180

Qy 64 ArcTrpLeuLeuAenGlyGlnProLeuSerMetValProProAspProHisHisLeuLeu 83
Db 181 CGCTGGTTGCTGAATGGGAGCCCTTGAGCATGGTCCCCCAGCCACACCTCTCTG 240
Qy 84 ProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGln 103
Db 241 CCTGATGGGACCTTCTGCTGTCTACAGCCCTCCCGGGGACATGCCCACGATGGCC 300
Qy 104 AlaLeuSerThrAspLeuGlyValThrCysGluAlaSerAsnArgLeuGlyThrAla 123
Db 301 GCCCTGTCCACAGACCTGGGTGTCTACATGTGAGGCCAGCAACCGGCTGGCACGCA 360
Qy 124 ValSerArgGlyValAlaArgLeuSerValAlaValLeuArgGluAspPheGlnLeuPro 143
Db 361 GTGAGCAGAGCGCTCGGCTGTCTGGGTGTCTCTCGGGAGGATTTCCAGATCCAGCCT 420
Qy 144 ArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGly 163
Db 421 CGGACATGGTGGCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCGCCCTGGGG 480
Qy 164 HisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGly 183
Db 481 CACCCAGAGCCACAGTCTCATGTGGAAGATGGGAAACCCCTGGCCCTCCAGCCCGGA 540
Qy 184 ArcHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu** 203
Db 541 AGGCACACAGTGTCCGGGGGTCTCTGCTGATGTCAGACAGACAGAGAGATGACGARGG 600
Qy 204 ThrTrpMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgVal 223
Db 601 ACCTACATGTGTGGCCACCAACAGCGCAGGACATAGGAGAGAGCGCGAGCCGGGTT 660
Qy 224 SerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGln 243
Db 661 TCCATCCAGAGGCCCGCAGGACTACAGGAGCCTGTGGAGCTTCTGGCTGTGCGAATTCAG 720
Qy 244 LeuGluAenValThrLeuLeuAenProAspProAlaGluGlyProLysProArgProAla 263
Db 721 CTGGAAATGTGACATGCTGTAACCGGATCTTCAGAGAGGGCCCCCAGACCTTAGACCGCG 780
Qy 264 ValTrpLeu***TrpLysValSerGlyPro***ArgLeuProAsnLeuThrArgProCys 283
Db 781 GTGTGGCTCAGCTGGAAGGTGAGTGGGCTGCTGCGCTGCCCAATCTTACCGGCTTG 840
Qy 283 sSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArg 299
Db 841 TTCAGGACCCAGACTGCCCGGGAGGCGCAGGAGCTCCGTGGGCAGAGG 889

RESULT 14

US-09-999-833A-210
; Sequence 210, Application US/09999833A
; Publication No. US20030054405A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.

APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC65
CURRENT APPLICATION NUMBER: US/09/999,833A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR APPLICATION NUMBER: 60/085689
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:
Pred. No.: 2,98-136 Length: 3716
Score: 1550.00 Matches: 292
Percent Similarity: 98.65% Conservative: 1
Best Local Similarity: 98.32% Mismatches: 3
Query Match: 96.39% Indels: 1
DB: 11 Gaps: 0

US-10-047-021-86 (1-303) x US-09-999-833A-210 (1-3716)

Qy 4 GlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeuLeuMet 23
Db 1 GGAGAGACACCTCTCTGGGGGGGAGGGTTCCTGCTGCTGCTGCTGCTGCTCATG 60
Qy 24 GlyGlyMetAlaGlnAspSerProGlnLeuValHisProGlnAspGlnLeuPhe 43
Db 61 GGAGGCGATGGCTCAGGACTCCCGCCCGCCAGATCTAGTCCACCCCGAGGACCATGTC 120
Qy 44 GlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProProThrile 63
Db 121 CAGGCGCCCTGGCCCTGCCAGGATGCTGCCAAGCCTCAGGCGCACCTCCACCATC 180
Qy 64 ArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisLeuLeu 83
Db 181 CGCTGGTTCGTGAATGGGACCCCTGAGCATGTGGCCCGAGACCCACACCATCTCTG 240
Qy 84 ProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGln 103
Db 241 CCTGATGGGACCTCTGCTCTACGCCCCCTGCCCGGGAGACATGCCAGATGGCCAG 300
Qy 104 AlaLeuSerThrAspLeuGlyValThrCysGluAlaSerAsnArgLeuGlyThrAla 123
Db 301 GCCCTGTCCACAGACCTGGGTGTCTACATGTGAGGCGCAGCAACCGGCTTGGCAGCGCA 360
Qy 124 ValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnLeuPro 143
Db 361 GTGAGCAGAGCGCTCGGCTGTCTGTGGCTGTCTCCGGAGAGATTTCAGATCCAGCT 420
Qy 144 ArgAspMetValAlaValGlyGlnPheThrLeuGluCysGlyProProTrpGly 163

Db 421 CGGGACATGCTGGCTGGTGGGTGAGCAGCTTTACTCTGGAATGTGGGCCCGCCCTGGGGC 480
Qy 164 HisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGly 183
Db 481 CACCCAGAGCCCAAGTCTCATGTTGGAAGATGGGAACCCCTGGCCCTCCAGCCCGGA 540
Qy 184 ArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu*** 203
Db 541 AGGCACACAGTGTCCGGGGGCTCCCTGCTGATGCAAGAGCAGAGAGATGACAGAGG 600
Qy 204 ThrTyMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgVal 223
Db 601 ACCTACATGTGTGGCCCAACACAGCGCAGGACATAGGAGAGCCCGCAGCCCGGTT 660
Qy 224 SerIleGlnGluProGlnAspTrpThrGluProValGluLeuLeuAlaValArgIleGln 243
Db 661 TCCATCCAGAGGCCCGAGGACTACAGGACCTGTGGAGCTTCTGGCTGTGCGAATTCAG 720
Qy 244 LeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAla 263
Db 721 CTGGAAATGTGACACTGCTGAACCCGATCTCTGCAGAGGGCCCGCAGACCTAGACCGCG 780
Qy 264 ValTrpLeu***TrpLysValSerGlyPro***-ArgLeuProAsnLeuThrArgProCy 283
Db 781 GTGTGGCTCAGCTGGAAGGTCACTGGGCCCTGCTGCTGCTGCCCAATCTTACACGCGCTG 840
Qy 283 sSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArg 299
Db 841 TTCAGGACCCAGACTGCCCGGGAGGCCAGGAGCTCCGTGGGCGAGAGG 889

RESULT 15

US-09-981-915A-210
; Sequence 210, Application US/09981915A
; Publication No. US20030054986A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
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; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630F1C12
; CURRENT APPLICATION NUMBER: US/09/981,915A
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03

1	PRIOR FILING DATE: 1998-04-15
2	PRIOR APPLICATION NUMBER: 60/081819
3	PRIOR FILING DATE: 1998-04-15
4	PRIOR APPLICATION NUMBER: 60/081952
5	PRIOR FILING DATE: 1998-04-15
6	PRIOR APPLICATION NUMBER: 60/081838
7	PRIOR FILING DATE: 1998-04-15
8	PRIOR APPLICATION NUMBER: 60/082568
9	PRIOR FILING DATE: 1998-04-21
10	PRIOR APPLICATION NUMBER: 60/082569
11	PRIOR FILING DATE: 1998-04-21
12	PRIOR APPLICATION NUMBER: 60/082704
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14	PRIOR APPLICATION NUMBER: 60/082804
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21	PRIOR FILING DATE: 1998-04-23
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69	PRIOR FILING DATE: 1998-05-13
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73	PRIOR FILING DATE: 1998-05-15

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Alignment Scores:

Pred. NO.:	2.9e-136	Length:	3716
Score:	1550.00	Matches:	292
Percent Similarity:	98.65%	Conservative:	1
Best Local Similarity:	98.32%	Mismatches:	3
Query Match:	96.39%	Indels:	1
DB:	11	Gaps:	0

US-10-047-021-86 (1-303) x US-09-981-915A-210 (1-3716)

Qy	4	GlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeuLeuMet	23
Db	1	GGAGGAGACACCTCTCTGGGGGGGAGGGTTCCCTGCTCTGCTGCTCTCTCATG	60
Qy	24	GlyGlyMetAlaGlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPhe	43
Db	61	GGAGGCATGGCTCAGGACTCCCGCCCCAGATCTAGTCCACCCCGAGGACAGCTGTC	120
Qy	44	GlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIle	63
Db	121	CAGGGCCCTGCCCTGCCAGGATGCTGCCAAGCCTCAGGCCAGCCCTCCACCATC	180
Qy	64	ArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisLeuLeu	83
Db	181	CGCTGTTGCTGAATGGGACCCCTGAGCATGGTGGCCCCAGACCACACCTCTCTG	240
Qy	84	ProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGln	103
Db	241	CCTGATGGGACCCCTCTCTGCTCAGCCCTGCTGCCGGGACATGCCACGATGGCCAG	300
Qy	104	AlaLeuSerThrAspLeuGlyValTyThrCysGluAlaSerAsnArgLeuGlyThrAla	123
Db	301	GCCCTGTCCAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCAGCGCA	360
Qy	124	ValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnPro	143
Db	361	GTCAGCAGAGCGCTCGGCTGTCTGTGGCTGTCTCCGGAGGATTTCCAGATCCAGCCT	420
Qy	144	ArgAspMetValAlaValGlyGlnGlnPheThrLeuGluCysGlyProProTrpGly	163
Db	421	CGGGACATGGTGGCTGTGGTGAGCAGTTTACTCTGGAATGTGGGCCCGCTGGGGC	480
Qy	164	HisProGlnProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGly	183
Db	481	CACCCAGAGCCACAGTCTCATGTGTGGAAGATGGAAACCCCTGGCCCTCCAGCCCGGA	540
Qy	184	ArgHisThrValSerGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu**	203
Db	541	AGGCACACAGTGTCCGGGGGGTCCCTGCTGTATGGCAGAGCAGAGAGTACGAGGG	600
Qy	204	ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaArgVal	223
Db	601	ACCTACATGTGTGGGCCACCAACAGCGCAGCATAGGGAGAGCCCGCGAGCCCGGTT	660
Qy	224	SerIleGlnGluProGlnAspTyThrGlnProValGluLeuLeuAlaValArgIleGln	243
Db	661	TCCATCCAGGAGCCCCAGGACTACACGAGGCTGTGGAGCTTCTGGCTGTGCGAATTCAG	720
Qy	244	LeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAla	263

Db	721	CTGGAAATGTGACACTGCTGAACCCGCGATCCTGCAGAGGGCCCCAAGCCTAGACCGCG	780
Qy	264	ValTrpLeu***TrpLysValSerGlyPro***-ArgLeuProAsnLeuThrArgProCy	283
Db	781	GTGTGGCTCAGCTGGAGGTCAGTGGCCCTGCTGCGCTGCCCAATCTTACCGGCTTG	840
Qy	283	sSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArg	299
Db	841	TTCAGGACCCAGACTGCCCGGGAGGCCAGGGAGCTCCGTGGGCAGAGG	889

Search completed: January 31, 2004, 17:18:16
Job time : 345.352 secs

Result No.	Score	Query Match	Length	DB	ID	Description
1	448.5	27.9	1651	2	T14160	transmembrane rece
2	445.5	27.7	1612	2	T30805	dutt1 protein - mo
3	414.5	25.8	1344	2	T14316	rig-1 protein - mo
4	360	22.4	1273	2	T42405	sax-3 protein - Ca
5	356.5	22.2	423	2	T29549	hypothetical prote
6	253.5	15.8	1898	2	S46216	leukocyte antigen-
7	253	15.7	1535	2	S46224	peroxidasin - fru
8	251	15.6	1272	2	S26180	neurofascin - chic
9	245	15.2	1427	2	I51669	tumor suppressor -
10	244.5	15.2	1897	1	TDHULK	leukocyte antigen-
11	237.5	14.8	1501	2	I59148	protein-tyrosine-p
12	237.5	14.8	1863	2	S46217	protein-tyrosine-p
13	237.5	14.8	1907	2	S50893	protein-tyrosine-p
14	236.5	14.7	1040	2	A34695	axonal glycoprotei
15	232	14.4	1040	2	A49356	transient axonal g
16	231.5	14.4	3707	2	I82852	heparan sulfate pr
17	230	14.3	1912	2	A56178	protein-tyrosine-p
18	228	14.2	1028	2	A53449	plasmacytoma-assoc
19	228	14.2	1894	2	S34689	protein-tyrosine-p
20	228	14.2	5175	2	T20992	hypothetical prote
21	228	14.2	5198	2	T43290	hemikentlin precurs
22	227.5	14.1	1028	2	I59164	BIG-1 protein - ra
23	227.5	14.1	1262	1	B48758	protein-tyrosine-p
24	227.5	14.1	1496	1	A48758	protein-tyrosine-p
25	222	13.8	2029	1	TDPELK	protein-tyrosine-p
26	220.5	13.7	1499	2	I50212	protein-tyrosine-p
27	217.5	13.5	1070	2	JC4599	protein-tyrosine k
28	216	13.4	1239	1	A32579	neuroglian - fruit
29	215.5	13.4	1443	2	I50600	neogenin - chicken

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1612 <WUM>
A;Cross-references: EMBL:Y17793; NID:el329712; PID:el329713; PIDN:CAA76850.1
A;Experimental source: brain
C;Genetics:
A;Gene: dutt1
A;Map position: 16

Query Match 27.7%; Score 445.5; DB 2; Length 1612;
Best Local Similarity 41.7%; Pred. No. 4.6e-25;
Matches 91; Conservative 31; Mismatches 87; Indels 9; Gaps 2;

Qy 28 QDSPPQILVHPDQDLFQCGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHH--LLP 84
Db EDFFPRIVEHSDLIIVSGEPATLCAAGRPPTIIEWYKGGREVTDKDPRSHRMLLP 84
Qy 85 DGTLLLOPPARGHAHQDQALSTDLGVYTCASNLGLTAVSRGARGLSVAVLRDFOIQPR 144
Db 85 SGLSFFLR-----IVHGRKSRPDGVYICARNVGLGEAVSHNASLEVAILLRDDRQNP 138
Qy 145 DMVAVVGQFTLECGPPWHPPEPTVSWWKGKPLALOPGRUTVSGSLLMARAEKSDXT 204
Db 139 DMVAVGEPAVMECQPPRHPPEPTISWKKGSPLDDKDERITIRGKLMITYTRKSDAG 198
Qy 205 YMCVATNSAGHRESRAARVSIQEQDYTEPVELLAVRI 242
Db 199 YVCVGTNMVGERSEVAELTVLERPSFVKRPSNLAVTV 236

RESULT 3
T14316
rig-1 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T14316
R;Yuan, S.S.F.; Cox, L.A.; Dasika, G.K.; Lee, E.Y.H.P.
submitted to the EMBL Data Library, April 1998
A;Reference number: Z17975
A;Accession: T14316
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1344 <YUA>
A;Cross-references: EMBL:AF060570; NID:g4206385; PID:g4206386; PIDN:AAD11628.1

Query Match 25.8%; Score 414.5; DB 2; Length 1344;
Best Local Similarity 39.9%; Pred. No. 7.4e-23;
Matches 101; Conservative 27; Mismatches 94; Indels 31; Gaps 8;

Qy 28 QDSPPQILVHPDQDLFQCGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDP--HH-LLP 84
Db EDAMPRIVEQPPDLVVSERGEATLPCRAEGRPRIEWYKNGARVATAREDPRAHRLLLP 97
Qy 85 DGTLLLOPPARGHAHQDQALSTDLGVYTCASNLGLTAVSRGARGLSVAVLRDFOIQPR 144
Db 98 SGLAFF---PRIVH---GRRSRPDGVYTCARNVGLGAASNASLEVAILLRDDRQSPG 151
Qy 145 DMVAVVGQFTLECGPPWHPPEPTVSWWKGKPLALOPGRUTVSGSLLMARAEKSDXT 204
Db 152 NVWVAVGEPVMECQPPRHPPEPTVSWWKGKPLALOPGRUTVSGSLLMARAEKSDXT 211
Qy 205 YMCVATNSAGHRESRAAR-VSIQEQDYTEPVELLAVRIQLENTVLLNPDPAE----- 256
Db 212 YMCVASNMGRESGAELVLERPSFURRPI-----NQVLADAEVNFCEVQG 261
Qy 257 GPKRPAVWLXWK 269
Db 262 DFQPN-----LWR 270

RESULT 4
T42405
sax-3 protein - Caenorhabditis elegans

C;Species: Caenorhabditis elegans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C;Accession: T42405
R;Zallen, J.A.; Yi, B.A.; Bargmann, C.I.
Cell 92, 217-227, 1998
A;Title: The conserved immunoglobulin superfamily member SAX-3/Robo directs multiple asp
A;Reference number: Z22160; MUID:98117250; PMID:9458046
A;Accession: T42405
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1273 <ZAL>
A;Cross-references: EMBL:AF041053; NID:g2804773; PIDN:AAC38848.1; PID:g2804780
C;Genetics:
A;Note: sax-3
A;Function:
A;Description: sax-3 function is required at the time of axon guidance

Query Match 22.4%; Score 360; DB 2; Length 1273;
Best Local Similarity 32.7%; Pred. No. 7.7e-19;
Matches 101; Conservative 50; Mismatches 110; Indels 48; Gaps 12;

Qy 12 RGSPLLLLLIMGM-----AQDSPPQILVHPDQDLFQCGPGPARMSCRASGQPPPT-- 62
Db 4 RKTLLCTILLVQAVIRSFCEADSNLAPVIIIEHPIDVVVSGRSPATLNC---GAKPSTAK 60
Qy 63 IRWLLNGQPL--SMVPPDPHLLPD-GTLLLOPPARGHAHQDQALSTDLGVYTCASNR 119
Db 61 ITWKDQGPVITNKQVNSHRIVLDGSLFLKVNKGKGD-----SDAGAYCVASNE 115
Qy 120 LGTAVSRGARGLSVAVLRDFOIQPRDMVAVVGQFTLECGPPWHPPEPTVSWWKGKPLA 179
Db 116 HGEVKSNEGSKLMLREDFRVPRTVQALGEMAVLECSPPRGFPFVPSWRKDKELR 175
Qy 180 LQP-GRHTV--SGSLLMARAEKSDXTYCMVATNSAGHRESRAARVSI-----QSPD 230
Db 176 IQDMPRYTLSDGNLIIDPVDSDSGTYQCVAANNMGERVSNPARLSVFEKPKPEQBPDK 235
Qy 231 YTEPVELLAVRIQLENTVLLNPDPAEKPKRPAVWLXWKVSGPKRLNLTTPCSPGRLPR 290
Db 236 MT-----VDGAAVLFCRVTDGPQ-----ITWK-----RKNEPMPVTRAYIAK 276
Qy 291 EARELRGQR 299
Db 277 DNRGLRIER 285

RESULT 5
T29549
hypothetical protein ZK377.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T29549
R;Nhan, M.; Hawkins, J.
submitted to the EMBL Data Library, February 1997
A;Description: The sequence of C. elegans cosmid ZK377.
A;Reference number: Z20639
A;Accession: T29549
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-423 <NHA>
A;Cross-references: EMBL:U88183; PIDN:AA852658.1; GSPDB:GN00028; CESP:ZK377.3
A;Experimental source: strain Bristol N2; clone ZK377
C;Genetics:
A;Gene: CESP:ZK377.3
A;Map position: X
A;Introns: 24/1; 142/3; 229/3; 284/2; 408/3

Query Match 22.2%; Score 356.5; DB 2; Length 423;
Best Local Similarity 33.8%; Pred. No. 4.2e-19;
Matches 97; Conservative 45; Mismatches 104; Indels 41; Gaps 11;

Qy 27 AQDSPPQILVHPDQDLFQCGPGPARMSCRASGQPPPT--IRWLLNGQPL--SMVPPDPHLL 82

Db 25 ASNLAPVIEHPIDVWVRSGSPATLNC---GAKPSTAKITWKQGPVITNKEQVNSHRI 81
 QY 83 LPD-GTLLILQPPARGHAGDQALSTDLGVYTCASNRILGTAVSRGARSVAVLRFDFQI 141
 Db 82 VLDTSGLFLKYNKSGKNGK-----SDAGAYCVASNEHGEVKSNEGSLKLAWLREDFRV 136
 QY 142 QPRDMVAVVGEFTLECGPPHGPFTVSWWKDGKPLALQ-GRHTV-SGGSLLMARAEK 199
 Db 137 RPRVTQALGGENAVLECPSPRGFPFVWVRKDDKELRIQDMPRVYTLSDGNLIIDPVD 196
 QY 200 SDEXTYMCVATNSAGHRSRAARVSI-----QSPQDYTEPVELLAVRIQLENTVLNP 252
 Db 197 SDSGYTCQCVANMVGERVSNPARLSVFEKPEQPKDMT-----VDGAAVLDFC 247
 QY 253 DPAGCPKPRPAVWLKWKVSGPXRRLNLRPCSGPRLPREARELRQR 299
 Db 248 RVTGDPQPO-----ITWK-----RKNEMPVTRAVIANDKRLRIER 284

RESULT 6
 S46216
 N:leukocyte antigen-related protein precursor - rat
 N:Alternate names: leukocyte common antigen homolog
 C:Species: Rattus norvegicus (Norway rat)
 C:Comments: protein-tyrosine-phosphatase (EC 3.1.3.48)
 C:Date: 20-Feb-1995 #sequence revision 20-Feb-1995 #text_change 23-Jul-1999
 C:Accession: S46216; S23252; A41032; A33154
 R:Zhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, B.J.
 Biochem. J. 302, 39-47, 1994
 A:Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine-phosphatase
 A:Reference number: S46216; MUID:94347119; PMID:8068021
 A:Accession: S46216
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-1898 <ZHA>
 A:Cross-references: EMBL:L11586; NID:G205132; PIDN:AAC37655.1; PID:G205133
 R:Hashimoto, N.; Zhang, W.R.; Goldstein, B.J.
 Biochem. J. 284, 569-576, 1992
 A:Title: Insulin receptor and epidermal growth factor receptor dephosphorylation by three
 A:Reference number: S23126; MUID:92287069; PMID:1599438
 A:Accession: S23252
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1361-1604/1649-1898 <HAS>
 R:Pot, D.A.; Woodford, T.A.; Remboutsika, E.; Haun, R.S.; Dixon, J.E.
 J. Biol. Chem. 266, 19688-19696, 1991
 A:Title: Cloning, bacterial expression, purification, and characterization of the cytoplasmic
 A:Reference number: A41032; MUID:92011772; PMID:1918076
 A:Accession: A41032
 A:Molecule type: mRNA
 A:Residues: 1035-1072, 'S', 1074-1433, 'T', 1435-1638, 'N', 1640-1642, 'HT', 1645-1898 <POT>
 A:Cross-references: GB:M60103; NID:G205130; PIDN:AAA41510.1; PID:G205131
 R:Pot, D.A.; Woodford, T.A.; Remboutsika, E.; Haun, R.S.; Dixon, J.E.
 submitted to the Protein Sequence Database, December 1990
 A:Reference number: A33154
 A:Accession: A33154
 A:Molecule type: mRNA
 A:Residues: 1035-1072, 'S', 1074-1433, 'T', 1435-1638, 'N', 1640-1642, 'HT', 1645-1898 <POT>
 C:Comment: Only the first of the two domains homologous with protein-tyrosine-phosphatase
 C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
 ogy
 C:Keywords: duplication; glycoprotein; phosphoprotein; phosphoric monoester hydrolase; d
 F:1-27/Domain: (or 1-26) signal sequence #status predicted <SIG>
 F:28-1898/Product: (or 27-1898) leukocyte antigen-related protein #status predicted <MAT
 F:28-1251/Domain: (or 27-1251) extracellular #status predicted <EXT>
 F:47-109/Domain: immunoglobulin homology <IMM1>
 F:149-209/Domain: immunoglobulin homology <IMM2>
 F:246-300/Domain: immunoglobulin homology <IMM3>
 F:318-400/Domain: fibronectin type III repeat homology <FN3A>
 F:413-499/Domain: fibronectin type III repeat homology <FN3B>
 F:511-593/Domain: fibronectin type III repeat homology <FN3C>
 F:606-695/Domain: fibronectin type III repeat homology <FN3D>
 F:708-799/Domain: fibronectin type III repeat homology <FN3E>

F:811-895/Domain: fibronectin type III repeat homology <FN3F>
 F:906-990/Domain: fibronectin type III repeat homology <FN3G>
 F:1002-1079/Domain: fibronectin type III repeat homology <FN3H>
 F:1252-1275/Domain: (or 1259-1275) transmembrane #status predicted <TM>
 F:1276-1898/Domain: intracellular #status predicted <INT>
 F:1286-1898/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F:1366-1587/Domain: protein-tyrosine-phosphatase homology <PTP1>
 F:1655-1878/Domain: protein-tyrosine-phosphatase homology <PTP2>
 F:54-107, 156-207, 253-298/Disulfide bonds: #status predicted
 F:117, 250, 295, 721, 957/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:1539/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:1545/Binding site: substrate phosphate (Arg) #status predicted
 F:1830/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:1836/Binding site: substrate phosphate (Arg) #status predicted

Query Match 15.8%; Score 253.5; DB 2; Length 1898;
 Best Local Similarity 31.8%; Pred. No. 9.3e-11;
 Matches 75; Conservative 41; Mismatches 83; Indels 37; Gaps 10;

QY 11 GRGSLP-----LLLLLIMGMAQSPQILVHPQDLFQGPGRMCRASGQPPPTIRWL 66
 Db 8 GRMVPLVPLVLMGLMAGHDSKPVFVPEQIGLGGVASFVCOATGEPKPRITWM 67
 QY 67 LNCQPLS-----MVPPDPHLLPDGTLTLLLPARGHAGDQALSTDLGVYTCASNRILG 121
 Db 68 KKGKKVSSQRPEVIEFD-----GAGSVLRIQP-----LRVQDEAIYECTATNSLG 114
 QY 122 TAVSRGARSVAVLRE-----FQIQPRDMVAVVGEQFTLECGPPHGPHTVSWWK 173
 Db 115 -EINTSAKLS--VLEEDQLPSGFTIDMGPOLKVKVKARTATMLCA-AGGNPDPIISWPK 170
 QY 174 DGKPL--ALQPR--HTVSGSLLMARAEKSDXTYMCVATNSAGHRSRAARVSIQ 226
 Db 171 DFLPVDPASSNGRIKQLRSGLALQIESSESQGYECVATNSAGTRYISAPANLYR 226

RESULT 7
 S46224
 peroxidase - fruit fly (Drosophila sp.)
 C:Species: Drosophila sp.
 C:Date: 19-Mar-1997 #sequence revision 19-Mar-1997 #text_change 24-Oct-2000
 C:Accession: S46224
 R:Nelson, R.E.; Fessler, L.I.; Takagi, Y.; Blumberg, B.; Keene, D.R.; Olson, P.F.; Parke
 EMBO J. 13, 3438-3447, 1994
 A:Title: Peroxidase: a novel enzyme-matrix protein of Drosophila development.
 A:Reference number: S46224; MUID:94341255; PMID:8062820
 A:Accession: S46224
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1535 <NEL>
 A:Cross-references: GB:U11052; NID:G531384; PIDN:AAA61568.1; PID:G531385
 C:Superfamily: peroxidase; myeloperoxidase homology; proteoglycan amino-terminal homology
 F:19-44/Domain: proteoglycan amino-terminal homology <PAH4>
 F:661-1350/Domain: myeloperoxidase homology <MPX>

Query Match 15.7%; Score 253; DB 2; Length 1535;
 Best Local Similarity 30.3%; Pred. No. 8e-11;
 Matches 80; Conservative 33; Mismatches 109; Indels 42; Gaps 13;

QY 30 SPPQILVHPQDL--FQGPGRMCRASGQPPPTIRWLNGQPLSMVPPDPHLLPDGT 87
 Db 367 SPPHFTQHPDQI VALHSSGHVLLDCAASGWFPDQIQWVNGRQLQSTPS-LQLQANGS 425
 QY 88 LLLLOPPARGHAGDQALSTDLGVYTCASNRILGTAVSRGARSVAVLRFDFQIPRDMV 147
 Db 426 LILLQ-----NQLSA--GTYRCEARNSLG-SVQATARIELKELPE-ILTAPOSQT 472
 QY 148 AVVGEQFTLECGPPHGPHTVSWWKDGKPLALQF-----RHTVSGSLLMARAEKSD 202
 Db 473 IKGKAFVLECDAD-GNPLPTIDMQLNGVDL---PGNTPDQLENTVELVGAARQSHA 528
 QY 203 XYTCVATNSAGHRSRAARVSIQ-----PDYTEPVELLAV---RIQLENTVLNPDPA 255

Db 529 GYVRCIAHNENG-ETSVEATIKVERSQPPQALAEPSNLVAITGTIEL-----PC 578
Qy 256 EGPKEPRAVWLXMKVSGPRLPNL 279
Db 579 QADQPEDGLQISWRHGRLLDPNV 602

RESULT 8
S26180
neurofascin - chicken
C:Species: Gallus gallus (chicken)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C:Accession: S26180
R:Volkmer, H.; Haesel, B.; Wolff, J.M.; Frank, R.; Rathjen, F.G.
J. Cell Biol. 118, 149-161, 1992
A:Title: Structure of the axonal surface recognition molecule neurofascin and its relationship to the cell adhesion molecule L1; fibronectin type III repeat homology; F:275-336/Domain: immunoglobulin homology <IMM>
A:Reference number: S26180; MUID:92317154; PMID:1377696
A:Accession: S26180
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1272 <VOL>
A:Cross-references: EMBL:X65224; NID:G63659; PIDN:CAA46330.1; PID:G63660
C:Superfamily: neural cell adhesion molecule L1; fibronectin type III repeat homology; F:275-336/Domain: immunoglobulin homology <IMM>

Query Match 15.6%; Score 251; DB 2; Length 1272;
Best Local Similarity 34.5%; Pred. No. 9.1e-11;
Matches 71; Conservative 34; Mismatches 71; Indels 30; Gaps 11;

Qy 32 PQILVHPQDLFQSPG-PARMSCRASGQPPPTIRWLNGQPLSMVPPDPHLLPDGTLL 90
Db 355 PYWLDEFQNL-LIAPGEDGLVCRANGNPKESIQWLVNGEPIEGSPNPSEVAGDIIVF 413
Qy 91 LOPPARHANHGOALSTDLGVYTCASNRLGTAVSRGRLSVAVLRDEFOIQPR 144
Db 414 -----RDTQIGSS--AVYQCWASNEHGYLL---ANAFVSVL----DVPPRILAPRN 455
Qy 145 DMVAVVGQFT-LEGPPWGHPEPTVSWKDGKPLALQPGHRTV-SGSLMARAESKDE 202
Db 456 QLIKVIQVNRLLDC-PFGSPGPIFLRWKNGQNLMDGGYKAHENGSLMSMARKEDQ 514
Qy 203 XYTMCVATNSAGHRESRAARVSIQEP 228
Db 515 GIYTCVATNILGKVEAQ-VRLVKDP 539

RESULT 9
151669
tumor suppressor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: 151669
R:Pierceall, W.E.; Reale, M.A.; Candia, A.F.; Wright, C.V.; Cho, K.R.; Fearon, E.R.
Dev. Biol. 166, 654-665, 1994
A:Title: Expression of a homologue of the deleted in colorectal cancer (DCC) gene in the developing frog
A:Reference number: 151669; MUID:95113183; PMID:7813784
A:Accession: 151669
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1427 <PIE>
A:Cross-references: EMBL:U10986; NID:G606873; PIDN:AAA70168.1; PID:G606874
C:Genetics: XDCa
A:Gene: XDCa

Query Match 15.2%; Score 245; DB 2; Length 1427;
Best Local Similarity 31.0%; Pred. No. 2.9e-10;
Matches 75; Conservative 32; Mismatches 99; Indels 36; Gaps 10;

Qy 49 ARMSCRASGQPPPTIRWLNGQPLSMVPPDPHLL-LPDGTLILLQPPARGHAHQALST 107
Db 157 ALLRCEITGEMPTISWQNEEDLKVTPGDPRLVLPSTGLQI-----SRLQTADG----- 207
Qy 108 DLGVYTCASNRLGTAVSRGRLSVAVLRDE-----FQIQPRDMVAVVGEQFTLECGP 160

Db 208 --GVYRCLAKNPGSARVGNEL--RILSSGLHRQVFLQPSNVVAIEQDVALECAV 263
Qy 161 PWGHPPTVSWKDGKPLALQPGHRTVSGS-LIMARAESKDEXTYMCVATNSAGHRESR 219
Db 264 S-GYPTPTIYMQGDEFPVIRTRKYSVLGGSNLLISNVTDDAGAYTCVATYKNVTSFS 322
Qy 220 AARVSIQEPDYTEPEVELLA---VRIQLENVTLLNPDPAEGPKRPAVWLXMKVSGPRL 276
Db 323 ADLTVMVPPQFLNHPANLAYESMDIEFE-----CAVSGKPSPTV--KWTQNGEVI 372
Qy 277 PN 278
Db 373 PS 374

RESULT 10
TDHULK
leukocyte antigen-related protein precursor - human
N:Alternate names: leukocyte common antigen homolog
N:Contains: protein-tyrosine-phosphatase (EC 3.1.3.48)
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 22-Jun-1999
C:Accession: S03841; JLO051
R:Streuli, M.; Krueger, N.X.; Hall, L.R.; Schlossman, S.F.; Saito, H.
J. Exp. Med. 168, 1523-1530, 1988
A:Title: A new member of the immunoglobulin superfamily that has a cytoplasmic region homologous to protein-tyrosine-phosphatase; fibronectin type III repeat homology; F:116-1897/Domain: signal sequence #status predicted <SIG>
A:Reference number: JLO051; MUID:89035978; PMID:2972792
A:Accession: S03841
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1897 <STR>
A:Cross-references: EMBL:Y00815; NID:G34266; PIDN:CAA68754.1; PID:G34267
C:Genetics: LAR
A:Gene: GDB:PTPRF; LAR
A:Cross-references: GDB:120138; OMIM:179590
A:Map position: lp34-lp34
C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology; F:116-1897/Domain: signal sequence #status predicted <SIG>
F:116-1897/Domain: signal sequence #status predicted <SIG>
F:17-1250/Domain: extracellular #status predicted <EXT>
F:37-99/Domain: immunoglobulin homology <IMM1>
F:113-199/Domain: immunoglobulin homology <IMM2>
F:236-290/Domain: immunoglobulin homology <IMM3>
F:308-390/Domain: fibronectin type III repeat homology <FN3A>
F:403-489/Domain: fibronectin type III repeat homology <FN3B>
F:501-583/Domain: fibronectin type III repeat homology <FN3C>
F:596-685/Domain: fibronectin type III repeat homology <FN3D>
F:698-798/Domain: fibronectin type III repeat homology <FN3E>
F:810-893/Domain: fibronectin type III repeat homology <FN3F>
F:905-989/Domain: fibronectin type III repeat homology <FN3G>
F:1001-1078/Domain: fibronectin type III repeat homology <FN3H>
F:1251-1274/Domain: transmembrane #status predicted <TM>
F:1275-1897/Domain: intracellular #status predicted <INT>
F:1285-1897/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F:1365-1586/Domain: protein-tyrosine-phosphatase homology <PTP1>
F:1654-1877/Domain: protein-tyrosine-phosphatase homology <PTP2>
F:44-97, 146-197, 243-288/Disulfide bonds: #status predicted
F:107, 240, 285, 711, 956/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:1538/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1544/Binding site: substrate phosphate (Arg) #status predicted
F:1829/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1835/Binding site: substrate phosphate (Arg) #status predicted

Query Match 15.2%; Score 244.5; DB 1; Length 1897;
Best Local Similarity 31.3%; Pred. No. 4.3e-10;
Matches 73; Conservative 41; Mismatches 80; Indels 39; Gaps 10;

Qy 15 LPLLLLLLIMGMAQ-----DSPQILVHPQDLFGGPGPARMSCRASGQPPPTIRWLNGQ 70
Db 2 VPLPALVLMGLVAGAHGDSKPVFKVPEDQTLGSGVASFVCQATGEPKPRITWKKKGK 61

Db 174 PVDPSASNGRIKQLRGALQIESSETDQKQECVATNSAGVRYSSPANLYVR 226

RESULT 12

S46217

protein-tyrosine-phosphatase (EC 3.1.3.48) type sigma precursor - rat
N;Alternate names: leukocyte common antigen-related phosphatase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-May-1995 #sequence revision 03-Nov-1995 #text_change 23-Jul-1999
C;Accession: S46217; S51174; A49104
R;Zhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, B.J.
Biochem. J. 302: 39-47, 1994
A;Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine-phosphatase
A;Reference number: S46216; MUID:94347119; PMID:8068021
A;Accession: S46217
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1863 <ZHA>
R;Goldstein, B.J.
submitted to the EMBL Data Library, February 1993
A;Reference number: S51174
A;Accession: S51174
A;Molecule type: mRNA
A;Residues: 1-1788, 'G', 1790-1863 <GOL>
A;Cross-references: EMBL:L11587; NID:G205134; PIDN:AAC37656.1; PID:G205135
R;Yan, H.; Grossman, A.; Wang, H.; D'Eustachio, P.; Mossie, K.; Musacchio, J.M.; Silver
J. Biol. Chem. 268, 24880-24886, 1993
A;Title: A novel receptor tyrosine phosphatase-sigma that is highly expressed in the
A;Reference number: A49104; MUID:94043351; PMID:8227050
A;Accession: A49104
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-596, 'R', 598-603, 'I', 967-1788, 'G', 1790-1863 <YAN>
A;Experimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBIP:139669)
C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
Cg
C;Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hy
F;1-26/Domain: signal sequence #status predicted <Sig>
F;27-1863/Product: protein-tyrosine-phosphatase #status predicted <MAT>
F;149-209/Domain: immunoglobulin homology <IMM1>
F;246-300/Domain: immunoglobulin homology <IMM2>
F;318-400/Domain: fibronectin type III repeat homology <FN3A>
F;413-499/Domain: fibronectin type III repeat homology <FN3B>
F;511-592/Domain: fibronectin type III repeat homology <FN3C>
F;1244-1863/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F;1331-1552/Domain: protein-tyrosine-phosphatase homology <PTP1>
F;1504/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1510/Binding site: substrate phosphate (Arg) #status predicted
F;1795/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1801/Binding site: substrate phosphate (Arg) #status predicted

Query Match 14.8%; Score 237.5; DB 2; Length 1863;
Best Local Similarity 30.9%; Pred. No. 1.4e-09;
Matches 72; Conservative 40; Mismatches 82; Indels 39; Gaps 11;

QY 13 GSPLPLLLLLIMGMAQDSPPIILVHQDLFGQGGPARMSCRASGQPPPIRW-----LL 67
Db 14 GPVGLFLVLLARGLAEAEPRFRTRDPKQGVGGVAFVCQATGDPKPRVTWNKGGKV 73
QY 68 NGQPLSMVPDPHHLLPDGTLTLLQLPARGHADGQALST--DLGVVTCASNLRLGTAVS 125.
Db 74 NSQRFITFD-----SSGAVLRIQP-----LRTPRDNVECVQNSVG-EIT 117
QY 126 RGLARSAVLRFDFQIQPRDMVAVGEQF-----TLECGPPGHGPEPTVSWKDGK 176
Db 118 VHAULT--VLRED-QLPPGPFNDMGPLQKVVERTRTATMLCAAS--GNPDPFITWFKDFL 173
QY 177 PL--ALQPR--HTVSGSLLMARAEKSDXTYMCVATNSAGHRESRAARVSIQ 226
Db 174 PVDPSASNGRIKQLRGALQIESSETDQKQECVATNSAGVRYSSPANLYVR 226

RESULT 13

S50893
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type sigma precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C;Accession: S50893; S40281
R;Wagner, J.; Boerboom, D.; Tremblay, M.L.
Eur. J. Biochem. 226, 773-782, 1994
A;Title: Molecular cloning and tissue-specific RNA processing of a murine receptor-type
A;Reference number: S50893; MUID:95112841; PMID:7529177
A;Accession: S50893

A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1907 <WAG>
A;Cross-references: EMBL:X82288; NID:9587483; PIDN:CAAS7732.1; PID:9587484
R;Hendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.
submitted to the EMBL Data Library, June 1993
A;Description: Assessment of the expression levels of murine protein-tyrosine phosphatase
A;Reference number: S40280
A;Accession: S40281

A;Molecule type: mRNA
A;Residues: 1441-1501, E', 1503-1546 <HEN>
A;Cross-references: EMBL:Z23050; NID:9438137; PIDN:CAA80585.1; PID:9438138
C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
cgy

C;Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane
F;149-209/Domain: immunoglobulin homology <IMM1>
F;246-300/Domain: immunoglobulin homology <IMM2>
F;413-506/Domain: fibronectin type III repeat homology <3FR>
F;1288-1907/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F;1375-1596/Domain: protein-tyrosine-phosphatase homology <PTP1>
F;1664-1887/Domain: protein-tyrosine-phosphatase homology <PTP2>
F;1548/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1554/Binding site: substrate phosphate (Arg) #status predicted
F;1839/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1845/Binding site: substrate phosphate (Arg) #status predicted

Query Match 14.8%; Score 237.5; DB 2; Length 1907;
Best Local Similarity 30.9%; Pred. No. 1.4e-09;
Matches 72; Conservative 40; Mismatches 82; Indels 39; Gaps 11;

Qy 13 GSLPLLLLLMGMAQSPQILVHPDQLFQPGPARMSCRASGQPPPTIRW-----LL 67

Db 14 GPVGLFVLLARGCLAEPPFIREPRDQIGVSGVASFVQATGDPKPRVTWNKKGKV 73

Qy 68 NQPLSVPPDPHLLPDGTLILLQPPARGHAHDGQALST--DLGVYTCESNRLGTAVS 125

Db 74 NSQRFETIDFE---SSGAVLRIQP-----LRTPRDENVYECVAQNSVG-EIT 117

Qy 126 RGARLSVAVLRDEFQIOPRDMVAVVVGQF-----TLFCGPPWGHPEPTVSMWKDGK 176

Db 118 IHAKLT--VLRED-QLPPGFNIDMPQLKVVETRTATMLCAAS-GNPDPETWFKDEL 173

Qy 177 PL--ALQGR--HTVSGGSLMARAEKSDXTYMCVATNSAGHRSRAARVSIQ 226

Db 174 PVDPSASNGRIKQLRSALQETSEETDQGYECVATNSAGVRYSSPANLYVR 226

RESULT 14

A34695
axonal glycoprotein TAG-1 precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-Jun-1990 #sequence_revision 29-Jun-1990 #text_change 21-Jan-2000
C;Accession: A34695
R;Furley, A.J.; Morton, S.B.; Manalo, D.; Karagogeos, D.; Dodd, J.; Jessell, T.M.
Cell 61, 157-170, 1990
A;Title: The axonal glycoprotein TAG-1 is an immunoglobulin superfamily member with neur
A;Reference number: A34695; MUID:90199890; PMID:2317872
A;Accession: A34695

A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1040 <FUR>

A;Cross-references: GB:M31725; NID:G207148; PIDN:AAA42201.1; PID:G207149
C;Superfamily: contactin; fibronectin type III repeat homology; immunoglobulin homology
C;Keywords: glycoprotein
F;343-399/Domain: immunoglobulin homology <IMM>

Query Match 14.7%; Score 236.5; DB 2; Length 1040;
Best Local Similarity 28.2%; Pred. No. 8.7e-10;
Matches 84; Conservative 43; Mismatches 100; Indels 71; Gaps 15;

Qy 18 LALLIMG-----GMAQDSP-----PQILVHPDQLFQPGPARMSCRASG 57

Db 11 LLLLVLATVALVSSPGWSPAGTPTGPIFEQPIGLLPPEE---SAEDQVTLACARA 67

Qy 58 QPPPTIRWLLNGQPLSMVPPDPHLLPDGTLILLQPPARGHAHDGQALSDGLVYTCEAS 117

Db 68 SPATYRWKNGTDMLEFSGSRHQLM-GGNLVIMSP-----TKTODAGVYQCLAS 116

Qy 118 NRLGTAVSRGARSVALVRDEFQIQPRDMVAV-VGEQFTLECGPPWGHPEPTVSMWKDGK 176

Db 117 NPVGTVVSKAVLRFGFLQF-FSKERDPVKTHEGWMGLPCNPPPAHYPGLSYRWLLNEF 175

Qy 177 PLAL-QGRHTVTS--CGSLLMARAEKSDXTYMCVATNSAGHRE-----SRAARVSI- 225

Db 176 PNFTPTDGRHFVSQTTGNLYIARTNASDLGNYSCLATS---HMDFTSKVSFKPAQLNLA 232

Qy 226 -QSPQDVT-----EPVELLAVRIQLENVTLLNPDPAEGPKPRPAVWLXW-KVSG 272

Db 233 AEDPRLFAPSIKARFPETVALVQQVTLFCFAGFNPVR-----IKRWKVDG 280

RESULT 15

A49356

transient axonal glycoprotein TAG-1 precursor - human

N;Alternate names: axonin-1

C;Species: Homo sapiens (man)

C;Date: 20-Feb-1995 #sequence_revision 23-Mar-1995 #text_change 24-Sep-1999

C;Accession: S35508; S28830; A49356

R;Hasler, T.

submitted to the EMBL Data Library, September 1992

A;Reference number: S35508

A;Accession: S35508

A;Molecule type: mRNA

A;Residues: 1-1040 <HAS>

A;Cross-references: EMBL:X68274; NID:G36674; PIDN:CAA48335.1; PID:G36675

R;Hasler, T.H.; Rader, C.; Stoekli, E.T.; Zuellig, R.A.; Sonderegger, P.

Eur. J. Biochem. 211, 329-339, 1993

A;Title: cDNA cloning, structural features, and eucaryotic expression of human TAG-1/axo

A;Reference number: S28830; MUID:93145965; PMID:8425542

A;Accession: S28830

A;Molecule type: mRNA

A;Residues: 1-296, 'T', 298-1040 <HA2>

A;Cross-references: EMBL:X68274

R;Siotra, P.C.; Karagogeos, D.; Theodorakis, K.; Michaelidis, T.M.; Modi, W.S.; Furley,

Genomics 18, 562-567, 1993

A;Title: Isolation of the cDNA and chromosomal localization of the gene (TAG1) encoding

A;Reference number: A49356; MUID:94140354; PMID:8307567

A;Accession: A49356

A;Molecule type: mRNA

A;Residues: 1-1001, 'G', 1003-1040 <TSI>

A;Cross-references: GB:X67734

C;Genetics:

A;Gene: GDB:TAX1

A;Cross-references: GDB:138782

A;Map position: 1q32-1q32

C;Superfamily: contactin; fibronectin type III repeat homology; immunoglobulin homology

C;Keywords: cell adhesion; glycoprotein

F;1-28/Domain: signal sequence #status predicted <SIG>

F;29-1040/Product: axonal glycoprotein TAG-1 #status predicted <MAT>

F;254-308/Domain: immunoglobulin homology <IMM1>

F;341-397/Domain: immunoglobulin homology <IMM2>

F;76,196,204,461,477,498,525,775,830,904,918,940/Binding site: carbohydrate (Asn) (coval

Query Match 14.4%; Score 232; DB 2; Length 1040;

Best Local Similarity 28.7%; Pred. No. 1.9e-09;
Matches 84; Conservative 41; Mismatches 108; Indels 60; Gaps 14;

QY	3	SGGDSLLGGRGSLPLLLLLIMGMAODSPQILVHPDQLFQPGPGPARMSCRASGQPPPT	62
Db	23	SAWSSALGSQTT-----FGPVFEDQLSLVL-FPEESTER---QVLLACRARASPPAT	70
QY	63	IRWLLNGQPLSMVPPDPHLLPDGTLILLQPPARGHAHDGQALSTDGLGYTCEASNRLGT	122
Db	71	YRWKMGTEMKLEPGSRHQLV-GGNLVINP-----TKAQDAGVYQCLASNPVGT	119
QY	123	AVSRGARLSVAVLREDFQIQPRDMV-AVVGEOFTLECGPPWGHPEPTVSWWKDGKPLAL-	180
Db	120	VVSREAILRFGFLQE-FSKEERDPVKAHEGWGMFLCNPFAHYPCGLSYRWLLNEFFNFIP	178
QY	181	QPCRHTVS--GGSLLMARAEKSDEXTYMCVATNSAGHRE-----SRAARVSIQ-----	226
Db	179	TGRHFVSQTTGNLYTARTNASDLGNYSCLATS---HMDFTSKSVFSKFAQLNLAAEDTR	235
QY	227	-----EPQDYTEPVVELLAVRIQLENVTLLNPDPAEGPKPRPAVMLXW-KVSG	272
Db	236	LFAPSIKARPAETALVGQQVTLECFAGNPVPR-----IKWRKVDG	278

Search completed: January 30, 2004, 15:57:08
Job time : 14.6529 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 30, 2004, 15:45:39 ; Search time 10.4663 Seconds
(without alignments)
1361.423 Million cell updates/sec

Title: US-10-047-021-86
Perfect score: 1608
Sequence: 1 MGSGGDSILGGRGSLPILL.....SGPRLPREARLGRQRRNTG 303

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	244.5	15.2	1897	PTPF_HUMAN	P10586 homo sapien
2	236.5	14.7	1040	AXOI_RAT	P22063 rattus norv
3	232	14.4	1040	AXOI_HUMAN	Q02246 homo sapien
4	231.5	14.4	3707	PGEM_MOUSE	Q05793 mus musculu
5	230	14.3	1912	PTPD_HUMAN	P23468 homo sapien
6	223	13.9	1493	NEO1_MOUSE	P97798 mus musculu
7	222	13.8	2029	LAR_DROME	P18621 drosophila
8	221.5	13.8	1377	NEO1_RAT	P97603 rattus norv
9	217.5	13.5	1070	PTK7_HUMAN	Q13308 homo sapien
10	217.5	13.5	1461	NEO1_HUMAN	Q92859 homo sapien
11	215.5	13.4	1443	NEO1_CHICK	Q90610 gallus gall
12	214	13.3	1036	AXOI_CHICK	P28685 gallus gall
13	209	13.0	1447	DCC_MOUSE	P70211 mus musculu
14	207.5	12.9	1302	NRG_DROME	P20241 drosophila
15	206	12.8	1447	DCC_HUMAN	P43146 homo sapien
16	206	12.8	4391	PGEM_HUMAN	P98160 homo sapien
17	202	12.6	837	NCM2_MOUSE	O35136 mus musculu
18	196.5	12.2	1914	KMLS_HUMAN	Q13746 homo sapien
19	195.5	12.2	1091	NCAL_CHICK	P13590 gallus gall
20	195.5	12.2	6632	UN89_CABEL	O01761 caenorhabdi
21	194.5	12.1	1284	NRCA_CHICK	P33331 gallus gall
22	193	12.0	837	NCM2_HUMAN	O15394 homo sapien
23	193	12.0	1266	NCGA_CHICK	Q03696 gallus gall
24	191	11.9	1260	CAML_MOUSE	P11627 mus musculu
25	188.5	11.7	2200	LAR_CABEL	Q98m8 caenorhabdi
26	186	11.6	416	RAGE_BOVIN	Q28173 bos taurus
27	186	11.6	1257	CAML_HUMAN	P32004 homo sapien
28	185	11.5	725	NCM2_MOUSE	P13594 mus musculu
29	185	11.5	1115	NCAL_MOUSE	P13595 mus musculu
30	184.5	11.5	333	AMAL_DROME	P15364 drosophila
31	184	11.4	1051	PTK7_CHICK	Q91048 gallus gall
32	184	11.4	3375	UN52_CABEL	Q06561 caenorhabdi
33	183.5	11.4	1010	CONT_CHICK	P14781 gallus gall

RESULT 1

ID	PTPF_HUMAN	STANDARD;	PRT;	1897 AA.
AC	P10586;			
DT	01-JUL-1989	(Rel. 11, Created)		
DT	01-JUL-1989	(Rel. 11, Last sequence update)		
DT	15-SEP-2003	(Rel. 42, Last annotation update)		
DE	LAR protein precursor (Leukocyte antigen related) (EC 3.1.3.48).			
GN	PTPRF OR LAR.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Tonsil;			
RX	MEDLINE=89033578; PubMed=2972792;			
RA	Streuli M., Krueger N.X., Hall L.R., Schlossman S.F., Saito H.;			
RT	"A new member of the immunoglobulin superfamily that has a			
RT	cytoplasmic region homologous to the leukocyte common antigen.";			
RL	J. Exp. Med. 168:1523-1530(1988).			
RN	[2]			
RP	MUTAGENESIS.			
RX	MEDLINE=90046860; PubMed=2554325;			
RA	Streuli M., Krueger N.X., Tsai A.Y.M., Saito H.;			
RT	"A family of receptor-linked protein tyrosine phosphatases in humans			
RT	and Drosophila.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 86:8698-8702(1989).			
RN	[3]			
RP	MUTAGENESIS.			
RX	MEDLINE=90316093; PubMed=1695146;			
RA	Streuli M., Krueger N.X., Thai T., Tang M., Saito H.;			
RT	"Distinct functional roles of the two intracellular phosphatase like			
RT	domains of the receptor-linked protein tyrosine phosphatases LCA and			
RT	LAR.";			
RL	EMBO J. 9:2399-2407(1990).			
CC	-!- FUNCTION: IT IS POSSIBLE THAT DLAR IS A CELL ADHESION RECEPTOR.			
CC	IT POSSESSES AN INTRINSIC PROTEIN TYROSINE PHOSPHATASE ACTIVITY			
CC	(PTPASE).			
CC	-!- FUNCTION: THE FIRST PTPASE DOMAIN HAS ENZYMATIC ACTIVITY, WHILE			
CC	THE SECOND ONE SEEMS TO AFFECT THE SUBSTRATE SPECIFICITY OF THE			
CC	FIRST ONE.			
CC	-!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein			
CC	tyrosine + phosphate.			
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.			
CC	-!- SIMILARITY: Contains 8 fibronectin type III domains.			
CC	-!- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
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CC	entities requires a license agreement (See http://www.iesb-sib.ch/announce/			
CC	or send an email to license@iesb-sib.ch).			

P13596 rattus norv
Q05695 rattus norv
O60469 homo sapien
P31836 bos taurus
P34082 drosophila
P13592 homo sapien
P13591 homo sapien
Q15109 homo sapien
Q12860 homo sapien
Q63198 rattus norv
Q28730 oryctolagus
P12960 mus musculu

ALIGNMENTS

```
CC -----
DR EMBL; Y00815; CAA68754.1; -.
DR PIR; S03841; TDHULK.
DR PDB; 1IAR; 25-APR-00.
DR GENE; HGNC:9670; PTPRF.
DR MIM; 179530; -.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005001; F:transmembrane receptor protein tyrosine pho. .; TAS.
DR GO; GO:0007155; P:cell adhesion; TAS.
DR GO; GO:0007185; P:transmembrane receptor protein tyrosine pho. .; TAS.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR003962; FNIII subd.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig c2.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00041; fn3; 7.
DR Pfam; PF00047; ig; 3.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00014; FNTYPEIII.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00060; FN3; 4.
DR SMART; SM00194; PTPC; 2.
DR PROSITE; PS00835; IG LIKE; 3.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS00556; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 2.
KW Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane;
KW Cell adhesion; Immunoglobulin domain; Repeat; 3D-structure.
FT SIGNAL 1 16
FT CHAIN 17 1897
FT DOMAIN 17 1250
FT TRANSMEM 1251 1274
FT DOMAIN 1275 1897
FT DOMAIN 123 113
FT DOMAIN 125 214
FT DOMAIN 222 304
FT DOMAIN 1360 1806
FT DOMAIN 1649 1897
FT ACT SITE 1538 1538
FT ACT SITE 1829 1829
FT CARBOHYD 107 107
FT CARBOHYD 240 240
FT CARBOHYD 285 285
FT CARBOHYD 711 711
FT CARBOHYD 956 956
FT MUTAGEN 1538 1538
SQ SEQUENCE 1897 AA; 211844 MW; 439850F1D5C031FF CRC64;

Query Match 15.2%; Score 244.5; DB 1; Length 1897;
Best Local Similarity 31.3%; Pred. No. 1e-10;
Matches 73; Conservative 41; Mismatches 80; Indels 39; Gaps 10;

QY 15 LPLLLLLMGWAQ----DSPQLIVHPDQLFQGPGRMCRASGPPPTIIRLLNGQ 70
DB 2 VPLVPLVMLGLVAGAHGDSRPVFKVPEDDTGLSGGVASFCVQATGPKPRITWKKKGK 61
QY 71 PLS-----MVPDPDPLHLLPDGTLTLLQPPARGHAGDQALSTDLGVYTCEASNRIGTAVS 125
DB 62 KVSQRFEVIFDD-----GAGSVLRIQP-----LRVQDEAIVECTATNSLG-EIN 107
QY 126 RGALSLVAVLREDFOIQPRDMVAVVGEQF-----TLGCGPWHGHPETVSNWKDGK 176
DB 108 TSAKLSVL---EEQLPGFPFSDMGPPQPKVKEKARTATMLCA-AGNPDPFISWFKDFL 163
QY 177 PL--ALQGR-HTVSGGSLMARKEKSDXTVMCVATNSAGHRSRAARVSIQ 226
DB 164 PVDPATSNRIKQLRSGALQIESSESDQGYKECVATNSAGTRYSAFANLYVR 216

RESULT 2
```

```
AXO1 RAT
ID AXO1 RAT STANDARD; PRT; 1040 AA.
AC P22063;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Contactin 2 precursor (Axonin-1) (Axonal glycoprotein TAG-1)
DE (Transient axonal glycoprotein 1) (TAX-1).
GN CNTN2 OR TAXI.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 31-41.
RC TISSUE=spinal cord;
RX MEDLINE=9019890; PubMed=2317872;
RA Furlley A.J., Morton S.B., Manalo D., Karagoce D., Dodd J.,
RA Jessell T.M.;
RT "The axonal glycoprotein TAG-1 is an immunoglobulin superfamily
member with neurite outgrowth-promoting activity.";
RL Cell 61:157-170(1990).
CC -1- FUNCTION: MAY PLAY A ROLE IN THE INITIAL GROWTH AND GUIDANCE OF
AXONS. MAY BE INVOLVED IN CELL ADHESION.
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE NEURONAL MEMBRANE BY A
GPI-ANCHOR AND IS ALSO RELEASED FROM NEURONS.
CC -1- TISSUE SPECIFICITY: IN NEURAL TISSUES IN EMBRYOS, AND IN ADULT
BRAIN, SPINAL CORD AND CEREBELLUM.
CC -1- DEVELOPMENTAL STAGE: TRANSIENTLY EXPRESSED ON A SUBSET OF AXONS
IN THE DEVELOPING RAT NERVOUS SYSTEM.
CC -1- SIMILARITY: Contains 6 immunoglobulin-like C2-type domains..
CC -1- SIMILARITY: Contains 4 fibronectin type III domains.
CC -----
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M31725; AAA42201.1; -.
DR PIR; A34695; A34695.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR003962; FNIII subd.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig c2.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00041; fn3; 4.
DR Pfam; PF00047; ig; 6.
DR PRINTS; PR00014; FNTYPEIII.
DR SMART; SM00060; FN3; 4.
DR SMART; SM00408; IGC2; 5.
DR PROSITE; PS00835; IG LIKE; 6.
KW Immunoglobulin domain; Glycoprotein; Signal; GPI-anchor;
KW Cell adhesion; Repeat;
FT SIGNAL 1 30
FT CHAIN 31 1015
FT PROPEP 1016 1040
FT DOMAIN 39 130
FT DOMAIN 135 224
FT DOMAIN 241 324
FT DOMAIN 329 413
FT DOMAIN 419 506
FT DOMAIN 511 605
FT DOMAIN 608 614
FT DOMAIN 613 708
FT DOMAIN 716 811
FT DOMAIN 818 910
FT DOMAIN 911 1005
FT SITE 796 798
FT CARBOHYD 78 78
FT CARBOHYD 200 200
CONTACTIN 2.
REMOVED IN MATURE FORM (POTENTIAL).
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 5.
IG-LIKE C2-TYPE 6.
GLY/PRO-RICH.
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 4.
CELL ATTACHMENT SITE (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
```


Query Match 14.4%; Score 232; DB 1; Length 1040;
Best Local Similarity 28.7%; Pred. No. 4.6e-10;
Matches 84; Conservative 41; Mismatches 108; Indels 60; Gaps 14;

```
QY 3 SGGSLGGRGSLPLLLLLLMGMAQSPPOILVHPDQLFQGGPARMSCRAGSQPPPT 62
DB 23 SAMSALGSQTT-----FGPVFEOQLSVL-FPESTEE---QVLLACRASPAT 70
QY 63 IRWLLNGPLSMVPPDPHLLPDGTLTLLLOPPARGHAHQALSTDLGVYTCESNRLGT 122
DB 71 YRWKMGNTKMLPGSRHQLV-GGNLVIMNP-----TKAQDAGVYQCLASNPVGT 119
QY 123 AVSFCARLSVAVAREFOIQPRDMV-AVVGQFTLECGPPMGHPPTVSWKDKPLAL- 180
DB 120 VVSREAILRFGFLOE-FSKERDPPKAHEGVGMWLPNCPNPAHYGLSYRMLNFPFIP 178
QY 181 QPGRHTVS--GGSLLMARAERSDEXTYMCVATNSAGHRE-----SRAARVSIQ----- 226
DB 179 TDGRHFVSQTTGNLYIARTNASDLGNYSCLATS-----HMDFTKSVFSKFAQLNLAEDTR 235
QY 227 -----EPQDYTEPVVELLAVRIQIENVTLNPDPAEGPKPRPAVWLXW-KVSG 272
DB 236 LFAPSIKARFPAETAYLVGQQVTLCEFAFGNFPVR-----IKWRKVDG 278
```

RESULT 4

```
PCBM MOUSE
ID PGSM MOUSE STANDARD; PRT; 3707 AA.
AC Q05793;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Basement membrane-specific heparan sulfate proteoglycan core
DE protein precursor (HSPG) (Perlecan) (PLC).
GN HSPG2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Melanoma;
RX MEDLINE=92078153; PubMed=1744087;
RA Noonan D.M., Fulle A., Valente P., Cai S., Horigan E., Sasaki M.,
RA Yamada Y., Hassell J.R.;
RT "The complete sequence of perlecan, a basement membrane heparan
RT sulfate proteoglycan, reveals extensive similarity with laminin A
RT chain, low density lipoprotein-receptor, and the neural cell adhesion
RT molecule.";
RL J. Biol. Chem. 266:22939-22947(1991).
RN [2]
RP SEQUENCE OF 940-1601 AND 1870-2600 FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=89034110; PubMed=2972708;
RA Noonan D.M., Horigan E.A., Ledbetter S.R., Vogeli G., Sasaki M.,
RA Yamada Y., Hassell J.R.;
RT "Identification of cDNA clones encoding different domains of the
RT basement membrane heparan sulfate proteoglycan.";
RL J. Biol. Chem. 263:16379-16387(1988).
CC -!- FUNCTION: This protein is an integral component of basement
CC membranes. It is responsible for the fixed negative electrostatic
CC charge and is involved in the charge-selective ultrafiltration
CC properties. It serves as an attachment substrate for cells.
CC -!- SUBUNIT: Purified perlecan has a strong tendency to aggregate in
CC dimers or stellate structures. It interacts with other basement
CC membrane components such as laminin, prolargin and collagen type
CC IV.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES.
CC -!- PTM: CONTAINS THREE HEPARAN SULFATE CHAINS AS WELL AS N-LINKED
CC AND O-LINKED OLIGOSACCHARIDES.
CC -!- SIMILARITY: Contains 4 LDL-receptor class A domains.
CC -!- SIMILARITY: Contains 11 laminin EGF-like domains.
```

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CC -!- SIMILARITY: Contains 3 laminin IV domains.
CC -!- SIMILARITY: Contains 15 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 3 laminin G-like domains.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC -!- SIMILARITY: Contains 1 SEA domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M77174; AAA39911.1; --
CC EMBL; J04054; AAA39899.1; --
CC EMBL; J04055; AAA39912.1; --
CC PIR; S18252; S18252.
CC PDB; 1GL4; 28-NOV-01.
CC MGD; MGI:96257; Hspg2.
CC GO; GO:0005604; C:basement membrane; IDA.
CC GO; GO:0008104; P:protein localization; IMP.
CC InterPro; IPR000742; EGF 2.
CC InterPro; IPR006209; EGF-like.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003598; Ig c2.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR000034; Laminin_B.
CC InterPro; IPR002049; Laminin_EGF.
CC InterPro; IPR001791; Laminin_G.
CC InterPro; IPR002172; LDL receptor_A.
CC InterPro; IPR000082; SEA_domain.
CC Pfam; PF00008; EGF; 4.
CC Pfam; PF00047; Ig; 15.
CC Pfam; PF00052; laminin_B; 3.
CC Pfam; PF00053; laminin_EGF; 7.
CC Pfam; PF00054; laminin_G; 3.
CC Pfam; PF00057; ldl_recept_a; 4.
CC Pfam; PF01330; SEA; 1.
CC PRINTS; PR00261; LDLRECEPTOR.
CC ProDom; PD003031; Laminin_B; 3.
CC SMART; SM00180; EGF_Lam; 7.
CC SMART; SM00408; IGC2; 14.
CC SMART; SM00281; Lamb; 3.
CC SMART; SM00282; LamG; 3.
CC SMART; SM00192; LDLA; 4.
CC SMART; SM00200; SEA; 1.
CC PROSITE; PS00022; EGF_1; 8.
CC PROSITE; PS01186; EGF_2; 5.
CC PROSITE; PS50835; IG_LIKE; 15.
CC PROSITE; PS50025; LAM_G_DOMAIN; 3.
CC PROSITE; PS01248; LAMININ_TYPE_EGF; 11.
CC PROSITE; PS01209; LDLRA_1; 4.
CC PROSITE; PS50068; LDLRA_2; 4.
CC PROSITE; PS50024; SEA; 1.
CC Signal; Basement membrane; Proteoglycan; Repeat; Glycoprotein;
CC Heparan sulfate; Laminin EGF-like domain; Immunoglobulin domain;
CC Extracellular matrix; EGF-like domain; 3D-structure.
CC SIGNAL 1 21 POTENTIAL.
CC CHAIN 22 3707 BASEMENT MEMBRANE-SPECIFIC HEPARAN
CC SULFATE PROTEOGLYCAN CORE PROTEIN.
CC SEGA.
CC DOMAIN 80 194 LDL-RECEPTOR CLASS A 1.
CC DOMAIN 195 234 LDL-RECEPTOR CLASS A 2.
CC DOMAIN 281 319 LDL-RECEPTOR CLASS A 3.
CC DOMAIN 320 359 LDL-RECEPTOR CLASS A 4.
CC DOMAIN 360 403 IG-LIKE C2-TYPE 1.
CC DOMAIN 404 504 LAMININ EGF-LIKE 1 (N-TERMINAL).
CC DOMAIN 521 530 LAMININ DOMAIN IV 1 (DOMAIN III A).
CC DOMAIN 531 730 LAMININ EGF-LIKE 1 (C-TERMINAL).
CC DOMAIN 731 763 LAMININ EGF-LIKE 2.
CC DOMAIN 764 813 LAMININ EGF-LIKE 3.
CC DOMAIN 814 871 LAMININ EGF-LIKE 4.
CC DOMAIN 879 923 LAMININ EGF-LIKE 4 (INCOMPLETE).
```


FT		/FTID=VSP_002594.
FT	VARSPLIC	863 878 Missing (in isoform 3).
FT	FT	/FTID=VSP_002595.
FT	VARSPLIC	1086 1096 Missing (in isoform 4).
FT	FT	/FTID=VSP_002596.
FT	VARSPLIC	1279 1331 Missing (in isoform 5).
FT	FT	/FTID=VSP_002597.
SQ	SEQUENCE	1493 AA; 163159 MW; 441DE919D5E17C0E CRC64;
 Query Match 13.9%; Score 223; DB 1; Length 1493; Best Local Similarity 29.6%; Pred. No. 3.3e-09; Matches 74; Conservative 32; Mismatches 104; Indels 40; Gaps 8;		
OY	15 LPLLLLL---	IMGMAQDSPPQ-----ILVHPQDLFQCGGPARMSCRAS 56
DB		: : : : : : : : : : : : : : : : :
DB	29 LPLLLLLRPASC	AATAATKGPRRQSQCASVRTPTFPFLVEPVDTLSVRSSVILNC SAY 88
OY	57 GQPPPTIRWLLNG	OPSLMVPPDPHLLPGTLLLQLQPPARGHAHQALSTDLGVYTCEA 116
DB		: : : : : : : : : : : : : : : : :
DB	89 SEPSPNIEWKKDG	TPLNLSEDRRLQPLPGSLFISNVVHSKH-----KPDEGFYCVA 142
OY	117 S-NRLCTAVSRGAR	LSSVAVLREDFQIQPRDMVAVGEQFTLEGCPWHGPE-----PTV 169
DB		: : : : : : : : : : : : : : : : :
DB	143 TVDNLTGISRTAK	LTVAGLPR-FTSQPESPVVUGNSAILNC-----EVNADLVPFV 194
OY	170 SNWKGGKLALOPGR	HVTSGGSLLMARAKSDEXTVMCVATNSAGHRESRAARVSI-QEP 228
DB	: : :	: : : : : : : : : : : : : : : : :
DB	195 RWEQNRPQLLDRI	VKLPSPGLTIVINATEGDGLRYRCIVESGPKFKFSDEAE LKVLQDP 254
OY	229 QDYTEPVELL	238
DB	: : :	:
DB	255 EELVDLVFLM	264
 RESULT 7 LAR_DROME STANDARD; PRT; 2029 AA. ID_LAR_DROME AC PL6621; DT 01-AUG-1990 (Rel. 15, Created) DT 01-AUG-1990 (Rel. 15, Last sequence update) DT 15-SEP-2003 (Rel. 42, Last annotation update) DE Protein-tyrosine phosphatase Lar precursor (EC 3.1.3.48) (Protein- tyrosine-phosphate phosphohydrolase) (dLAR). GN dLAR. OS Drosophila melanogaster (fruit fly). OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; OC Ephydroidea; Drosophilidae; Drosophila. OX NCBI_TaxID=7227; RN [1] RN RP SEQUENCE FROM N.A. RX MEDLINE=90046860; PubMed=2554325; RA Streuli M., Krueger N.X., Tsai A.Y.M., Saito H.; RA "A family of receptor-linked protein tyrosine phosphatases in humans and Drosophila."; RL Proc. Natl. Acad. Sci. U.S.A. 86:8698-8702(1989). RN [2] RN RP SEQUENCE FROM N.A. RC STRAIN=Canton-S; RX MEDLINE=96178473; PubMed=8598047; RA Krueger N.X., van Pactor D., Wan H.I., Gelbart W.M., Goodman C.S., RA Saito H.; RL "The transmembrane tyrosine phosphatase DLAR controls motor axon guidance in Drosophila."; RT Cell 84:611-622(1996). CC - - FUNCTION: IT IS POSSIBLE THAT DLAR IS A CELL ADHESION RECEPTOR. CC IT POSSESSES AN INTRINSIC PROTEIN TYROSINE PHOSPHATASE ACTIVITY (PTPASE). IT CONTROLS MOTOR AXON GUIDANCE. CC - - CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein CC tyrosine + phosphate. CC - - SUBCELLULAR LOCATION: Type I membrane protein. CC - - TISSUE SPECIFICITY: SELECTIVELY EXPRESSED IN A SUBSET OF AXONS AND CC PIONEER NEURONS IN THE EMBRYO.		

DR MIM; 601890; --
DR GO; GO:0005886; C:plasma membrane; TAS.
DR GO; GO:0005888; C:proteoglycan integral to plasma membrane; TAS.
DR GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . .; TAS.
DR GO; GO:0007155; P:signal transduction; TAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig c2.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002011; Rtkinase1.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00047; Ig; 7.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD00001; Prot_kinase; 1.
DR SMART; SM00408; IGC2; 5.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00835; IG LIKE; 7.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00239; RECEPTOR_TYR_KIN_II; FALSE NEG.
KW Receptor; Transmembrane; Signal; Glycoprotein; Cell adhesion;
KW Immunoglobulin domain; Repeat.
FT SIGNAL 1 30
FT CHAIN 31 1070
FT DOMAIN 31 704
FT TRANSMEM 705 725
FT DOMAIN 726 1070
FT DOMAIN 31 120
FT DOMAIN 128 218
FT DOMAIN 225 317
FT DOMAIN 309 407
FT DOMAIN 412 497
FT DOMAIN 503 586
FT DOMAIN 578 680
FT DOMAIN 796 1066
FT DISULFID 53 101
FT DISULFID 150 200
FT DISULFID 246 301
FT DISULFID 343 391
FT DISULFID 433 481
FT DISULFID 524 570
FT DISULFID 613 664
FT CARBOHYD 116 116
FT CARBOHYD 175 175
FT CARBOHYD 184 184
FT CARBOHYD 214 214
FT CARBOHYD 268 268
FT CARBOHYD 283 283
FT CARBOHYD 405 405
FT CARBOHYD 463 463
FT CARBOHYD 567 567
FT CARBOHYD 646 646
FT CONFLICT 92 92
FT CONFLICT 147 147
FT CONFLICT 207 207
FT CONFLICT 495 495
FT CONFLICT 515 515
FT CONFLICT 881 881
FT CONFLICT 969 969
FT CONFLICT 992 992
SQ SEQUENCE 1070 AA; 118260 MW; 47CDF25B8E3698A5 CRC64;

Query Match 13.5%; Score 217.5; DB 1; Length 1070;
Best Local Similarity 29.2%; Pred. No. 5.9e-09;
Matches 63; Conservative 35; Mismatches 93; Indels 25; Gaps 7;

Qy 26 MAQSPFQILVHPDQFGGPGARMSCASQGPPTIRWLLNQ-PLSMVPPDPH---- 80
Db 219 IADESFARVLAQDVVVARVEEAMFHCQFSAQPPSLQWLFEDETPITNRSRPPHLRA 278
Qy 81 HLLPDGTLILLQPPARGHAHQALSTDLGVYTCEASNRLGTAVSRGALSVAVLRDFQ 140

Db 279 TVFANGSLLLTQVRPR-----NAGIYRCIGQGQRPPIILEATLHLAEIDMPL 327
Qy 141 IQRDMYAVVGEQFTLECGPWPWGPPTVSMWKGKPLALQPGRHTVSGSLLMARAES 200
Db 328 FEPR--VFTAGSBERVTLPPKGLPEPSV-WWEHAGVRLPTHGRVYOKGHELVLANTAES 384
Qy 201 DEXTYMCVATNSAGHRES-----RAARVS--IQBPQD 230
Db 385 DAGVYTCHAAANLAGQRQDVNITVATVPSWLKPKQD 420

RESULT 10
NEO1_HUMAN
ID NEO1_HUMAN STANDARD; PRT; 1461 AA.
AC Q92859; O00340;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Neogenin precursor.
GN NEO1 OR NGN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN 1
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Fetal brain;
RX MEDLINE=97236653; PubMed=9121761;
RA Meyerhardt J.A., Look A.T., Bigner S.H., Fearon E.R.;
RT "Identification and characterization of neogenin, a DCC-related
gene.";
RL Oncogene 14:1129-1136 (1997).
[2]
RN 2
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Fetal brain;
RX MEDLINE=97312699; PubMed=9169140;
RA Vielmetter J., Chen X.-N., Miskevich F., Lane R.P., Yamakawa K.,
RT Korenberg J.R., Dreyer W.J.;
RT "Molecular characterization of human neogenin, a DCC-related protein,
and the mapping of its gene (NEO1) to chromosomal position 15q22.3-
q23.";
RL Genomics 41:414-421 (1997).
CC -1- FUNCTION: MAY BE INVOLVED AS A REGULATORY PROTEIN IN THE
TRANSITION OF UNDIFFERENTIATED PROLIFERATING CELLS TO THEIR
DIFFERENTIATED STATE. MAY ALSO FUNCTION AS A CELL ADHESION
MOLECULE IN A BROAD SPECTRUM OF EMBRYONIC AND ADULT TISSUES.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
Name=1;
IsoId=Q92859-1; Sequence=Displayed;
Name=2;
IsoId=Q92859-2; Sequence=VSP_002593;
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED AND ALSO IN CANCER CELL
LINES.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. DCC
SUBFAMILY.
CC -1- SIMILARITY: Contains 4 immunoglobulin-like C2-type domains.
CC -1- SIMILARITY: Contains 6 fibronectin type III domains.
CC -----
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CC -----
CC EMBL; U61262; AAB17263.1; -.
DR EMBL; U72931; AAC51287.1; -.
DR HSP; P02751; ITTF.
DR Genew; HGNC:7754; NEO1.

DR MIM; 601907; --
DR GO; 0005887; C: integral to plasma membrane; TAS.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR003962; FNIII subd.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_C2.
DR Pfam; PF00041; fn3; 6.
DR Pfam; PF00047; IG; 4.
DR PRINTS; PR00014; FNTYPEIII.
DR SMART; SM00060; FN3; 6.
DR SMART; SM00408; IGC2; 3.
DR PROSITE; PS50835; IG_LIKE; 4.
DR Cell adhesion; Repeat; Signal; Transmembrane; Immunoglobulin domain;
KW Glycoprotein; Alternative splicing.
FT SIGNAL 1 33
FT CHAIN 34 1461
FT DOMAIN 34 1105
FT TRANSMEM 1106 1126
FT DOMAIN 1127 1461
FT DOMAIN 52 141
FT DOMAIN 152 238
FT DOMAIN 243 336
FT DOMAIN 341 426
FT DOMAIN 436 533
FT DOMAIN 536 629
FT DOMAIN 630 729
FT DOMAIN 735 829
FT DOMAIN 850 950
FT DOMAIN 951 1052
FT DOMAIN 1118 1121
FT DISULFID 74 129
FT DISULFID 173 221
FT DISULFID 270 320
FT DISULFID 362 410
FT CARBOHYD 73 73
FT CARBOHYD 210 210
FT CARBOHYD 326 326
FT CARBOHYD 470 470
FT CARBOHYD 489 489
FT CARBOHYD 639 639
FT CARBOHYD 715 715
FT CARBOHYD 909 909
FT VARSPLIC 1248 1300
FT CONFLICT 168 168
FT SEQUENCE 1461 AA; 159958 MW; 7AAE897E69635A21 CRC64;
Query Match 13.5%; Score 217.5; DB 1; Length 1461;
Best Local Similarity 22.6%; Pred. No. 8.3e-09;
Matches 86; Conservative 40; Mismatches 122; Indels 133; Gaps 11;
QY 17 LLLLLL-----GMAQDPP-----QILVHPDQLFQGPARGMCRAS 56
DB 18 LYCLLLGRRAPGAAARSGAPQSGASIRTFPFYFLVPEVDLTLSVRGSSVILNCAY 77
QY 57 GPPPTIRWLNGQPLSMVPPDPHLLPDGTLTLLQPPARGHAHQALSTDLGVYTCEA 116
DB 78 SEPSKIEWKDGTGLNLVSDRRQLLPDGLSLFISNVVHSKRN-----KPDGYIQCA 131
QY 117 S-NRLGTAVSRGALSVA-----133
DB 132 TVESLGTIISRTAKLIVAGLPRTSQPSPSSVYAGNALLCEVNADLVPPFVRWQNRQP 191
QY 134 VLRED-----F 139
DB 192 LLLDDRVIKPSGLMVLISNATEGDGLYRCVVGSGPPKYSDVELKVLDPPEVISDLVF 251
QY 140 QIQPRDMVAVCEQTLTCGPPWGHPEPTVSWKDGKPLALQPGHVT--SGSLLMARA 197
DB 252 LKQPSPLVRVIGQDVVLPCVAS-GLPTPTIKMKNEALDTSESRLLVLAGGSLEISDV 310
QY 198 EKSDXTYMCVATNSAGHSRAARVSIOEQPDYTPVELLAVRIQLENVTLLNPDPAEG 257

DB 311 TEDDAGTYFCIADNGNETIEAQLTVQAQPEFLKQPTNIYA----HESMDIVFECEVTG 366
QY 258 PKRPAVWLXKVGSPXRLPN 278
DB 367 -KPTPTV--KVRKNGDMWVIPS 384
RESULT 11
NEO1_CHICK
ID NEO1_CHICK STANDARD; PRT; 1443 AA.
AC Q90610;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Neogenin (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=White leghorn; TISSUE=Embryonic brain;
RX MEDLINE=95105243; PubMed=7806578;
RA Vielmetter J., Roman J.M., Dreyer W.J.;
RT "Neogenin, an avian cell surface protein expressed during terminal
neural differentiation, is closely related to the human tumor
suppressor molecule deleted in colorectal cancer.";
RL J. Cell Biol. 127:2009-2020(1994).
CC -!- FUNCTION: MAY BE INVOLVED AS A REGULATORY PROTEIN IN THE
TRANSITION OF UNDIFFERENTIATED PROLIFERATING CELLS TO THEIR
DIFFERENTIATED STATE. MAY ALSO FUNCTION AS A CELL ADHESION
MOLECULE IN A BROAD SPECTRUM OF EMBRYONIC AND ADULT TISSUES.
CC -!- SUBCELLULAR LOCATION: Type 1 membrane protein.
CC -!- DEVELOPMENTAL STAGE: IN RETINA, EXPRESSED ON GANGLION CELL FIBERS
AS SOON AS THEY BEGIN TO EXTEND THEIR AXONS.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. DCC
SUBFAMILY.
CC -!- SIMILARITY: Contains 4 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 6 fibronectin type III domains.
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or send an email to license@isb-sib.ch).
EMBL; U07644; AAC59662.1; --
DR PIR; I50600; I50600.
DR HSPF; P11276; 2MFN.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR003962; FNIII subd.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_C2.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00041; fn3; 6.
DR Pfam; PF00047; IG; 4.
DR PRINTS; PR00014; FNTYPEIII.
DR SMART; SM00060; FN3; 6.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS50835; IG_LIKE; 4.
DR Cell adhesion; Repeat; Transmembrane; Immunoglobulin domain;
KW Glycoprotein.
FT NON TER 1 1090
FT DOMAIN <1 1091
FT TRANSMEM 1091 1111
FT DOMAIN 1112 1443
FT DOMAIN 118 113
FT DOMAIN 118 204
FT DOMAIN 212 302
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.

FT DOMAIN 307 392 IG-LIKE C2-TYPE 4.
FT DOMAIN 422 519 FIBRONECTIN TYPE-III 1.
FT DOMAIN 522 615 FIBRONECTIN TYPE-III 2.
FT DOMAIN 616 714 FIBRONECTIN TYPE-III 3.
FT DOMAIN 720 814 FIBRONECTIN TYPE-III 4.
FT DOMAIN 835 935 FIBRONECTIN TYPE-III 5.
FT DOMAIN 936 1037 FIBRONECTIN TYPE-III 6.
FT DISULFID 40 95 BY SIMILARITY.
FT DISULFID 139 187 BY SIMILARITY.
FT DISULFID 236 286 BY SIMILARITY.
FT DISULFID 328 376 BY SIMILARITY.
FT CARBOHYD 39 376 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 456 456 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 475 475 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 700 700 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 894 894 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1443 AA; 158050 MW; 558C6795579C0E26 CRC64;
Query Match 13.4%; Score 215.5; DB 1; Length 1443;
Best Local Similarity 31.4%; Pred. No. 1.2e-08;
Matches 80; Conservative 27; Mismatches 117; Indels 31; Gaps 9;
Qy 30 SPQQLVHPQDLPQPGPARMSCRASQPPPTIRWLLNGQPLSMVPPDPHLLPDGTL 89
Db 17 TPFYFLVPMDLVSRGASVIMNCSSYCTPPKIEWKKDGTLLNLVSDRRQLLPDGSLL 76
Qy 90 LLQPPARGHAHQALSTDLGYTCEAS-NRLGTAVSRGARSVAVLREDFQIQPRDMVA 148
Db 77 INSVHSHN-----KDEGYQCVATVSELSGIVSTAKLTAGLPR-FTSQPELSSV 129
Qy 149 VVGQFTLECPWPCHPE-----PTVSNWKGKPLALQPGRHVTVSGSLMARAEKSD 202
Db 130 YKGSAILNC-----EVNVDLAPFVRWEODRPLSDRVFKLPGLGALLGNATDTG 182
Qy 203 XYTMCVATNSAGHRESRAARVSIQEPDYTPVVELLAVR--IQLENTVTLN---PDAEG 257
Db 183 GFYRCVIESGGTPKYSERAEKIL--PDPEPQSLVFRVQPSLLTKVTGQNAVFPVAGG 240
Qy 258 PKPRAVWLXWVSG 272
Db 241 ---PPTPVRTKNG 252

RESULT 12

ID AXO1 CHICK STANDARD; PRT; 1036 AA.
AC P28685;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Contact 2 precursor (Axonin-1).
GN CNTN2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI TaxID=9031;
RN [1]_SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=92174898; PubMed=1311675;
RA Zuehlig R.A., Rader C., Schroeder A., Kalousek M.B.,
RA von Bohlen Und Halbach F., Osterwalder T., Inan C., Stoeckli E.T.,
RA Affolter H.-U., Fritz A., Hafen E., Sonderegger P.;
RT "The axonally secreted cell adhesion molecule, axonin-1. Primary
RT structure, immunoglobulin-like and fibronectin-type-III-like domains
RT and glycosyl-phosphatidylinositol anchorage."
RL Eur. J. Biochem. 204:453-463(1992).
CC -1- FUNCTION: AXON-ASSOCIATED CELL ADHESION MOLECULE (AXCAM) WHICH
CC PROMOTES NEURITE OUTGROWTH BY INTERACTION WITH THE AXCAM L1 (G4)

CC OF NEURITIC MEMBRANE.
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE NEURONAL MEMBRANE BY A
CC GPI-ANCHOR.
CC -1- PFM: The N-terminus is blocked.
CC -1- SIMILARITY: Contains 6 immunoglobulin-like C2-type domains.
CC -1- SIMILARITY: Contains 4 fibronectin type III domains.
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; X63101; CAA44815.1; --
CC PIR; S22383; S22383.
CC PDB; 1CS6; 19-MAY-00.
CC InterPro; IPR003961; FN III.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003598; Ig_c2.
CC InterPro; IPR003006; Ig_MHC.
CC Pfam; PF00041; fn3; 3.
CC Pfam; PF00047; Ig; 6.
CC SMART; SM00060; FN3; 4.
CC SMART; SM00408; IGC2; 5.
CC PROSITE; PS00835; IG-LIKE; 6.
CC Immunoglobulin domain; Glycoprotein; Signal; GPI-anchor;
CC Cell adhesion; Repeat; 3D-structure.
FT SIGNAL 1 23 OR 25 (POTENTIAL).
FT CHAIN 24 ? CONTACTIN 2.
FT PROPEP 2 1036 REMOVED IN MATURE FORM.
FT DOMAIN 32 123 IG-LIKE C2-TYPE 1.
FT DOMAIN 128 223 IG-LIKE C2-TYPE 2.
FT DOMAIN 234 317 IG-LIKE C2-TYPE 3.
FT DOMAIN 322 406 IG-LIKE C2-TYPE 4.
FT DOMAIN 412 499 IG-LIKE C2-TYPE 5.
FT DOMAIN 504 598 IG-LIKE C2-TYPE 6.
FT DOMAIN 599 608 HINGE (POTENTIAL).
FT DOMAIN 601 607 GLY/PRO-RICH.
FT DOMAIN 608 709 FIBRONECTIN TYPE-III 1.
FT DOMAIN 710 811 FIBRONECTIN TYPE-III 2.
FT DOMAIN 812 912 FIBRONECTIN TYPE-III 3.
FT DOMAIN 913 1009 FIBRONECTIN TYPE-III 4.
FT CARBOHYD 71 71 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 199 199 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 456 456 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 472 472 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 493 493 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 520 520 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 770 770 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 900 900 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 914 914 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1036 AA; 113301 MW; 08B80143BE779794 CRC64;
Query Match 13.3%; Score 214; DB 1; Length 1036;
Best Local Similarity 28.7%; Pred. No. 1e-08;
Matches 81; Conservative 40; Mismatches 107; Indels 54; Gaps 16;
Qy 9 LGGRG-----SLPLLLLI-----MGGMADSPQQLVHPQDLPF-QGPGPAR--MSCRAS 56
Db 1 MGTAAFICTSLAVIICVNCQAQSGM-RSYGVPFEEQPAHTLPFGSAEKVTLTCAR 59
Qy 57 GQPPPTIRWLLNGQPLSMVPPDPHLLPDGTLTLLQLPPARGHAHQALSTDLGYTCEA 116
Db 60 ANPPATYRWKNGTELKX-GPDSRYRLVAGDLVISNP-----VKANDAGSYQCVA 108
Qy 117 SNRLGTAVSRGARSVAVLREDFQIQPRDMVAV---GEQFTLECGPPWGHPEPTVSMWK 173
Db 109 TNARGTVVSREASLRFQFLQE-FSAERDPPVKITEGVMVMT--CSPPHYPALUSYRWLL 165
Qy 174 DGKPLAL-QPGRHTVS--GGSLMARAEKSDXTYMCVATNSAGHRE-----SRAARV 223

DE Neuroglial precursor.
GN NRG OR CG1634.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM SHORT), AND SEQUENCE OF 24-41 AND 737-751.
RX MEDLINE=90030418; PubMed=2805067;
RA Bieber A.J., Snow P.M., Hortsch M., Patel N.H., Jacobs J.R.,
RA Traquina Z.R., Schilling J., Goodman C.S.;
RT "Drosophila neuroglial: a member of the immunoglobulin superfamily
RT with extensive homology to the vertebrate neural adhesion molecule
RT L1";
RL Cell 59:447-460(1989).
RN [2]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=98332718; PubMed=9666073;
RA Zhao G., Hortsch M.;
RT "The analysis of genomic structures in the L1 family of cell adhesion
RT proteins provides no evidence for exon shuffling events after the
RT separation of arthropod and chordate lineages.";
RL Gene 215:47-55(1998).
RN [3]
RP REVISIONS.
RA Hortsch M.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RX STRAIN=Berkley;
RC MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Burton R.C., Rogers Y.-H.C., Blaise R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Jajall M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Sampson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster";
RL Science 287:2185-2195(2000).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RX STRAIN=Berkley; TISSUE=Head;
RC

RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE OF 1182-1302 FROM N.A., FUNCTION, ALTERNATIVE SPLICING, AND
RP TISSUE SPECIFICITY.
RX MEDLINE=90262720; PubMed=1693086;
RA Hortsch M., Bieber A.J., Patel N.H., Goodman C.S.;
RT "Differential splicing generates a nervous system-specific form of
RT Drosophila neuroglial";
RL Neuron 4:697-709(1990).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 610-814.
RX MEDLINE=94213741; PubMed=7512815;
RA Huber A.H., Wang Y.-M.E., Bieber A.J., Bjorkman P.J.;
RT "Crystal structure of tandem type III fibronectin domains from
RT Drosophila neuroglial at 2.0 A.";
RL Neuron 12:717-731(1994).
RN [8]
RP FUNCTION: THE LONG ISOFORM MAY PLAY A ROLE IN NEURAL AND GLIAL
RP CELL ADHESION IN THE DEVELOPING EMBRYO. THE SHORT ISOFORM MAY BE A
RP MORE GENERAL CELL ADHESION MOLECULE INVOLVED IN OTHER TISSUES AND
RP IMAGINAL DISK MORPHOGENESIS. VITAL FOR EMBRYONIC DEVELOPMENT.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=P20241-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=P20241-2; Sequence=VSP_002601_VSP_002602;
CC -1- TISSUE SPECIFICITY: LONG ISOFORM IS RESTRICTED TO SURFACE OF
CC NEURONS AND GLIA IN THE DEVELOPING NERVOUS SYSTEM AND THE SHORT
CC ISOFORM TO OTHER NONNEURAL TISSUES.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -1- SIMILARITY: Contains 6 immunoglobulin-like C2-type domains.
CC -1- SIMILARITY: Contains 5 fibronectin type III domains.
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CC -----
CC EMBL; M28231; AAA28728.2; -;
CC EMBL; AF050085; AAC28613.2; -;
CC EMBL; AF050084; AAC28613.2; JOINED.
CC EMBL; AF050085; AAC28614.2; -;
CC EMBL; AF050084; AAC28614.2; JOINED.
CC EMBL; AF003444; AAF46387.1; -;
CC EMBL; AY058284; AAL1513.1; -;
CC EMBL; X76243; CAA53822.1; -;
CC EMBL; X76244; CAA53823.1; -;
CC PDB; 1CFB; 30-NOV-94.
CC FlyBase; FBgn0002968; Nrg.
CC GO; GO:0005886; C:plasma membrane; IEP.
CC GO; GO:0005194; F:cell adhesion molecule activity; IMP.
CC GO; GO:0007560; P:imaginal disc morphogenesis; IMP.
CC GO; GO:0007158; P:neutrophil cell adhesion; IMP.
CC InterPro; IPR003961; FN.III.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003598; Ig_C2.
CC Pfam; PF00041; fn3; 5.
CC Pfam; PF00047; ig; 6.
CC SMART; SM00060; FN3; 5.
CC SMART; SM00408; IGC2; 4.
CC PROSITE; PS00835; IG_LIKE; 6.
CC Cell adhesion; Glycoprotein; Transmembrane; Repeat; 3D-structure;
KW

Immunoglobulin domain; Signal; Developmental protein;		DCC HUMAN		STANDARD;	PRT; 1447 AA.
KW	ALTERNATIVE SPLICING.	ID	DT	AC	P43146;
FT	1	DT	01-NOV-1995	Rel. 32, Created	
FT	24	DT	01-NOV-1995	Rel. 32, Last sequence update	
FT	1139	DE	15-SEP-2003	Rel. 42, Last annotation update	
FT	1155	OS	Tumor suppressor protein DCC precursor (Colorectal cancer suppressor).		
FT	1302	GN	DCC.		
FT	29	OS	Homo sapiens (Human).		
FT	134	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
FT	245	OC	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.		
FT	339	OX	NCBI_TaxID=9606;		
FT	432	OX	[1]		
FT	521	RP	SEQUENCE FROM N.A.		
FT	629	RP	MEDLINE=95011532; PubMed=7926722;		
FT	729	RA	Hedrick L., Cho K.R., Fearon E.R., Wu T.-C., Kinzler K.W.,		
FT	792	RA	Vogelstein B.;		
FT	832	RT	"The DCC gene product in cellular differentiation and colorectal		
FT	932	RT	tumorigenesis.";		
FT	1024	RL	Genes Dev. 8:1174-1183(1994).		
FT	59	RN	[2]		
FT	111	RP	SEQUENCE OF 1-750 FROM N.A.		
FT	625	RP	MEDLINE=90100559; PubMed=2294591;		
FT	182	RA	Fearon E.R., Cho K.R., Nigro J.M., Kern S.E., Simons J.W.,		
FT	182	RA	Ruppert J.M., Hamilton S.R., Preisinger A.C., Thomas G., Kinzler K.W.,		
FT	411	RA	Vogelstein B.;		
FT	448	RA	"Identification of a chromosome 18q gene that is altered in		
FT	652	RT	colorectal cancers.";		
FT	683	RT	Science 247:49-56(1990).		
FT	821	RL	[3]		
FT	821	RP	SEQUENCE OF 107-472 FROM N.A. (SCRAMBLED EXONS).		
FT	1125	RA	MEDLINE=91121517; PubMed=1991322;		
FT	1224	RA	Nigro J.M., Cho K.R., Fearon E.R., Kern S.E., Ruppert J.M.,		
FT	1224	RA	Oliner J.D., Kinzler K.W., Vogelstein B.;		
FT	1224	RT	"Scrambled exons.";		
FT	1224	RL	Cell 64:607-613(1991).		
FT	1224	RN	[4]		
FT	1224	RP	GENE STRUCTURE, AND VARIANTS CARCINOMA HIS-1375.		
FT	1224	RA	MEDLINE=94245241; PubMed=8188295;		
FT	1224	RA	Cho K.R., Oliner J.D., Simons J.W., Hedrick L., Fearon E.R.,		
FT	1224	RA	Preisinger A.C., Hedge P., Silverman G.A., Vogelstein B.;		
FT	1224	RT	"The DCC gene: structural analysis and mutations in colorectal		
FT	1224	RT	carcinomas.";		
FT	1224	RL	Genomics 19:525-531(1994).		
FT	1224	RN	[5]		
FT	1224	RP	VARIANT CARCINOMA THR-168, AND VARIANT GLY-201.		
FT	1224	RA	MEDLINE=94243823; PubMed=8187090;		
FT	1224	RA	Miyake S., Nagai K., Yoshino K., Ota M., Endo M., Yusa Y.;		
FT	1224	RT	"Point mutations and allelic deletion of tumor suppressor gene DCC in		
FT	1224	RT	human esophageal squamous cell carcinomas and their relation to		
FT	1224	RT	metastasis.";		
FT	1224	RL	Cancer Res. 54:3007-3010(1994).		
FT	1224	CC	-!- FUNCTION: IMPLICATED AS A TUMOR SUPPRESSOR GENE.		
FT	1224	CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.		
FT	1224	CC	-!- TISSUE SPECIFICITY: FOUND IN AXONS OF THE CENTRAL AND PERIPHERAL		
FT	1224	CC	NERVOUS SYSTEM AND IN DIFFERENTIATED CELL TYPES OF THE INTESTINE.		
FT	1224	CC	-!- DISEASE: COLORECTAL TUMORS THAT LOST THEIR CAPACITY TO		
FT	1224	CC	DIFFERENTIATE INTO MUCUS PRODUCING CELLS UNIFORMLY LACK DCC		
FT	1224	CC	EXPRESSION. INACTIVATION OF DCC DUE TO ALLELIC DELETION AND/OR		
FT	1224	CC	POINT MUTATIONS MAY CAUSE BOTH LYMPHATIC AND HEMATOGENOUS		
FT	1224	CC	METASTASIS OF OBESOPHAGEAL SQUAMOUS CELL CARCINOMAS.		
FT	1224	CC	-!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. DCC		
FT	1224	CC	SUBFAMILY.		
FT	1224	CC	-!- SIMILARITY: Contains 4 immunoglobulin-like C2-type domains.		
FT	1224	CC	-!- SIMILARITY: Contains 6 fibronectin type III domains.		
FT	1224	CC	-----		
FT	1224	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
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FT	1224	CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/		
FT	1224	CC	or send an email to license@sib-sib.ch).		
FT	1224	CC	-----		

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OM protein - protein search, using sw model

Run on: January 30, 2004, 15:51:24 ; Search time 31.9223 Seconds
(without alignments)
2449.385 Million cell updates/sec

Title: US-10-047-021-86
Perfect score: 1608
Sequence: 1 MGSGDSILGGRGSLPLILL.....SGPLPREARELRQRRNTG 303

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 23:**

- 1: sp_archaea:**
- 2: sp_bacteria:**
- 3: sp_fungi:**
- 4: sp_human:**
- 5: sp_invertebrate:**
- 6: sp_mammal:**
- 7: sp_mhc:**
- 8: sp_oxganelle:**
- 9: sp_phase:**
- 10: sp_plant:**
- 11: sp_rodent:**
- 12: sp_virus:**
- 13: sp_vertebrate:**
- 14: sp_unclassified:**
- 15: sp_rvirus:**
- 16: sp_bacteriap:**
- 17: sp_archaeap:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1444	89.8	1007	Q8WZ75	Q8wz75 homo sapien
2	1436	89.3	792	Q96JV6	Q96jv6 homo sapien
3	1112.5	69.2	1016	Q8C310	Q8c310 mus musculus
4	791	49.2	702	Q8TEG1	Q8tegl1 homo sapien
5	452.5	28.1	1034	Q96MS0	Q96ms0 homo sapien
6	448.5	27.9	1651	Q55005	Q55005 rattus norv
7	446.5	27.8	1651	Q916N7	Q916n7 homo sapien
8	445.5	27.7	1612	Q89026	Q89026 mus musculus
9	444.5	27.6	330	Q90242	Q90242 gallus gall
10	432	26.9	1614	Q8UV7	Q8uvd7 xenopus lae
11	423	26.3	1513	Q90270	Q90270 brachydanio
12	414.5	25.8	1344	Q92214	Q92214 mus musculus
13	407	25.3	333	Q90241	Q90241 gallus gall
14	406	25.2	1419	Q98SW3	Q98sw3 brachydanio
15	405	25.2	1389	Q90269	Q90269 brachydanio
16	405	25.2	1395	Q9W213	Q9w213 drosophila

17	405	25.2	1395	5	O44924	O44924 drosophila
18	404.5	25.2	1380	4	Q9HCK4	Q9hck4 homo sapien
19	400.5	24.9	1675	13	Q98SW4	Q98sw4 brachydanio
20	398.5	24.8	227	11	Q8BJ59	Q8bj59 mus musculus
21	397.5	24.7	1342	5	Q9GPP6	Q9gpp6 drosophila
22	397.5	24.7	1342	5	Q9VP27	Q9vp27 drosophila
23	360	22.4	1269	5	O01632	O01632 caenorhabdi
24	360	22.4	1273	5	O44928	O44928 caenorhabdi
25	358	22.3	1406	5	Q9GPP7	Q9gpp7 drosophila
26	358	22.3	1463	5	Q9VQ08	Q9vq08 drosophila
27	351	21.8	1060	11	Q9QZ13	Q9qz13 rattus norv
28	348.5	21.7	376	13	Q90271	Q90271 brachydanio
29	267.5	16.6	1496	4	Q92626	Q92626 homo sapien
30	261.5	16.3	1151	11	Q9QVN5	Q9qvn5 rattus sp.
31	261.5	16.3	1174	11	Q91260	Q91260 rattus norv
32	261.5	16.3	1217	11	P97685	P97685 rattus norv
33	260.5	16.2	298	4	Q96HT1	Q96ht1 homo sapien
34	260.5	16.2	1028	11	P97528	P97528 rattus norv
35	260.5	16.2	1041	4	O94856	O94856 homo sapien
36	259	16.1	1311	5	O961K8	O961k8 drosophila
37	259	16.1	1527	5	Q9VZ24	Q9vz24 drosophila
38	258.5	16.1	1898	11	Q9EQ17	Q9eq17 mus musculus
39	254.5	15.8	1948	4	Q13332	Q13332 homo sapien
40	254	15.8	498	11	Q8BET6	Q8bet6 mus musculus
41	254	15.8	705	11	Q8CBD3	Q8cbd3 mus musculus
42	253.5	15.8	814	4	Q81VU1	Q81vu1 homo sapien
43	253.5	15.8	1898	11	O64604	O64604 r protein-t
44	253	15.7	1535	5	Q23991	Q23991 drosophila
45	252.5	15.7	1028	11	Q8C6X1	Q8c6x1 mus musculus

ALIGNMENTS

RESULT 1

Q8WZ75	PRELIMINARY;	PRT; 1007 AA.
ID	Q8WZ75	
AC	Q8WZ75;	
DT	01-MAR-2002 (Tremblrel. 20, Created)	
DT	01-MAR-2002 (Tremblrel. 20, Last sequence update)	
DT	01-MAR-2003 (Tremblrel. 23, Last annotation update)	
DE	Magic roundabout.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX	NCBI_taxid=9606;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=20530916; PubMed=11076864;	
RA	Huminiecki L., Bicknell R.;	
RT	"In silico cloning of novel endothelial-specific genes.";	
RL	Genome Res. 10:1796-1806(2000).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RA	Huminiecki L., Bicknell R.;	
RL	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; AF361473; AAL31867.1;	
DR	Genew; HGNC:17985; ROBO4.	
DR	InterPro; IPR003961; FN III.	
DR	InterPro; IPR007110; IG-like.	
DR	InterPro; IPR003598; IG_c2.	
DR	InterPro; IPR003006; IG_MHC.	
DR	Pfam; PF00041; fn3; 2.	
DR	Pfam; PF00047; ig; 2.	
DR	SMART; SM00060; FN3; 2.	
DR	SMART; SM00408; IGC2; 1.	
DR	PROSITE; PS50835; IG_LIKE; 2.	
KW	Immunoglobulin domain	
SQ	SEQUENCE 1007 AA; 107457 MW; E43F246CS9BE1415 CRC64;	

Query Match 89.8%; Score 1444; DB 4; Length 1007;
Best Local Similarity 98.9%; Pred. No. 2.6e-115;
Matches 270; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

RC TISSUE=Spleen;
RA Jikuya H., Takano J., Nomura N., Kikuno R., Nagase T., Ohara O.;
RT "The nucleotide sequence of a long cDNA clone isolated from human
RT spleen."
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK074163; BAB84989.1; -
DR InterPro; IPR003961; FN.III.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin domain
FT NON TER 1
SQ SEQUENCE 702 AA; 75340 MW; D668FEE4BCAFDCC6 CRC64;

Query Match 49.2%; Score 791; DB 4; Length 702;
Best Local Similarity 59.0%; Pred. No. 1.9e-59;
Matches 161; Conservative 0; Mismatches 2; Indels 110; Gaps 1;

Qy 1 MSGGDSLLGGRGSLPLLLIMMGMAQDSPQILVHPQDLQFGPGPARMSCRSGQPP 60
Db 1 MSGGDSLLGGRGSLPLLLIM-
Qy 61 PTIRWLNGQPLSMVPPDPHLLPDGTLTLLQPPARGHAGDQALSTDLGYVTCEASNRL 120
Db 24 -----
Qy 121 GTAVSRGARLSVAVLRDFQIQPRDMVAVGGEQFTLECGPPGWGHPETVSWKDGKPLAL 180
Db 24 -----VLREDFQIQPRDMVAVGGEQFTLECGPPGWGHPETVSWKDGKPLAL 70
Qy 181 QGRHTVSGSLLMARAEKSDXTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAV 240
Db 71 QGRHTVSGSLLMARAEKSDXTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAV 130
Qy 241 RIQLENTVLLNPDPAEGKPRPAVWLXWVSGP 273
Db 131 RIQLENTVLLNPDPAEGKPRPAVWLXWVSGP 163

RESULT 5
Q96MS0 PRELIMINARY; PRT; 1034 AA.
AC Q96MS0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein FLJ31982.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
RA Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamiyama K.,
RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K.,
RA Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahara K., Masuho Y., Nagai K., Isogai T.;
RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK056544; BAB71212.1; -
DR InterPro; IPR003961; FN.III.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR003006; IG_MHC.

DR Pfam; PF00041; fn3; 3.
DR Pfam; PF00047; ig; 5.
DR SMART; SM00060; FN3; 3.
DR SMART; SM00408; IGC2; 5.
DR PROSITE; PS0835; IG LIKE; 5.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 1034 AA; 110723 MW; 09E13C7B424F7E30 CRC64;

Query Match 28.1%; Score 452.5; DB 4; Length 1034;
Best Local Similarity 40.7%; Pred. No. 3.5e-30;
Matches 118; Conservative 27; Mismatches 104; Indels 41; Gaps 10;

Qy 1 MSGGDSLLGGRGSLPLLLIMMGMA-----QDSPQILVHPQDLQFGQPPAR 50
Db 23 ISNSSELLGFNSLAALNHTLLPPGDPSLNGSRVGPEDAMPRIQVEPPDLLVSRGEPAT 82
Qy 51 MSCRASQPPPTIRWLNGQPLSMVPPDP--HH-LLPDGTLLLLQPPARGHAGDQALST 107
Db 83 LPCRAEGRPRPNIEWYKNGARVATVREDPRAHRLLLPSGALFF---PRIVH---GRRARP 136
Qy 108 DLGYVTCEASNRLCTAVSRGARLSVAVLRDFQIQPRDMVAVGGEQFTLECGPPGWGHP 167
Db 137 DEGYTCVARNYLGAASRNASLEAVLRDDFROSGNVVAVGEPVAVLEVCVPRGHP 196
Qy 168 TVSWKDGKPLALQGRHTVSGSLLMARAEKSDXTYMCVATNSAGHRESRAARVSIQ 227
Db 197 SVSWKDGARLKEBEGRTITRGKLMWSHTLKS DAGMYVCVSNMAGERESAAAEVVMLE 256
Qy 228 -PDYTEPVELLAVRIQLENTVLLNPDPAE-----GPKRPAVWLXWK 269
Db 257 RPSFLRPV-----NOVVLADAPVTFLCEVKGDPPTPR-----LWR 292

RESULT 6
O55005 PRELIMINARY; PRT; 1651 AA.
ID O55005
AC O55005;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Transmembrane receptor Robol.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spinal cord;
RX MEDLINE=98117249; PubMed=9458045;
RA Kidd T., Brose K., Mitchell K.J., Fetter R.D., Tessier-Lavigne M.,
RA Goodman C.S., Tear G.
RT "Roundabout controls axon crossing of the CNS midline and defines a
RT novel subfamily of evolutionarily conserved guidance receptors."
RL Cell 92:205-215 (1998).
DR EMBL; AF041082; AAC39960.1; -
DR HSSP; P56276; 1TLK.
DR InterPro; IPR003961; FN.III.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00041; fn3; 3.
DR Pfam; PF00047; ig; 5.
DR SMART; SM00060; FN3; 3.
DR SMART; SM00408; IGC2; 5.
DR PROSITE; PS0835; IG LIKE; 5.
KW Immunoglobulin domain; Receptor.
SQ SEQUENCE 1651 AA; 180747 MW; FA2452DD46E186B7 CRC64;

Query Match 27.9%; Score 448.5; DB 11; Length 1651;
Best Local Similarity 42.2%; Pred. No. 1.4e-29;
Matches 92; Conservative 31; Mismatches 86; Indels 9; Gaps 2;

Qy 28 QDSPQILVHPQDLQFGPGPARMSCRSGQPPPTIRWLNGQPLSMVPPDPH-----LLP 84

Db 64 EDFPRIVEHPSDLIVSGEPATLNCRAEGRPTTIEWYKGERVETDKDDPRSHRMLLP 123
Qy 85 DGTLLLOPPARGHAHQALSTDLGVYTCASNRLGTAVSRGRLSVAVLREDFOIQPR 144
Db 124 SGSLFFLR-----IVHGKSRPDEGVYICVARNYLGEAVSHNASLEVAILLRDFRQNP 177
Qy 145 DMVAVGQFTLECGPPWGHPEPTVSWWKGKPLALQPGHRTVSGGSLMARAEKSDXT 204
Db 178 DMVAVGEPVMECPQPRGHEPTISWKGSPDLDDKDERITIRGGKLMITYTRKSDAGK 237
Qy 205 YMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRI 242
Db 238 YVCVTNNVGERSEVAELTLERPSFVKRPSNLAIVT 275

RESULT 7

Q9Y6N7 PRELIMINARY; PRT; 1651 AA.
AC Q9Y6N7
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Roundabout 1.
GN ROBO1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98117249; PubMed=9458045;
RA Kidd T., Brose K., Mitchell K.J., Fetter R.D., Tessier-Lavigne M.,
RA Goodman C.S., Tear G.;
RT "Roundabout controls axon crossing of the CNS midline and defines a
RT novel subfamily of evolutionarily conserved guidance receptors.";
RL Cell 92:205-215(1998).
DR EMBL; AF040990; AAC39575.1; -.
DR HSSP; P56276; ITLK.
DR Genew; HGNC:10249; ROBO1.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00041; fn3; 3.
DR Pfam; PF00047; ig; 5.
DR SMART; SM00060; FN3; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 5.
SQ SEQUENCE 1651 AA; 180929 MW; 9D98CD7CAB73074D CRC64;

Query Match 27.8%; Score 446.5; DB 4; Length 1651;
Best Local Similarity 41.7%; Pred. No. 2e-29;
Matches 91; Conservative 31; Mismatches 87; Indels 9; Gaps 2;
Qy 28 QDSPPOILVHPDOLFOGPGPARMSCRASGPPPTIRWLLNGQPLSMVPPDPHH---LLP 84
Db 64 EDFPRIVEHPSDLIVSGEPATLNCRAEGRPTTIEWYKGERVETDKDDPRSHRMLLP 123
Qy 85 DGTLLLOPPARGHAHQALSTDLGVYTCASNRLGTAVSRGRLSVAVLREDFOIQPR 144
Db 124 SGSLFFLR-----IVHGKSRPDEGVYICVARNYLGEAVSHNASLEVAILLRDFRQNP 177
Qy 145 DMVAVGQFTLECGPPWGHPEPTVSWWKGKPLALQPGHRTVSGGSLMARAEKSDXT 204
Db 178 DMVAVGEPVMECPQPRGHEPTISWKGSPDLDDKDERITIRGGKLMITYTRKSDAGK 237
Qy 205 YMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRI 242
Db 238 YVCVTNNVGERSEVAELTLERPSFVKRPSNLAIVT 275

RESULT 8

O89026 PRELIMINARY; PRT; 1612 AA.
AC O89026
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Dutt1 protein.
GN ROBO1 OR DUTT1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Wu M.C., Lowe N., Fordham R., Rabbitts P.;
RT "The mouse homologue of human DUTT1/H-robol gene: protein sequence and
RT chromosomal location.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y17793; CAA76850.1; -.
DR HSSP; P56276; ITLK.
DR MGD; MGI:1274781; Robol.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00041; fn3; 3.
DR Pfam; PF00047; ig; 5.
DR SMART; SM00060; FN3; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 5.
SQ SEQUENCE 1612 AA; 176406 MW; 5F2988C544796B4B CRC64;
Query Match 27.7%; Score 445.5; DB 11; Length 1612;
Best Local Similarity 41.7%; Pred. No. 2.4e-29;
Matches 91; Conservative 31; Mismatches 87; Indels 9; Gaps 2;
Qy 28 QDSPPOILVHPDOLFOGPGPARMSCRASGPPPTIRWLLNGQPLSMVPPDPHH---LLP 84
Db 25 EDFPRIVEHPSDLIVSGEPATLNCRAEGRPTTIEWYKGERVETDKDDPRSHRMLLP 84
Qy 85 DGTLLLOPPARGHAHQALSTDLGVYTCASNRLGTAVSRGRLSVAVLREDFOIQPR 144
Db 85 SGSLFFLR-----IVHGKSRPDEGVYICVARNYLGEAVSHNASLEVAILLRDFRQNP 138
Qy 145 DMVAVGQFTLECGPPWGHPEPTVSWWKGKPLALQPGHRTVSGGSLMARAEKSDXT 204
Db 139 DMVAVGEPVMECPQPRGHEPTISWKGSPDLDDKDERITIRGGKLMITYTRKSDAGK 198
Qy 205 YMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRI 242
Db 199 YVCVTNNVGERSEVAELTLERPSFVKRPSNLAIVT 236
RESULT 9
Q90242 PRELIMINARY; PRT; 330 AA.
AC Q90242
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Roundabout1 protein (Fragment).
GN ROBO1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21366016; PubMed=11472852;
RA Vargesson N., Luria V., Messina I., Erskine L., Laufer E.;
RT "Expression patterns of slit and Robo family members during vertebrate

```
limb development.";
RL Mech. Dev. 106:175-180(2001).
EMBL; AF364047; AAK94293.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00408; IGC2; 3.
DR PROSITE; PS50835; IG LIKE; 3.
KW Immunoglobulin domain.
FT NON_TER 1
FT TER 330
SQ SEQUENCE 330 AA; 36725 MW; 0613488F78CEBE61 CRC64;

Query Match 27.6%; Score 444.5; DB 13; Length 330;
Best Local Similarity 40.9%; Pred. No. 4.1e-30;
Matches 94; Conservative 32; Mismatches 93; Indels 11; Gaps 3;

QY 18 LLLLMGG--NAQDSPQILVHPQDLFGPGPARMSCRAGQPPTIRWLLNGQPLSMV 75
DB 7 LLLASGSLRQEDPPRIVEHPSDLIIVSGEPATLNCKAEGRPPTIEWYKGGERVETD 66
QY 76 PDPHH---LLPDGTLILLOPPARGHAGDQALSTDLGVYTCASNRLGTAVSRGARSLSV 132
DB 67 KDDPRSHRMLLPSSGLFFLR-----IVHGRKSRDEGVYVCVARNYLGEAVSHNASLEV 120
QY 133 AVLREDFQIQRDMVAVVGEQFTLECGPPGWGHPPTVSWMKDGKPLALQPGRHHTVSGSL 192
DB 121 AILRDDFRQNSDVMVAVGEPAVMCEQPPRGHPPTISWKKGDTPIDDDKDERITIRGGKL 180
QY 193 LMARAKSDEXTYMCVATNSAGHRESRAARVSIQEPDQYTEPVELLAVRI 242
DB 181 MITTRKNDAGKYCVGNTMVGERSEVAELTVLERPSFLRRPSNNAVTV 230

RESULT 10
Q8UVD7 PRELIMINARY; PRT; 1614 AA.
AC Q8UVD7;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DE Roundabout-1.
GN ROBO1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Connor R.M., Key B.;
RT "Dual role for Roundabout-1 in neural differentiation and axon
pathfinding in the Xenopus forebrain.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF461119; AAL66361.1; -.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00041; fn3; 3.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00060; FN3; 3.
DR SMART; SM00408; IGC2; 5.
KW Immunoglobulin domain.
SQ SEQUENCE 1614 AA; 176733 MW; 01D2C3D6593F3935 CRC64;

Query Match 26.9%; Score 432; DB 13; Length 1614;
Best Local Similarity 40.6%; Pred. No. 3.5e-28;
Matches 89; Conservative 32; Mismatches 88; Indels 10; Gaps 3;

QY 28 QDSPQILVHPQDLFGPGPARMSCRAGQPPTIRWLLNGQPLSMVPPDPHH---LLP 84

limb development.";
RL Mech. Dev. 106:175-180(2001).
EMBL; AF364047; AAK94293.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00408; IGC2; 3.
DR PROSITE; PS50835; IG LIKE; 3.
KW Immunoglobulin domain.
FT NON_TER 1
FT TER 330
SQ SEQUENCE 330 AA; 36725 MW; 0613488F78CEBE61 CRC64;

Query Match 27.6%; Score 444.5; DB 13; Length 330;
Best Local Similarity 40.9%; Pred. No. 4.1e-30;
Matches 94; Conservative 32; Mismatches 93; Indels 11; Gaps 3;

QY 18 LLLLMGG--NAQDSPQILVHPQDLFGPGPARMSCRAGQPPTIRWLLNGQPLSMV 75
DB 7 LLLASGSLRQEDPPRIVEHPSDLIIVSGEPATLNCKAEGRPPTIEWYKGGERVETD 66
QY 76 PDPHH---LLPDGTLILLOPPARGHAGDQALSTDLGVYTCASNRLGTAVSRGARSLSV 132
DB 67 KDDPRSHRMLLPSSGLFFLR-----IVHGRKSRDEGVYVCVARNYLGEAVSHNASLEV 120
QY 133 AVLREDFQIQRDMVAVVGEQFTLECGPPGWGHPPTVSWMKDGKPLALQPGRHHTVSGSL 192
DB 121 AILRDDFRQNSDVMVAVGEPAVMCEQPPRGHPPTISWKKGDTPIDDDKDERITIRGGKL 180
QY 193 LMARAKSDEXTYMCVATNSAGHRESRAARVSIQEPDQYTEPVELLAVRI 242
DB 181 MITTRKNDAGKYCVGNTMVGERSEVAELTVLERPSFLRRPSNNAVTV 230

RESULT 10
Q8UVD7 PRELIMINARY; PRT; 1614 AA.
AC Q8UVD7;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DE Roundabout-1.
GN ROBO1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Connor R.M., Key B.;
RT "Dual role for Roundabout-1 in neural differentiation and axon
pathfinding in the Xenopus forebrain.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF461119; AAL66361.1; -.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00041; fn3; 3.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00060; FN3; 3.
DR SMART; SM00408; IGC2; 5.
KW Immunoglobulin domain.
SQ SEQUENCE 1614 AA; 176733 MW; 01D2C3D6593F3935 CRC64;

Query Match 26.9%; Score 432; DB 13; Length 1614;
Best Local Similarity 40.6%; Pred. No. 3.5e-28;
Matches 89; Conservative 32; Mismatches 88; Indels 10; Gaps 3;

QY 28 QDSPQILVHPQDLFGPGPARMSCRAGQPPTIRWLLNGQPLSMVPPDPHH---LLP 84

limb development.";
RL Mech. Dev. 106:175-180(2001).
EMBL; AF364047; AAK94293.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00408; IGC2; 3.
DR PROSITE; PS50835; IG LIKE; 3.
KW Immunoglobulin domain.
FT NON_TER 1
FT TER 330
SQ SEQUENCE 330 AA; 36725 MW; 0613488F78CEBE61 CRC64;

Query Match 27.6%; Score 444.5; DB 13; Length 330;
Best Local Similarity 40.9%; Pred. No. 4.1e-30;
Matches 94; Conservative 32; Mismatches 93; Indels 11; Gaps 3;

QY 18 LLLLMGG--NAQDSPQILVHPQDLFGPGPARMSCRAGQPPTIRWLLNGQPLSMV 75
DB 7 LLLASGSLRQEDPPRIVEHPSDLIIVSGEPATLNCKAEGRPPTIEWYKGGERVETD 66
QY 76 PDPHH---LLPDGTLILLOPPARGHAGDQALSTDLGVYTCASNRLGTAVSRGARSLSV 132
DB 67 KDDPRSHRMLLPSSGLFFLR-----IVHGRKSRDEGVYVCVARNYLGEAVSHNASLEV 120
QY 133 AVLREDFQIQRDMVAVVGEQFTLECGPPGWGHPPTVSWMKDGKPLALQPGRHHTVSGSL 192
DB 121 AILRDDFRQNSDVMVAVGEPAVMCEQPPRGHPPTISWKKGDTPIDDDKDERITIRGGKL 180
QY 193 LMARAKSDEXTYMCVATNSAGHRESRAARVSIQEPDQYTEPVELLAVRI 242
DB 181 MITTRKNDAGKYCVGNTMVGERSEVAELTVLERPSFLRRPSNNAVTV 230

RESULT 10
Q8UVD7 PRELIMINARY; PRT; 1614 AA.
AC Q8UVD7;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DE Roundabout-1.
GN ROBO1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee J.S., Ray R., Chien C.B.;
RT "Cloning and expression of three zebrafish roundabout homologs suggest
roles in axon guidance and cell migration.";
RL Dev. Dyn. 221:216-230(2001).
DR EMBL; AF337035; AAK58427.1; -.
DR ZFIN; ZDB-GENE-001019-1; robo2.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00041; fn3; 3.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00060; FN3; 3.
DR SMART; SM00408; IGC2; 5.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50835; IG LIKE; 5.
KW Immunoglobulin domain.
SQ SEQUENCE 1513 AA; 165181 MW; D1743BACCC089F0 CRC64;

Query Match 26.3%; Score 423; DB 13; Length 1513;
Best Local Similarity 35.1%; Pred. No. 1.9e-27;
Matches 97; Conservative 40; Mismatches 97; Indels 42; Gaps 7;

QY 16 PLLLLLLLGMG-----AQDSPQILVHPQDLFGPGPARMSCRAGQPPTIR 64
DB 3 PLTHLLCGLVYFNQVDSRLRQEDSPRIVEHPSDLIIVSGEPATLNCKAEGRPPTVE 62
QY 65 WLLNGQPLSMVPPDPHH---LLPDGTLILLOPPARGHAGDQALSTDLGVYTCASNRLG 121
DB 63 WYKQGERVETDKDPRSHRMLLPSSGLFFLR-----IVHGRKSPDGEAVCVARNYL 116
QY 122 TAVSRGARSLSVAVLREDFQIQRDMVAVVGEQFTLECGPPGWGHPPTVSWMKDGKPLAQ 181
DB 117 EAVSENASLEVALLRDDFRQNPTDVMVAAGPAILECVPRGHPPTIYWKDKVRIDEK 176
QY 182 PGRHTVSGSLLMARAKSDEXTYMCVATNSAGHRESRAARVSI-QEPDQYTEPV----- 235
DB 177 DDRIKIRGGKLMINSTRKSDAGMVICVGTNMVGERDSETAQVTFPERPTFLRRPTNQVVL 236
```

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Qy 236 --ELLAVRIQLENTLLNPDPAEGPKPRPAVLXWK 269
      | | | | | | | | | | | | | | | | | |
Db 237 EEAVDFRCVQOG-----DPQPS-----IRWK 258

RESULT 12
ID Q92214 PRELIMINARY; PRT; 1344 AA.
AC Q92214;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DE 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Rig-1 protein.
GN RBIG1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN PROSITE 10090;
SQ SEQUENCE FROM N.A.
RA Yuan S.-S.F., Cox L.A., Dasika G.K., Lee E.Y.-H.P.;
RA Submitted (APR-1998) to the ENBL/GenBank/DBJ databases.
DR EMBL; AF060570; AAD11628.1; -.
DR HSSP; P56276; ITLK.
DR MGD; MGI:1343102; Rbig1.
DR InterPro; IPR003961; FN.III.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig.C2.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR00041; fn3; 3.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00408; IGC2; 3.
DR PROSITE; PS00835; IG_LIKE; 5.
KW Immunoglobulin domain.
SQ SEQUENCE 1344 AA; 143439 MW; 8B0060341C49CFEA CRC64;

Query Match 25.8%; Score 414.5; DB 11; Length 1344;
Best Local Similarity 39.9%; Pred. No. 8.9e-27;
Matches 101; Conservative 27; Mismatches 94; Indels 31; Gaps 8;

Qy 28 QDSPQILVHPDQDFOGPGPARMSCRASGQPPPTIRWLNQPLSMVPPDP--HH-LLP 84
      | | | | | | | | | | | | | | | | | |
Db 38 EDAMPRIVEQPDVLSRGEATLPCRAEGRPENIEWYKNGARVATAREDPRAHRLLP 97

Qy 85 DGTLLLOPPARGHAHQALSTDLGVYTCASNRLGTAVSRGARLSVAVLRDFQIQPR 144
      | | | | | | | | | | | | | | | | | |
Db 98 SGALFF---PRVH---GRRSRPDEGVYTCVARNYLGAASRNASLEVALRLDDFROSPG 151

Qy 145 DMVAVVGQFTLECGPPMGHPPTVSWWKGKPLALOPGRHTVSGSLLMARAEKSDXT 204
      | | | | | | | | | | | | | | | | | |
Db 152 NVVAVGEPVAVMECVPPKGPHEPLVWTKGKIKLKEBEGRTIRGGKLMKSHTFKSDAGM 211

Qy 205 YMCVATNSAGHRESRAAR-VSIQEPQDYTEPVVELLAVRIQLENTLLNPDPAE----- 256
      | | | | | | | | | | | | | | | | | |
Db 212 YMCVASNMAGRESGAELVLERPSFLRRPI-----NQWLADAPVNFCEVQOG 261

Qy 257 GPKPRPAVLXWK 269
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Db 262 DPQPN-----LHWR 270

RESULT 13
ID Q90241 PRELIMINARY; PRT; 333 AA.
AC Q90241;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DE 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Roundabout2 protein (Fragment).
GN ROBO2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

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OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21366016; PubMed=11472852;
RA Vargesson N., Luria V., Messina I., Erskine L., Laufer E.;
RT "Expression patterns of Slit and Robo family members during vertebrate
RT limb development.";
RL Mech. Dev. 106:175-180(2001).
DR EMBL; AF364048; AAK94294.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig.C2.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00408; IGC2; 3.
DR PROSITE; PS00835; IG_LIKE; 3.
KW Immunoglobulin domain.
RN NON TER 333 333
SQ SEQUENCE 333 AA; 37689 MW; 47607C05AD84C7B3 CRC64;

Query Match 25.3%; Score 407; DB 13; Length 333;
Best Local Similarity 34.9%; Pred. No. 6.9e-27;
Matches 96; Conservative 38; Mismatches 99; Indels 42; Gaps 7;

Qy 17 LLLLLLGGMA-----ODSPQILVHPDQDFOGPGPARMSCRASGQPPPTIRW 65
      | | | | | | | | | | | | | | | | | |
Db 3 LPTLLLLFGPFPQVYGSRLRQEDFPRIVEHSDIVSKEPTTLNCKAEGRTPTIEW 62

Qy 66 LLMGQPLSMVPPDPFH---LLPDGTLTLLQPPARGHAHQALSTDLGVYTCASNRLGT 122
      | | | | | | | | | | | | | | | | | |
Db 63 YKDERVETKDDPRSHRMLPSGLFFLR-----IVHGRSRKPDGSGYCVARNYLGE 116

Qy 123 AVSRGARLSVAVLRDFQIQPRDMVAVVGQFTLECGPPMGHPPTVSWWKGKPLALQP 182
      | | | | | | | | | | | | | | | | | |
Db 117 AVSRNASLEVALRLDDFQNPQPTDVVVAAGEPAILECQPPRGHPPTIYWKDKVRIIDRE 176

Qy 183 GRHTVSGSLLMARAEKSDXTYMCVATNSAGHRESRAARVSI-OEPQDYTEPV----- 235
      | | | | | | | | | | | | | | | | | |
Db 177 ERISIRGGKLMINSTRKSDAGMTCTGTNNVGERDSDPAELTVFERFTFLRRPINQVLE 236

Qy 236 -ELLAVRIQLENTLLNPDPAEGPKPRPAVLXWK 269
      | | | | | | | | | | | | | | | | | |
Db 237 EEAVDFRCVQOG-----DPQTV--RWK 257

RESULT 14
ID Q98SW3 PRELIMINARY; PRT; 1419 AA.
AC Q98SW3;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Transmembrane receptor Roundabout3.
GN ROBO3.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=AB+.
RX MEDLINE=21152912; PubMed=11231085;
RA Challa A.K., Beattie C.E., Seeger M.A.;
RT "Identification and characterization of roundabout orthologs in
RT zebrafish.";
RL Mech. Dev. 101:249-253(2001).
DR EMBL; AF304131; AAK28043.1; -.
DR HSSP; P08921; IA64.
DR ZFIN; ZDB-GENE-000209-4; robo3.
DR InterPro; IPR003962; FN.III subd.
DR InterPro; IPR003961; FN.III.
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 31, 2004, 12:28:30 ; Search time 1838.41 Seconds
(without alignments)
4005.776 Million cell updates/sec

Title: US-10-047-021-86
Perfect score: 1608
Sequence: 1 MGSGDLSLGGSGSLPLLL.....SGPRLPREARELRQRRNTG 303

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US10047021/runat_30012004_145453_24574/app_query.fasta_1.910
-DB=EST -QFMT=fastap -SUFFIX=est -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -ENDS=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10047021 -CGEN 1 1 4399 -runat_30012004_145453_24574 -NCPU=3
-NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: em_estba.*
2: em_esthum.*
3: em_estin.*
4: em_estmu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_hcc.*
9: gb_est1.*
10: gb_est2.*
11: gb_hcc.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: em_gss_hum.*
18: em_gss_inv.*
19: em_gss_pln.*
20: em_gss_vrt.*
21: em_gss_fun.*
22: em_gss_mam.*
23: em_gss_mus.*
24: em_gss_pro.*
25: em_gss_rod.*
26: em_gss_phg.*
27: em_gss_vrl.*
28: gb_gss1.*

29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1565	97.3	3758	11	BC039602	BC039602 Homo sapi
2	1520	94.5	1201	9	AL553360	AL553360 AL553360
3	1345	83.6	1019	12	BM921911	BM921911 AGENCOURT
4	1265	78.7	922	13	BX418142	BX418142 BX418142
5	1234	76.7	826	14	CB994099	CB994099 AGENCOURT
6	1214.5	75.5	860	14	CB996189	CB996189 AGENCOURT
7	1146.5	71.3	941	13	BQ890126	BQ890126 AGENCOURT
8	1145.5	71.2	3689	11	AK004723	AK004723 Mus muscu
9	1145.5	71.2	3865	11	AK087355	AK087355 Mus muscu
10	1135.5	70.6	803	14	CB997292	CB997292 AGENCOURT
11	1112	69.2	729	12	BI762862	BI762862 603048384
12	1030	64.1	1230	12	BM906521	BM906521 AGENCOURT
13	1025.5	63.8	771	14	CB959649	CB959649 AGENCOURT
14	1017	63.2	798	14	CB961529	CB961529 AGENCOURT
15	980	60.9	688	14	CB961818	CB961818 AGENCOURT
16	967	60.1	797	14	CB961002	CB961002 AGENCOURT
17	936	58.2	558	9	AL602474	AL602474 DKFZp6860
18	920	57.2	1087	12	BM914311	BM914311 AGENCOURT
19	891.5	55.4	610	10	BG745318	BG745318 602723637
20	865	53.8	502	13	BX474842	BX474842 DKFZp686M
21	863	53.7	570	10	BE233526	BE233526 139756 MA
22	825.5	51.3	662	14	BY727209	BY727209 BY727209
23	789	49.1	532	13	BX475138	BX475138 DKFZp6860
24	787.5	49.0	620	10	BB664621	BB664621 BB664621
25	784	48.8	526	14	CA394658	CA394658 c954c07.Y
26	775	48.2	501	13	BX474746	BX474746 DKFZp686B
27	730.5	45.4	631	10	BE376779	BE376779 601227331
28	700	43.5	438	13	BX475177	BX475177 DKFZp686F
29	660.5	41.1	529	4	BX520802	BX520802 RZPD Mus
30	660	41.0	424	13	BX475172	BX475172 DKFZp686E
31	660	41.0	426	2	HSM085795	Bx492967 Homo sapi
32	659.5	41.0	551	9	AI116483	AI116483 ud74c06.Y
33	657.5	40.9	557	14	BY704924	BY704924 BY704924
34	585.5	36.4	1257	14	CB993951	CB993951 AGENCOURT
35	574	35.7	344	9	AA577940	AA577940 nl20d01.a
36	572.5	35.6	455	10	BB839755	BB839755 BB839755
37	566	35.2	450	9	AL039859	AL039859 DKFZp434E
38	541	33.6	555	12	BI836220	BI836220 603085778
39	529	32.9	532	12	BI159602	BI159602 602920006
40	507.5	31.6	444	13	BY270114	BY270114 BY270114
41	486.5	30.3	441	13	BY285423	BY285423 BY285423
42	476.5	29.6	379	10	BB871780	BB871780 BB871780
43	451	28.0	428	10	BB849408	BB849408 BB849408
44	439.5	27.3	414	13	BY268765	BY268765 BY268765
45	424.5	26.4	391	9	AA388861	AA388861 mp13e06.r

ALIGNMENTS

RESULT 1
LOCUS BC039602 3758 bp mRNA linear HTC 06-NOV-2002
DEFINITION Homo sapiens, Similar to roundabout homolog 4, magic roundabout
(Drosophila), clone IMAGE:5590503, mRNA.
ACCESSION BC039602
VERSION BC039602.1 GI:24660430
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3758)

AUTHORS
TITLE
JOURNAL

Strausberg, R.
Direct Submission
Submitted (01-NOV-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK
COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
Contact: amadaneysystemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAC Plate: 84 Row: 1 Column: 5
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis, GenomeScan gene prediction
This clone has the following problem: frame shifted.

FEATURES
source

Location/Qualifiers
1..3758
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5590503"
/tissue_type="Ovary, pooled from 3 adults"
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/lab_host="DH10B"
/note="vector: pCMV-SPORT6"
772 a 1232 c 1046 g 708 t

Alignment Scores:

Pred. No.: 5.78e-107 Length: 3758
Score: 1565.00 Matches: 295
Percent Similarity: 98.67% Conservative: 1
Best Local Similarity: 98.33% Mismatches: 3
Query Match: 97.33% Indels: 1
DB: 11 Gaps: 0

US-10-047-021-86 (1-303) x BC039602 (1-3758)

Qy 1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeu 20
Db 29 ATGGGCTCTGGAGAGACAGGCTCTGGGGGCGAGGGTTCCTGCTCTCTCTG 88
Qy 21 LeuLeuMetGlyMetAlaGlnAspSerProGlnLeuLeuValHisProGlnAsp 40
Db 89 CTCATCATGGAGGAGCATGGCTCAGGACTCCCGCCGCCAGATCCTAGTCCACCCCGAGAC 148
Qy 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60
Db 149 CAGTGTGTCCAGGGCCCTGGGCGCTGCCAGGATGAGTGCACCAAGCTCAGGCGACCCACCT 208
Qy 61 ProThrLeuArgTTPLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80
Db 209 CCCACCATCCCTGGTGTCTGATGGGCGAGCCCTGAGCATGGTGGCCCGAGACCCACAC 268
Qy 81 HisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100
Db 269 CACCTCTCTGCTGATGGAGCCCTTCTGCTGCTACAGCCCTGCGCGGGGACATGCCAC 328
Qy 101 AspGlyGlnAlaLeuSerThrAspLeuGlyValThrCysGluAlaSerAsnArgLeu 120
Db 329 GATGCCAGGGCCCTGTCCACAGACTGGGTGTCTACACATGTGAGGGCCAGCAACCGCTT 388
Qy 121 GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln 140

Db 389 GGACGCGCAGTCAGCAGAGGGCTCGGCTGCTGTGGCTGTCTCCCGGAGATTCCAG 448
Qy 141 IleGlnProArgAspMetValAlaValValGlyGlnGlnPheThrLeuGluCysGlyPro 160
Db 449 ATCCAGCCTCGGACATGCTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG 508
Qy 161 ProTTPGlyHisProGluProThrValSerTTPTrpLysAspGlyLysProLeuAlaLeu 180
Db 509 CCCTGGGGGCCACCCAGAGCCACAGTCTCATGTGTGGAAAGATGGGAAACCCCTGGCCCTC 568
Qy 181 GlnProGlyArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSer 200
Db 569 CAGCCCGGAAGGCACACAGTGTCCGGGGGGTCCCTGTGTGTGTGTGTGTGTGTGTGT 628
Qy 201 AspGlu***ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAla 220
Db 629 GACGAAGGGACCTACATGTGTGTGGCCACCAACAGCGCAGGACATAGGAGAGCGCGCA 688
Qy 221 AlaArgValSerIleGlnGluProGlnAspTyrThrGluProValGluLeuAlaVal 240
Db 689 GCCCGGGTTCCTATCCAGGAGCCCGCAGGACTACACGAGGCTGTGGAGCTTCTGGCTGTG 748
Qy 241 ArgIleGlnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysPro 260
Db 749 CGAATTCAGCTGGAAATGTGACACTGCTGAACCCGGATCTCGCAGAGGGCCCCAAGCCT 808
Qy 261 ArgProAlaValTTPLeu***TTPLysValSerGlyPro***ArgLeuProAsnLeuTh 280
Db 809 AGACCGCGGTGTGGCTCAGCTGGAAGGTCACTGGCGGCTGTGTGGCTGTGGCTATCTTAC 868
Qy 280 rArgProCysSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArg 299
Db 869 ACGGCTTGTTCAGGACCCAGACTGCCCCGGAGGCGAGGAGCTCCGTGGGCGAGAG 926

RESULT 2

AL553360

LOCUS

DEFINITION

AL553360 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA

AL553360

VERSION

AL553360.2

KEYWORDS

EST.

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1201)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished

On Feb 15, 2001 this sequence version replaced gi:12893123.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 6206.r For

more information about this cluster, see

<http://www.genoscope.cns.fr/>

cgi-bin/cluster.cgi?seq=CS0D1075CH07QPI&cluster=6206.r. Contact :

Feng Liang Email : fliang@lifetech.com URL :

<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0D1075CH07QPI.

FEATURES
source

1..1201
Location/Qualifiers
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/clone="CS0D1075YPI3"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dtr)

primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 236 a 348 c 369 g 212 t 36 others

ORIGIN

Alignment Scores:

Pred. No.: 3.5e-104 Length: 1201

Score: 1520.00 Matches: 290

Percent Similarity: 96.68% Conservativity: 1

Best Local Similarity: 96.35% Mismatches: 8

Query Match: 94.53% Indels: 2

DB: 9 Gaps: 0

US-10-047-021-86 (1-303) x AL553360 (1-1201)

QY 1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeu 20

DB 81 ATGGGCTCTGGAGGACAGCTCTCTGGGGGAGGGGTTCCCTGCTGCTGCTG 140

QY 21 LeuIleMetGlyGlyMetAlaGlnAspSerProGlnIleLeuValHisProGlnAsp 40

DB 141 CTCATCATGGAGGATGCTCAGACTCCCGCCCGATCTAGTCCACCCCGAGAC 200

QY 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60

DB 201 CAGCTGTTCCAGGGCCCTGGCCCTCCAGGATGAGTGCAGAGCTCCAGGCGGCACT 260

QY 61 ProThrIleArgTrpLeuLeuGlnGlyGlnProLeuSerMetValProProAspProHis 80

DB 261 CCCACATCCGCTGGTGTGTAATGGGAGCCCTCCGAGCATGGTGGCCCGACCCACAC 320

QY 81 HisLeuLeuProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100

DB 321 CACCTCTGCTGATGGAGCTTCTGCTGCTACAGCCCTCCCGGGGACATGCCAC 380

QY 101 AspGlyGlnAlaLeuSerThrAspLeuGlyValThrCysGluAlaSerAsnArgLeu 120

DB 381 GATGCCAGGCTGTCACAGCTGGGTGTCTACATGTGAGGCGAGCAACCGGCTT 440

QY 121 GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln 140

DB 441 GGCAGCGCATGTAGCAGAGCGCTCGGCTGTCTGGCTGTCTCCGGAGGATTTCCAG 500

QY 141 IleGlnProArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyPro 160

DB 501 ATCCAGCTCGGACATGCTGCTGTGGGTGAGCAGTTTACTCTGGAAATGGGCGG 560

QY 161 ProTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeu 180

DB 561 CCTGGGGCCACCCAGAGCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTGGCCCTC 620

QY 181 Gln-ProGlyArgHisThrValSerGlySerLeuLeuMetAlaArgAlaGluLysE 200

DB 621 CACGCCCGAGAGGCACATGCTCGGGGGGTCCTGCTGTGATGGCAAGCAGAGAGAG 680

QY 200 rAspGlu***ThrTrpMetCysValAlaAlaThrAsnSerAlaGlyHisArgGluSerArgAl 220

DB 681 TGACGAGGGACCTACATGTGTGTGGCCACCAACAGCGGAGGACATAGGAGGCGGCG 740

QY 220 alaArgValSerIleGlnGluProGlnAspTrpThrGluProValGluLeuLeuAlaVa 240

DB 741 ACCCGGGGTTTCCATCCAGGAGCCCGAGGACTACACGAGCTGTGGAGCTTCTGGCTGT 800

QY 240 InArgIleGlnLeuGluAenValThrLeuLeuAsnProAspProAlaGluGlyProLysPr 260

DB 801 GCGAATTCAGCTGGAATAATGTGACACTGCTGAACCCGGATCTCCAGAGGGGCGGCAAGCC 860

QY 260 oArgProAlaValTrpLeu***TrpLysValSerGlyPro***ArgLeuProAsnLeuTr 280

DB 861 TAGACCGGGGTGTGGCTCAGCTGAGAGGTGAGTGGGCTGTGGCGCTCGGCAATCTTA 920

QY 280 hrArgProCysSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArg 299

DB 921 CACGCGCTTGTTCAGGACCCAGACTGCCCCGAGGAGCCAGGAGCTCTGTGGCGCAGAG 979

RESULT 3

BM921911

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT

EMAIL

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CDNA

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Db 196 GCGCGGACATGCCAGATGCCAGGCCCTGTCCACAGACCTGGGTGTCTACATGT 255
Qy 115 GluAlaSerAenArgLeuGlyThrAlaValSerArgGlyAlaArgLeuSerValAlaVal 134
Db 256 GAGGCCAGCAACCGCTTGGCAGCGCAGTACAGAGAGCGCTCGCTGTCTGTGGCTGTC 315
Qy 135 LeuArgGluAepPheGlnIleGlnProArgAspMetValAlaValGlyGluGlnPhe 154
Db 316 CTCGGGAGGATTTCCAGATCAGCCTCGGACATGTGGTGTGGTGGTGGTGGTGGTGGT 375
Qy 155 ThrLeuGluCysGlyProProTyrGlyHisProGluProThrValSerTyrTyrLeuAsp 174
Db 376 ACTCTGGATGTGGCGCCCTTGGGCGCACCCAGAGCCACAGTCTCATGTGGTGGATGAT 435
Qy 175 GlyIysProLeuAlaLeuGlnProGlyArgHisThrValSerGlyGlySerLeuLeuMet 194
Db 436 GGGAAACCCCTGGCCCTTCAGCCCGGAGGACACAGTGTCCGGGGGTCCCTGCTGATG 495
Qy 195 AlaArgAlaGluIysSerAspGlu**ThrTyrMetCysValAlaThrAsnSerAlaGly 214
Db 496 GCAAGAGCAGAGAGAGAGTGCAGAGGACCTTACATGTGTGGTGGTGGTGGTGGTGGTGG 555
Qy 215 HisArgGluSerArgAlaAlaArgValSerIleGlnGluProGlnAspTyrThrGluPro 234
Db 556 CATAGGAGAGCGCGCAGCCCGGGTTCATCCAGGAGCCCGAGGACTACACGGAGCCT 615
Qy 235 ValGluLeuLeuAlaValArgIleGlnLeuGluAenValThrLeuLeuAenProAspPro 254
Db 616 GTGGAGCTTCTGGCTGTGCGAATTTCAGCTGGGAAATGTGACATGCTGNAACCCGGATCCT 675
Qy 255 AlaGluGlyProIysProArgProAlaValThrLeu**TyrIysValSerGlyPro*** 274
Db 676 GCAGAGGGCCCAAGCCTAGACCGCGGTGGCTCAGTCAAGTCAAGTCAAGTCAAGTCAAG 735
Qy 275 -ArgLeuProAenLeuThrArgProCysSerGlyProArgLeuProArg-GluAlaArg 293
Db 736 CGGCTGGCCATCTTACACGGCCCTTGTTCAGGACCCAGATGCCCCGGGAGGCCAGG 794

RESULT 4
BX418142 922 bp mRNA linear EST 13-MAY-2003
LOCUS BX418142 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
DEFINITION CS0DF001YI24 5-PRIME, mRNA sequence.
ACCESSION BX418142
VERSION BX418142.1 GI:30642200
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 922)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6206.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DF001BE12QI&cluster=6206.r. Contact:
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID: CS0DF001BE12QI.
Location/Qualifiers
1..922
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/tissue_type="FETAL BRAIN"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
BASE COUNT 189 a 286 c 277 g 158 t 12 others
ORIGIN
Alignment Scores:
Pred. No.: 3,31e-85 Length: 922
Score: 1265.00 Matches: 244
Percent Similarity: 97.21% Conservative: 0
Best Local Similarity: 97.21% Mismatches: 7
Query Match: 78.67% Indels: 1
DB: 13 Gaps: 0
US-10-047-021-86 (1-303) x BX418142 (1-922)
Qy 1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeu 20
Db 170 ATGGGATCTGGAGAGACAGCCTCTCGGGGCGAGGGGTTCCTGTGCTCTGCTGCTG 229
Qy 21 LeuIleMetGlyGlyMetAlaGlnAspSerProGlnIleLeuValHisProGlnAsp 40
Db 230 CTATCATATGGAGGATGGCTCAGGATYCCCGCCCCAGATCTCTAGTCCACCCAGGAC 289
Qy 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60
Db 290 CAGCTGTTCAGGGCCCTGCGCCCTCCAGGATGAGTGCAGGAGCTCAGGCCACGACCT 349
Qy 61 ProThrIleArgTyrLeuLeuAenGlyGlnProLeuSerMetValProProAspProHis 80
Db 350 CCCACCATCCGCTGGTGTGCTGAAATGGGCGAGCCCTGAGCATGTGTGCGCCAGACCCAC 409
Qy 81 HisLeuLeuProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100
Db 410 CACCTCTGCTGATGGAGCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 469
Qy 101 AspGlyGlnAlaLeuSerThrAspLeuGlyValThrCysGluAlaSerAsnArgLeu 120
Db 470 GATGTTCAGGCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGCTT 529
Qy 121 GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln 140
Db 530 GGCACGGCAGTACAGAGAGCGCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 589
Qy 141 IleGlnProArgAspMetValAlaValAlaValGlyGlnPheThrLeuGluCysGlyPro 160
Db 590 ATCCAGCCTCGGACATGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG 649
Qy 161 ProTyrGlyHisProGluProThrValSerTyrTyrIysAspGlyIysProLeuAlaLeu 180
Db 650 CCCTGGGGCCACCCAGAGCCCACTCTCATGTGTGGAAAGATGGGAAACCTG-GCCCTC 708
Qy 181 GlnProGlyArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGlySer 200
Db 709 CAGCCCGGAAGGCACACAGTGTCCGGGGATCCCTGCTGATGGCAGAGCAGAGAGAGT 768
Qy 201 AspGlu**ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAla 220
Db 769 GACGAAGGAGCCTACATGTGTGGGCCCAACAGCAGGACACAGGAGGAGCGCGCA 828
Qy 221 AlaArgValSerIleGlnGluProGlnAspTyrThrGluProValGluLeuAlaVal 240
Db 829 SCCGGGTTCATCCAGGAGCCCGAGGACTACAGGAGGCTGTGGAGCTTCTGCTGCTG 888
Qy 241 ArgIleGlnLeuGluAenValThrLeuLeuAen 251
Db 889 CGAATACAGCTGGAAATGTGACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
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RESULT 5
CB994099
LOCUS
DEFINITION
AGENCOURT_13622710 NIH_MGC_148 Homo sapiens cDNA clone
IMAGE:30331943 5', mRNA sequence.
CB994099
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 826)
NIH-MGC http://mgi.nci.nih.gov/.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM348 row: c column: 24
High quality sequence stop: 637.
Location/Qualifiers
1..826
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30331943"
/tissue_type="pre-eclampsia placenta"
/lab_host="DH10B Tona"
/clone_lib="NIH_MGC_148"
/note="Organ: placenta; Vector: pBluescriptR; Site 1:
all-XhoI; Site 2: BamH; Library is oligo-dT primed and
directionally cloned using primer
5'-TTTTTTTTTTTTTTTTTTVN-3', size-selected for average insert
size 2.3 kb and normalized to ROT 5. This is a primary
library enriched for full-length clones and constructed
using the Cap-trapper method (Carninci, in preparation).
Library constructed by M. Brownstein (NIH/NHGRI,
National Institutes of Health). Note: this is a NIH_MGC
Library."
BASE COUNT 160 a 266 c 261 g 138 t 1 others
ORIGIN
Alignment Scores:
Pred. No.: 6,11e-83 Length: 826
Score: 1234.00 Matches: 243
Percent Similarity: 92.80% Conservative: 2
Best Local Similarity: 92.05% Mismatches: 14
Query Match: 76.74% Indels: 5
DB: 14 Gaps: 2
US-10-047-021-86 (1-303) x CB994099 (1-826)
QY 1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeu 20
DB 38 ATGGGCTCTGGAGGAGACAGCTCTCGGGGGGACGGGTTCCTGCTCTGCTCTCTG 97
QY 21 LeuLeuMetGlyGlyMetAlaGlnAspSerProGlnGlnLeuValHisProGlnAsp 40
DB 98 CTCATCATGGAGGAGCATGGCTCAGACTCCCGCCCGCCAGATCCTAGTCCACCCCGAG 157
QY 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnPro 60
DB 158 CAGCTGTTCCAGGGCCCTGGCCCTGCGAGGATGAGTGGCGGAGCTCAGGCCAGCCACT 217

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61 ProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80
218 CCCACCATCCGCTGGTGTGAATGGGAGCCCTGAGCATGGTCCGCCAGACCCACAC 277

81 HisLeuLeuProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100
278 CACCTCTCCCTGATGGGAGCCCTTCTGCTGTACAGCCCTGCTCCGGGAGACATGCCAC 337

101 AspGlyGlnAlaLeuSerThrAspLeuGlyValTyrCysGluAlaSerAsnArgLeu 120
338 GATGCCAGGCCCTGCTCCACAGACTGGGTGTACACATGTGAGGCCAGCAACCGGCTT 397

121 GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln 140
398 GGCACGGAGTGCAGCAGAGGGCTCGGCTGTCTGTGGTGTCTCTCCGGAGGATTTCCAG 457

141 IleGlnProArgAspMetValAlaValValGluGlnPheThrLeuGluCysGlyPro 160
458 ATCCAGCCTCGGAGCATGGTGGCTGTGGTGGTGGAGCAGTTTACTCTGGAATGTGGGCG 517

161 ProTrpGlyHisProGluProThrValSerTrpTyrLysAspGlyLysProLeuAlaLeu 180
518 CCCTGGGAGCCACCCAGAGCCACAGCTCTCATGGTGGAAAGATGGGAAACCCCTGCGCCTC 577

181 GlnProGlyArgHisThrValSerGlySerLeuLeuMetAlaArgAlaGluLysSer 200
578 CAGCCCGGAGGACACACAGTGTCCGGGGGTCTCCCTGTGTGATGGCAAGAGCAGAGAAGT 637

201 AspGlu***ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAla 220
638 GACGAAGGAGCTATCATGTGTGGCCACCAACAGCGCAAGCATANGAGAGAGCGCGCC 697

221 AlaArgValSerIleGlnGlu-ProGlnAspTyrThr-GluProVal-GluLeuLeu--- 238
698 ACCCGGGTTTCATCCAGAGAGCCCGCCAGAGCTACAGGAGGAGCTGTGGAGCTTCTGGGC 757

239 AlaValArgIleGlnLeuGluAsnValThrLeuLeu---AsnProAspProAlaGluGly 257
758 TGTGGAATTTTCAGCTGGGAAATGTGACACTGGTGGTGAACCCCGGATCTTGGCAAGGG 817

258 Prolys 259
818 CCCCAA 823

CB996189 860 bp mRNA linear EST 01-MAY-2003
AGENCOURT_13622686 NIH_MGC_148 Homo sapiens cDNA clone
IMAGE:30337143 5', mRNA sequence.
CB996189
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 860)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM361 row: 1 column: 16
High quality sequence stop: 578.
Location/Qualifiers

RESULT 6
CB996189
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 860)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM361 row: 1 column: 16
High quality sequence stop: 578.
Location/Qualifiers

QY 1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeu 20
DB 38 ATGGGCTCTGGAGGAGACAGCTCTCGGGGGGACGGGTTCCTGCTCTGCTCTCTG 97
QY 21 LeuLeuMetGlyGlyMetAlaGlnAspSerProGlnGlnLeuValHisProGlnAsp 40
DB 98 CTCATCATGGAGGAGCATGGCTCAGACTCCCGCCCGCCAGATCCTAGTCCACCCCGAG 157
QY 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnPro 60
DB 158 CAGCTGTTCCAGGGCCCTGGCCCTGCGAGGATGAGTGGCGGAGCTCAGGCCAGCCACT 217

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source
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/lab_host="DH10B Tona"
/clone_lib="NIH MGC 148"
/notes="Organ: placenta; Vector: pBlueScriptR; Site 1:
all-XhoI; Site 2: BamH; Library is oligo-dT primed and
directionally cloned using primer
5'-TTTTTTTTTTTTTTN-3', size-selected for average insert
size 2.3 kb and normalized to ROT 5. This is a primary
library enriched for full-length clones and constructed
using the Cap-trapper method (Carninci, in preparation).
Library constructed by M. Brownstein (NIMH/NHGR1,
National Institutes of Health). Note: this is a NIH_MGC
Library."
BASE COUNT 169 a 279 c 267 g 144 t 1 others
ORIGIN
Alignment Scores:
Pred. No.: 1.86e-81 Length: 860
Score: 1214.50 Matches: 242
Percent Similarity: 81.61% Conservative: 2
Best Local Similarity: 80.94% Mismatches: 11
Query Match: 75.53% Indels: 44
DB: 14 Gaps: 5

US-10-047-021-86 (1-303) x CB996189 (1-860)
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Db 38 ATGGCTCTGGAGGAGACAGCTCTCTGGGGGAGGGTTCCCTGCTCTCTCTCTCTG 97
Qy 21 LeulleMetGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAsp 40
Db 98 CTCATCTGGGAGGATGGCTCAGACTCCCGCCGACAGTCTAGTCCACCCCGGAC 157
Qy 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60
Db 158 CAGCTGTTCAGGGCCCTGGCCCTGCCAGGATGAGTGCAGGCTCAGGCGACCCACCT 217
Qy 61 ProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80
Db 218 CCCACCATCCGCTGCTGCTGAATGGGAGGCCCTTGACATGGTGCCTCCAGACCCAC 277
Qy 81 HisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100
Db 278 CACCTCTCTGCTGATGGACCTTCTGCTGCTACAGCCCTCGCCGGGACATGCCAC 337
Qy 101 AspGlyGlnAlaLeuSerThrAspLeuGlyValTyThrCysGluAlaSerAsnArgLeu 120
Db 338 GATGCCAGGCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTT 397
Qy 121 GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln 140
Db 398 GGCACGGCAGTCAGCAGAGGGCGCTGCTGCTGTGGTGTCTCCCGGAGGATTTCCAG 457
Qy 141 IleGlnProArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyPro 160
Db 458 ATCCAGCCTCGGACATGGTGGCTGTGGTGGTGAGCAGTTTACTCTGGAATGTGGCCG 517
Qy 161 ProTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeu 180
Db 518 CCCTGGGGCCACCCAGAGCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTGGCCCTC 577
Qy 181 GlnProGlyArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSer 200
Db 578 CAGCCCGGAGGACACAGTGTCCGGGGGTGCTCTGCTGATGGCAGGACAGAGAGT 637
Qy 201 AspGlu***ThrTyMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAla 220
Db 201 AspGlu***ThrTyMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAla 220

103 638 GACGAGGGACCTACATGTGTGTGGCCACCAACAGCGCAGGACATAGGAGCGCGCA 697
Qy 221 AlaArg-ValSerIleGlnGluProGlnAspTyThrGluProValGluLeuAlaVa 240
Db 698 GCCCGGGGTTCATCCAGGAA
Qy 240 lArgIleGlnGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysPr 260
Db 720 -----GCCCGGAGGAACTACACC 736
Qy 260 oArgProAlaValTrpLeu***TrpLysValSerGlyPro***Arg----- 275
Db 737 GGAGCCCTGT-----TGGGAGCTTCTTGGGCTGTGCGAANTTTTCACGCTGGG 784
Qy 276 -----LeuPro---AsnLeuThrArgProCys---SerGlyPro 286
Db 785 TAAAAATGTTGACACCTTGCTGGAAACCCCGGGAATCTCTGCCAAGAGGGCCC 839

RESULT 7
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LOCUS
DEFINITION AGENCOURT 7982449 lupski_dorsal_root_ganglion Homo sapiens cDNA
clone IMAGE:6186214 5', mRNA sequence.
ACCESSION BO890126
VERSION BO890126.1 GI:22282140
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 941)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-x@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13578 row: d column: 23
High quality sequence start: 6
High quality sequence stop: 612.
Location/Qualifiers
1. .941
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/dev_stage="adult, 36 yr"
/lab_host="DH10B"
/clone_lib="Lupski dorsal root ganglion"
/notes="Vector: pCMV-SPOK6 (Life Technologies); Site_1:
NotI; Site 2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACCGCTCCG-3' and
5'-GACTAGTCTAGATCGAGCGCCGCT(15)-3'. Size selected >
1 kb for average insert length 1.7 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies."
```

Percent Similarity: 81.88% Conservatives: 3
 Best Local Similarity: 80.87% Mismatches: 31
 Query Match: 71.30% Indels: 24
 DB: 13 Gaps: 7

US-10-047-021-86 (1-303) x B0890126 (1-941)

QY 1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeu 20
 Db 53 ATGGGCTCTGGAGGAGACAGCCTCTCTGGGGGCGAGGGTTCCCTGCTGCTGCTCTG 112
 QY 21 LeuLeuMetGlyGlyMetAlaGlnAspSerProGlnIleLeuValHisProGlnAsp 40
 Db 113 CTCATCATGGAGGAGATGCTCAGACTCCCGCCGCCAGATCTAGTCCACCCCGAGGAC 172
 QY 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60
 Db 173 CAGCTGTTCAGGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 232
 QY 61 ProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80
 Db 233 CCCACATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 292
 QY 81 HisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100
 Db 293 CACCTCTCTGCTGATGGGACCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 352
 QY 101 AspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeu 120
 Db 353 GATGCCAGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 412
 QY 121 GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln 140
 Db 413 GGCAGCGCAGTCAGCAGAGCGCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 472
 QY 141 IleGlnProArgAspMetValAlaValValGlyGlnGlnPheThrLeuGluCysGlyPro 160
 Db 473 ATCCAGCCTCGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 532
 QY 161 ProTrpGlyHisProGluProThrValSerTrpTrpLeuAspGlyValPheLeuAlaLeu 180
 Db 533 CCTCGGGGCCACCCAGAGCCCATGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 592
 QY 181 GlnProGlyArgHis--ThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysS 200
 Db 593 CAGCCCGGAGGACACAGTGTGTCGGGGGGTCCCTGCTGATGTCAGCAGAGAGAGA 652
 QY 200 erAspGlu***ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArg---GluSerA 219
 Db 653 GTGACGAAGAGGACCTACATGTGTGTGGCCACCAACAGCGCAGCAGCATAGAGAGAG 712
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RESULT 8
 AK004723
 LOCUS
 DEFINITION Mus musculus adult male lung cDNA, RIKEN full-length enriched library, clone:1200012D01 product:similar to MAGIC ROUNDABOUT [Homo sapiens], full insert sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 AUTHORS

TITLE
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TITLE
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 PUBMED
 REFERENCE
 AUTHORS

AK004723
 GI:26334429
 CAP trapper.
 Mus musculus (house mouse)
 Mus musculus

Carninci, P., and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
 99279253
 10349636

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)
 20499374
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Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
 Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M.,
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
 Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
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Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
 Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,
 Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamakawa, I.,
 Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,
 Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,
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 Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,
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 Carninci, P., de Bonaldo, M.P., Brownstein, M.J., Bult, C.,
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 and Hayashizaki, Y.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409 (6821), 685-690 (2001)
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 11217851

The FANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 6 (bases 1 to 3689)

Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H.,
 Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y.,
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Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
 Direct Submission
 Submitted (10-JUL-2000) Yoshihide Hayaehizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
 On Dec 10, 2002 this sequence version replaced gi:12836108.
 Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGCGCGCACTCGAGTTTCTTTTCTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGAGATCCAGAGCTCAATTAATTAATTAACCCGCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: SstI; 3' end: XhoI. Host: SOLR.

FEATURES

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BASE COORDINATE

802 a 1115 c 1011 g 761 t

Alignment Scores:

Pred. No.: 1.57e-75 Length: 3689
 Score: 1145.50 Matches: 223
 Percent Similarity: 82.06% Conservative: 24

Best Local Similarity: 74.09% Mismatches: 52
 Query Match: 71.24% Indels: 2
 DB: 11 Gaps: 1

US-10-047-021-86 (1-303) x AK004723 (1-3689)

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 Qy 21 LeulleMetGlyGlyMetAlaGlnAspSerProGlnleLeuValHisProGlnAsp 40
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 Db 277 TACCTTTGGCGATGGAGCCCTCTCTTACATCGGCCCTCTGTCCAGGAGCGCCACAA 336
 Qy 101 AspGlyGln--AlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArg 119
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RESULT 9
 AK087355
 LOCUS

3865 bp mRNA linear HTC 05-DEC-2002

DEFINITION Mus musculus 0 day neonate lung cDNA, RIKEN full-length enriched library, clone:E030049D17 product:similar to MAGIC ROUNDABOUT [Homo sapiens], full insert sequence.

ACCESSION AK087355

VERSION AK087355.1 GI:26352439

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253

10349636

2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.
Genome Res. 10 (10), 1617-1630 (2000)
20499374

11042159

3 Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yanamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913

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4 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsumoto, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Brownstein, M.J., Bult, C., Carninci, P., de Bonaldo, M.P., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzei, J., Mombert, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y.
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
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11217851

5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3865)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirao, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,

Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akashira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suenro-cho, Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@ec.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/.

FEATURES
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BASE COUNT 826 a 1188 c 1038 g 813 t

ORIGIN

Alignment Scores:
Pred. No.: 1.66e-75 Length: 3865
Score: 1145.50 Matches: 223
Percent Similarity: 82.06% Conservative: 24
Best Local Similarity: 74.09% Mismatches: 52
Query Match: 71.24% Indels: 2
DB: 11 Gaps: 1

US-10-047-021-86 (1-303) x AK087355 (1-3865)

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RESULT 10
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IMAGE:30336795 5', mRNA sequence.
ACCESSION CB997292
VERSION CB997292.1 GI:30291812
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 803)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rc@mail.nih.gov
Tissue Procurement: Dr. Stefan Hanson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: NDAM360 row: n column: 04
High quality sequence stop: 535.

FEATURES

source
1..803
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30336795"
/tissue_type="pre-eclamptic placenta"
/lab_host="DH10B Tona"
/clone_lib="NIH_MGC_148"
/notes="Organ: Placenta; Vector: pBluescriptR; Site_1:
alt-XhoI; Site_2: BamH; Library is oligo-dT primed and
directionally Cloned using primer
5'-TTTTTTTTTTTTTTTNN-3', size-selected for average insert
size 2.3 kb and normalized to ROT 5. This is a primary
library enriched for full-length clones and constructed
using the Cap-trapper method (Carninci, in preparation).
Library constructed by M. Brownstein (NIH/NHGRI,
National Institutes of Health). Note: this is a NIH_MGC
Library."
BASE COUNT 156 a 262 c 247 g 138 t
ORIGIN

Alignment Scores:

Pred. No.: 1,43e-75 Length: 803
Score: 1135.50 Matches: 221
Percent Similarity: 95.42% Conservative: 8
Best Local Similarity: 92.08% Mismatches: 7
Query Match: 70.62% Indels: 4
DB: 14 Gaps: 1

US-10-047-021-86 (1-303) x CB997292 (1-803)

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Qy 1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeu 20
Db ATGGGCTCTGAGGAGACAGCTCTCTGGGGGAGGGGTTCCTGCTCTGCTCTGCTG 97
Qy 21 LeuIleMetGlyGlyMetAlaGlnAspSerProGlnIleLeuValHisProGlnAsp 40
Db CTATCATGGGAGGATGGTCTAGGACTCCCGGCCCCAGATCCTAGTCCACCCAGGAC 157
Qy 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60
Db CAGCTGTTCAGGGCCCTGGCCCTGCCAGGATGAGTGGCCGAGCCTCAGGCGACCACT 217
Qy 61 ProThrIleArgTrpLeuLeuLeuAsnGlyGlnProLeuSerMetValProAspProHis 80
Db CCACCATTCGCTGTGCTGAATGGGACGCCCTTGAGCATGGTGGCCCGACAGACCCAC 277
Qy 81 HisLeuLeuProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100
Db CACTCTCTGCTGATGGGACCTTCTGCTGCTACAGCCCTTGCCTGGGGACATGCCAC 337
Qy 101 AspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeu 120
Db GATGGCCAGGCGCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCGCAGCAACCG 397
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QY 121 GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln 140
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 Db 398 GGCAGCGCAGTCAGCAGAGCGCTGGCTGTCTGTGGCTGTCTCTCGGGAGGATTCCAG 457
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 QY 141 IleGlnProArgAspMetValAlaValGlyGlnPheThrLeuGluCysGlyPro 160
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 Db 458 ATCCAGCCTCGGAGCATGTGGCTGTGGTGGGTGACAGTCTTACTCTGGAATGTGGCGG 517
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 QY 161 ProTtpGlyHisProGluProThrValSerTtpTtpLysAspGlyLysProLeuAlaLeu 180
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 Db 518 CCTGGGCGCACCAGAGCCACAGTCATGTGTGGAAGATGGGAACCCCTGCGCCCTC 577
 |||||
 QY 181 GlnProGlyArgHisThrValSerGlySerLeuLeuMetAlaAlaGlaGluYsser 200
 |||||
 Db 578 CAGCCCCGGAAGACACACAGTCTCGGGGGTCCCTGCTGATGCCAAGAGCAAAAAGAT 637
 |||||
 QY 201 AspGlu**ThrTyrMetCysValAlaThrAsnSerAlaGlyHis-ArgGluSerArgNl 220
 |||||
 Db 638 GACGAAGGAAGTACTCTGTGTGGCCACCCAGCGCAGGACATGAAGGAGAGCGCGC 697
 |||||
 QY 220 aAla-ArgValSer-IleGln--GluProGlnAspTyrThrGluProValGlu 236
 |||||
 Db 698 AACCCCGGGTTTCCCATCCAGGAGCCCTTAGAATACCCCGAGCCTGTGAA 751
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 RESULT 11
 Bi762862
 LOCUS 603048384F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5188652 5',
 mRNA sequence.
 Bi762862
 VERSION 1
 KEYWORDS NIH-MGC http://mgc.nci.nih.gov/
 SOURCE National Institutes of Health, Mammalian Gene Collection (MGC)
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 729)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgaapb@roaail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM11471 row: g column: 21
 High quality sequence stop: 723.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5188652"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_116"
 /note="Organ: pooled colon, kidney, stomach; Vector:
 pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
 source anonymous pool of 3 colons, age 26 yo male, 49 yo
 female, 71 yo male colon; 46 yo male kidney, and pool of 2
 stomachs, 62 yo male and 70 yo female. Library is
 oligo-dr primed and directionally cloned (EcoRV site is
 destroyed upon cloning). Average insert size 1.4 kb,
 insert size range 1-3 kb. Library is normalized and
 enriched for full-length clones and was constructed by C.
 Gruber (Invitrogen). Research Genetics tracking code
 023. Note: this is a NIH_MGC Library."
 137 a 240 c 229 g 123 t

Alignment Scores:
 Pred. No.: 7,33e-74 Length: 729
 Score: 1112.00 Matches: 224
 Percent Similarity: 93.90% Conserv: 7
 Best Local Similarity: 91.06% Mismatches: 10
 Query Match: 69.15% Indels: 6
 DB: 12 Gaps: 1
 US-10-047-021-86 (1-303) x Bi762862 (1-729)
 QY 4 GlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeuLeuMet 23
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 Db 3 GGAGGAGACAGCTCTCTGGGGGCA--GGGTTCCTGCTCTGCTCTGCTCATCATG 60
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 QY 24 GlyGlyMetAlaGlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPhe 43
 |||||
 Db 61 GGAGCATGGCTCAGGACTCCCGTCCGAGATCTTAGTCCACCCCGAGCAGCTGTT--- 117
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 QY 44 GlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIle 63
 |||||
 Db 118 CCAGGCCCTGGCCCTGCCAGGATGAGTGCACAGCTTCAGGCCACCCACCTCCACCATC 177
 |||||
 QY 64 ArgTtpLeuLeuAsnGlyGln-ProLeuSerMetValProProAspProHisHisLeu 83
 |||||
 Db 178 CGCTGGTGTGTAATGGCAGCCCATGAGCATGGTGGCCCGCAGACCCACCATCTCTCT 237
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 QY 83 uProAspGlyThrLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuGln 103
 |||||
 Db 238 GCCTGATGGGACCTTCTGCTGTCTACAGCCCTCTCCCGGGGACATGCCAGATGGCCA 297
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 QY 103 nAlaLeuSerThrAsp-LeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThra 123
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 Db 298 GGCCCTGTCCACAGACCATGGGTGTCTACATATGTGAGSCCAGCAACCGCTTGCACGG 357
 |||||
 QY 123 laValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnP 143
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 Db 358 CAGTCAGCAGAGGCGCTCGGCTGTGTGGCTGTCTCTCCGGGAGGATTTCCAGATCCAGC 417
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 QY 143 roArgAspMetValAlaValValGlyGlnPheThrLeuGluCysGlyProProTtpG 163
 |||||
 Db 418 CTCGGACATGGTGGCTGTGGTGGGTGAGCAGTTTACTCTGGATGTGGGCGCCCTGGG 477
 |||||
 QY 163 lyHisProGluProThrValSerTtpTtpLysAspGlyLysProLeuAlaLeuGlnProG 183
 |||||
 Db 478 GCCACCCAGAGCCACAGCTCTCATGGTGGAAAGATGGGAACCCCTGGCCCTCCAGCCCG 537
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 QY 183 lyArgHisThrValSerGlySerLeuLeuMetAlaAlaGluYsserAspGlu* 203
 |||||
 Db 538 GAAGGCACACAGTGTCCGGGGTCCCTGCTGTGATGGCAAGAGCAGAGAAGAGTGCAGAG 597
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 QY 203 **ThrTyr--MetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaAr 222
 |||||
 Db 598 GGACTTACCATGCTGTGTGGCCACCAACAGCGCAGGACATAGGGAGAGCCCGCGCAGCG 657
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 QY 222 gValSerIleGlnProGlnAspTyrThrGluProValGluLeuLeuAlaValArgI 242
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 Db 658 GGTTCATCCAGGAGCCCGAGGAGTACACGGAGCTGTGGAGCTTCTGGCTGTGCCGNA 717
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 QY 242 eGlnLeuGlu 245
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 Db 718 TCAGCTGGAC 727
 RESULT 12
 Bi906521
 LOCUS 6620212 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5590503
 DEFINITION 5', mRNA sequence.
 Bi906521
 VERSION Bi906521.1 GI:19356900
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

FEATURES
 source

BASE COUNT
 ORIGIN

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1230)
NIH-MGC <http://mgi.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Invitrogen

cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: LHAM12364 row: o column: 16
High quality sequence stop: 535.
Location/Qualifiers

FEATURES

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1. 1230
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5590503"
/lab_host="DH10B"
/clone_lib="NIH_MGC_125"
/note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
Site 1: EcorV (destroyed); Site 2: NotI; RNA source pool
of three ovaries, from females ranging in age from 38 to
49 yo. Library is oligo-dT primed and directionally cloned
(EcorV site is destroyed upon cloning). Average insert
size 2.1 kb, insert size range 1-3.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 036."

BASE COUNT 257 a 429 c 326 g 217 t 1 others
ORIGIN

Alignment Scores:
Pred. No.: 1.92e-67 Length: 1230
Score: 1030.00 Matches: 222
Percent Similarity: 67.05% Conservative: 14
Best Local Similarity: 63.07% Mismatches: 37
Query Match: 64.05% Indels: 79
DB: 12 Gaps: 10

US-10-047-021-86 (1-303) x BM906521 (1-1230)

Qy 1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeu 20
Db 35 ATGGGCTCTGGAGAGACAGCTCTCTGGGGGCGAGGGTTCCTCTGCTGCTCTG 94
Qy 21 LeuileMetGlyGlyMetAlaGlnAspSerProGlnIleLeuValHisProGlnAsp 40
Db 95 CTCATCATGGAGGATGGCTCAGACTCCCGCCGACAGATCTCTAGTCCACCCCGAGAC 154
Qy 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60
Db 155 CAGCTGTCTCAGGGCCCTTGGCCCTGCGCAGGATGAGTGCCTGAGGAGCCACCT 214
Qy 61 ProThrileArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80
Db 215 CCCACCATCCCTGGTGTCTGAATGGGCGAGCCCTGAGCATGTGTGCCCGACCCACAC 274
Qy 81 HisLeuLeuProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100
Db 275 CACCTCTGCTGATGGAGCCCTTCTGCTGCTACAGCCCTTGCCTGCGGGAGACATGCCAC 334
Qy 101 AspGlyGlnAlaLeuSerThrAspLeuGlyValTrpCysGluAlaSerAsnArgLeu 120
Db 335 GATGGCAGGCGCCCTGTGCACAGACTGGGTGTCTACATGTGAGGCGCAGCAACCGGCTT 394
Qy 121 GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln 140

Db 395 GGCAAGCGGCTCAGCAGAGCGGCTCGGCTGCTGTGTGGCTGTCTCTCGGAGGATTTCCAG 454
Qy 141 IleGlnProArgAspMetValAlaValValGlyGlnPheThrLeuGluCysGlyPro 160
Db 455 ATCCAGCCTCGGACATGGTGGCTGTGTGGTGGAGCAGTTTACTCTGGAATGTGGCCG 514
Qy 161 ProTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeu 180
Db 515 CCTGGGGCCACCAGAGCCACAGTCTCATGTGGAAAGATGGAAACCCCTGGCCCTC 574
Qy 181 GlnProGlyArgHisThrVal----SerGlyGlySerLeuLeuMetAla----- 195
Db 575 CAGCCGGAAGGCACACAGTGTGCGGGGGGTCCTGTGTGATGGCCATAATGCCACG 634
Qy 196 -----ArgAlaGluLys----- 199
Db 635 TTTTCTGGCTAAAGGGCATTAATACTGTGTGTCGCCCGCCGCTAAACCCCAAGGCACC 694
Qy 200 -----SerAspGlu***ThrTyr 205
Db 695 CTTGGACAGCCACACACTACAGGGGCCCTTTCTCGGTATGACCCCGCTACATAC 754
Qy 206 MecCysVal-----AlaThrAsnSerAlaGlyHisArgGluSerArgAla 220
Db 755 TCATGCCACCCCATTCGTCTCCCGGTTCTCTGGCGCGGTGCGGCCACCTTACTTTC 814
Qy 221 AlaArgValSerIle-----GlnGluProGlnAsp----- 230
Db 815 TCGCGCTCGAACAAGCGCCACCTCGACTTTTACCGCGCGCGCCGAGACTAAGATCCG 874
Qy 231 -----TyrThrGluProValGluLeuAlaValArgIleGlnLeuGlu 245
Db 875 ACAGACAGCTATCTCTACACGCCGCCAGCA-----TCAGATGGCGGAGCCTCGAA 925
Qy 246 AsnValThrLeuLeuAsnProAspPro----- 254
Db 926 CGCGTTCCCTCCGTCACCGTTACCGCGGCTCTCTCTGTGTATGATCCAGCAGAGAAAT 985
Qy 255 -----AlaGluGlyProLysProArg-ProAlaValTrpLeu***TrpLysVa 270
Db 986 TGGCGCGCATCGGGCGAAGACCCGAA---AGAGCCCGCC-----TGCGGAAC 1030
Qy 270 lSerGlyPro***ArgLeuProAsnLeuThrArg 281
Db 1031 CGAGGACATATTAAGCGCCAGATCTATGAAGA 1064

RESULT 13

CB959649

LOCUS

DEFINITION

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

771 bp mRNA linear EST 29-APR-2003
AGENCOURT 13893577 NIH_MGC_147 Homo sapiens cDNA clone
IMAGE:30344820 5', mRNA sequence.

CB959649

CB959649.1 GI:30215765

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC <http://mgi.nci.nih.gov/>.

1 (bases 1 to 771)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. Stefan Hanson

cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help

and advice from Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: NDAM381 row: 1 column: 13

High quality sequence stop: 628.

FEATURES

source

1. .771
/organism="Homo sapiens"
/mol_type="mrna"
/db_xref="taxon:9606"
/clone="IMAGE:30344820"
/tissue_type="Human Placenta"
/lab_host="DH10B Tona"
/clone_lib="NIH MGC 147"
/note="Organ: Placenta; Vector: pBluescriptR; Site: 1:
all-XhoI; Site 2: BamH; Oligo-dT primed using primer
5'-TTTTTTTTTTTNN-3', size-selected for average
insert size 2.3 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIMH/NHGRI, National Institutes of Health). Note: This is
a NIH MGC library."

BASE COUNT 147 a 246 c 245 g 124 t 9 others
ORIGIN

Alignment Scores:
Pred. No.: 2,398-67 Length: 771
Score: 1025.50 Matches: 197
Percent Similarity: 89.43% Conservative: 6
Best Local Similarity: 86.70% Mismatches: 19
Query Match: 63.77% Indels: 5
DB: 14 Gaps: 2

US-10-047-021-86 (1-303) x CB959649 (1-771)

QY 1 MetGlySerGlyValAspSerLeuLeuGlyArgGlySerLeuProLeuLeuLeu 20
DB 66 ATGGGCTCTGGAGGAGACAGCTCTCTGGGGGAGGGGTTCCTGCTGCTGCTGCTG 125

QY 21 LeuLeuMetGlyGlyMetAlaGlnAspSerProProGlnLeuLeuValHisProGlnAsp 40
DB 126 CTCATCTGGGAGGATGGCTCAGGACTCCCGCCCGCCAGATCTAGTCCACCCCGGAG 185

QY 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60
DB 186 CAGCTGTCTTCCAGGGGCTGGCCCTCCAGGATGAGCTGCCAAGCCTCAGGCCAGCCT 245

QY 61 ProThrLeuArgTyrLeuLeuAsnGlyGlnProLeuSerMetValProAspProHis 80
DB 246 CCCACATCCGCTGTGTTGCTGAATGGGAGCCCTTGGAGATGTCCTCCCGCCAGCCAC 305

QY 81 HisLeuLeuProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100
DB 306 CACCTCTGCTGATGGGACCTTCTGCTGCTACAGCCCTGCGCGGGGACATGCCAC 365

QY 101 AspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeu 120
DB 366 GATGCCAGGCGCTCTCCACAGACCTGGTGTCTACATGTGAGGCCAGCAACCGGCTT 425

QY 121 GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln 140
DB 426 GGCAGGCGAGTCAGCAGAGGCGCTCGGCTGTCTGTGGCTGCTCTCCGGGAGGATTCAG 485

QY 141 IleGlnProArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyPro 160
DB 486 ATCCAGCTTCGGGACATGTTGGCTGTGGTGGGTGAGCAGATTACTCTGGAATGTGGCG 545

QY 161 ProTrpGlyHisProGluProThrValSerTrpTyrAspGlyLysProLeuAlaLeu 180
DB 546 CCTGGGGCCACCCAGAGCCACAGTCTCATGCTGGAAAGATGGAAACCCCTGCGCCCTC 605

QY 181 GlnProGlyArgHisThr----ValSerGlyGlySerLeuLeuMetAla----- 195
DB 606 CAGCCCGGAAGGACACACAGTGTCCGGGGGGTCCCTGCTGATGGCAANGAGCAGAAGA 665

QY 196 ArgAlaGluLysSerAspGlu***ThrTyrMetCysValAlaThrAsnSerAlaGlyHis 215

DB 666 AGACTGGACGAAGGGGACCTTANNCATGTGTGTGGCCANNCCACAGCGCAAGGAAC 725
QY 216 ArgGluSerArgAlaAlaArg 222
DB 726 CATAGGGGAGAAAGCCCCGC 746

RESULT 14
CB961529
LOCUS
DEFINITION CB961529 798 bp mRNA linear EST 29-APR-2003
IMAGE:30348011 5', mRNA sequence.
ACCESSION CB961529
VERSION CB961529
KEYWORDS EST.
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgs.nci.nih.gov/
1 (bases 1 to 798)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
CDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM390 row: a column: 12
High quality sequence stop: 565.

FEATURES
Location/Qualifiers
1. .798
/organism="Homo sapiens"
/mol_type="mrna"
/db_xref="taxon:9606"
/clone="IMAGE:30348011"
/tissue_type="pre-eclamptic placenta"
/lab_host="DH10B Tona"
/clone_lib="NIH MGC 148"
/note="Organ: placenta; Vector: pBluescriptR; Site 1:
all-XhoI; Site 2: BamH; Library is oligo-dT primed and
directionally cloned using primer
5'-TTTTTTTTTTTNN-3', size-selected for average insert
size 2.3 kb and normalized to ROT 5. This is a primary
library enriched for full-length clones and constructed
using the Cap-trapper method (Carninci, in preparation).
Library constructed by M. Brownstein (NIMH/NHGRI,
National Institutes of Health). Note: this is a NIH_MGC
Library."

BASE COUNT 155 a 261 c 242 g 139 t 1 others
ORIGIN

Alignment Scores:
Pred. No.: 1,088-66 Length: 798
Score: 1017.00 Matches: 195
Percent Similarity: 88.60% Conservative: 7
Best Local Similarity: 85.53% Mismatches: 22
Query Match: 63.25% Indels: 4
DB: 14 Gaps: 2

US-10-047-021-86 (1-303) x CB961529 (1-798)

QY 1 MetGlySerGlyGlyAspSerLeuLeuGlyArgGlySerLeuProLeuLeuLeu 20
DB 38 ATGGGCTCTGAGGAGACAGCTCTCTGGGGGAGGGGTTCCTGCTGCTGCTGCTG 97

QY 21 LeuLeuMetGlyGlyMetAlaGlnAspSerProGlnLeuLeuValHisProGlnAsp 40

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Db 98 CTCATCATGGAGCATGGCTCAGAGCTCCCGCCCGCCAGATCTCTAGTCCACCCCGCCAGGAC 157
Qy 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60
Db 158 CAGTGTTCAGAGGCCCTGGCCCTCCAGGATGAGCTGCCGAGCTCAGGCCACCCACCT 217
Qy 61 ProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80
Db 218 CCCACCATCCGCTGGTGTCTGAATGGGCAGCCCTGAGCATGTGGTCCCGCCAGACCCACAC 277
Qy 81 HisLeuLeuProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100
Db 278 CACCTCTGCTGATGAGACCTCTCTGTCTACAGCCCTGCTCCGCGGAGCATGCCAC 337
Qy 101 AspGlyGlnAlaLeuSerThrAspLeuGlyValThrCysGluAlaSerAsnArgLeu 120
Db 338 GATGGCCAGGCCCTGTCTCAGACACTGGTGTCTACATGTGAGGCAGCAACCGGCTT 397
Qy 121 GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln 140
Db 398 GGCACGCGAGTCAGCAGAGCGCTCGGCTGTCTGTGGCTGTCTCCGAGGATTTCCAG 457
Qy 141 IleGlnProArgAspMetValAlaValValGlyGlnPheThrLeuGluCysGlyPro 160
Db 458 ATCCAGCCTCGGACATGTGTGGCTGTGGTGTGAGCAGATTTACTCTGGAATGTGGCCG 517
Qy 161 ProTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeu 180
Db 518 CCCTGGGCGCACCCAGAGCCACAGTCTCATGTGGGAAAGATGGAAATCCCTGGCCCTC 577
Qy 181 GlnProGlyArgHisThrVal---SerGlyGlySerLeuLeuMetAlaArgAlaGluLys 199
Db 578 CCGCCCCGAGGACACAGATGATCCGGGGGGTCTCTCTGTATGGGCAAGCAATAAA 637
Qy 200 SerAsp-----Glu***ThrTyrMetCysValAlaThrAnSerAlaGlyHisArg 216
Db 638 AACAGTTGACGAAGGAGCCCTTTTGTGTGTGGTGGGCCCCACCAATCAAGCTCCAGGGAAA 697
Qy 217 GluSerArgAlaAlaArgValSer 224
Db 698 TTAGGGNAGAGCCCGGCCCAAC 721

RESULT 15
CB961818
LOCUS
DEFINITION AGNCOURT 13665726 NIH_MGC_148 Homo sapiens cDNA clone
IMAGE:30349135 5', mRNA sequence.
CB961818
VERSION
KEYWORDS EST.
SOURCE CB961818.1 GI:30217935
ORGANISM Homo sapiens (human)

REFERENCE
1 (bases 1 to 688)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM392 row: p column: 08
High quality sequence stop: 448.
Location/Qualifiers
1. .688
/organism="Homo sapiens".

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/clone="IMAGE:30349135"
/tissue_type="pre-clamptic placenta"
/lab_host="DH10B Tona"
/clone_lib="NIH_MGC_148"
/notes="Organ: placenta; Vector: pBluescriptR; Site 1:
alt-XhoI; Site 2: BamH; Library is oligo-dT primed and
directionally cloned using primer
5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert
size 2.3 kb and normalized to 5. This is a primary
library enriched for full-length clones and constructed
using the Cap-trapper method (Carninci, in preparation).
Library constructed by M. Brownstein (NIH/NHGRI,
National Institutes of Health). Note: this is a NIH_MGC
Library."
BASE COUNT 126 a 229 c 216 g 116 t 1 others
ORIGIN

Alignment Scores:
Pred. No.: 5 36e-64 Length: 688
Score: 980.00 Matches: 191
Percent Similarity: 94.09% Conservative: 0
Best Local Similarity: 94.09% Mismatches: 8
Query Match: 60.95% Indels: 4
DB: 14 Gaps: 2

US-10-047-021-86 (1-303) x CB961818 (1-688)
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Db 38 ATGGGCTCTGAGGAGACACGCTCTCTGGGGGCGAGGGTTCCTGCTCTGCTCTG 97
Qy 21 LeuIleMetGlyGlyMetAlaGlnAspSerProGlnIleLeuValHisProGlnAsp 40
Db 98 CTATCATGGAGGAGCATGTGCTCAGGACTCCCGCCCGCCAGATCTCTAGTCCACCCCGAGAC 157
Qy 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60
Db 158 CAGCTGTTCAGGGCCCTGGCCCTGCCAGATGAGCTGCCGAGCTCAGGCCACCCACCT 217
Qy 61 ProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80
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Qy 81 HisLeuLeuProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100
Db 278 CACCTCTGCTGTATGGGACCCCTTCTGTCTGTGTGGCTGTCTCTCCGCGGAGGATTTCCAG 337
Qy 101 AspGlyGlnAlaLeuSerThrAspLeuGlyValThrCysGluAlaSerAsnArgLeu 120
Db 338 GATGGCCAGGCCCTGTCTCAGACACTGGTGTCTACACATGTGAGGCAGCAACCGGCTT 397
Qy 121 GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln 140
Db 398 GGCACGCGAGTCAGCAGAGCGCTCGGCTGTCTGTGGCTGTCTCTCCGCGGAGGATTTCCAG 457
Qy 141 IleGlnProArgAspMetValAlaValValGlyGlnPheThrLeuGluCysGlyPro 160
Db 458 ATCCAGCCTCGGACATGTGTGGCTGTGGTGTGAGCAGATTTACTCTGGAATGTGGGCCG 517
Qy 161 ProTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLys---ProLeuAla 179
Db 518 CCCTGGGCGCACCCAGAGCCACAGTCTCATGTGGGAAAGATGGAAACCCCTGGGCC 577
Qy 180 LeuGlnProGlyArgHisThr---ValSerGlyGlySerLeuLeu---MetAlaArgAla 198
Db 578 TCAGCCCCGAAAGGACACACAGTGTCCGGGGGGGTCTCCCTGCTTGNATGGCAGAGCCG 637
Qy 198 LysLys 199
Db 638 AAAAG 642

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Search completed: January 31, 2004, 15:28:18
Job time : 1848.41 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 30, 2004, 15:44:59 ; Search time 35.7513 Seconds
(without alignments)
1225.369 Million cell updates/sec

Title: US-10-047-021-86_COPY_28_303

Perfect score: 1475

Sequence: 1 QDSPPQLVHPDQLFCGPG.....SGPRLPRELRGQRNTG 276

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A. Geneseq 15Jun03.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1469	99.6	303	23	ABP62033
2	1469	99.6	304	20	AA12934
3	1311	88.9	480	22	AAU00501
4	1311	88.9	985	20	AAV41716
5	1311	88.9	985	21	ABE44272
6	1311	88.9	985	24	ABU61102
7	1311	88.9	1007	23	ABB97310
8	1311	88.9	1104	23	AAU99419
9	1303	88.3	792	22	AA895515

10	1303	88.3	792	22	AAG67430	Amino acid sequenc
11	1029.5	69.8	1015	23	AAU99420	Mouse ECSM4 protei
12	955	64.7	934	22	AAU00500	Human TANGO 330 fo
13	446.5	30.3	753	20	AAW83927	Human T85 protein.
14	446.5	30.3	753	24	AAU04090	Human expressed pr
15	446.5	30.3	1649	20	AAU08404	Human ROBO1 protei
16	446.5	30.3	1649	24	ABU04091	Human expressed pr
17	446.5	30.3	1651	20	AAU13566	Human Robo 1 polyp
18	446.5	30.3	1651	24	ABU04089	Human expressed pr
19	446.5	30.3	1651	24	ABU04092	Human expressed pr
20	446.5	30.3	1651	24	ABU04093	Human expressed pr
21	446.5	30.3	1651	24	ABU04094	Human expressed pr
22	404.5	27.4	1515	23	AAO19185	Human neurotransmi
23	396.5	26.9	1422	23	AAO19179	Human neurotransmi
24	395.5	26.8	1395	20	AAU13563	Drosophila Robo 1
25	395.5	26.8	1395	20	AAU08401	Drosophila sp. ROB
26	395.5	26.8	1395	22	ABW8257	Drosophila melanog
27	354.5	24.0	1297	20	AAU13565	C. elegans Robo po
28	354.5	24.0	1297	20	AAU08403	C. elegans Robo pr
29	345	23.4	1380	20	AAU08402	Drosophila sp. ROB
30	345	23.4	1381	20	AAU13564	Drosophila Robo 2
31	323	21.9	823	22	ABW61552	Drosophila melanog
32	307	20.8	885	22	ABW61502	Drosophila melanog
33	267.5	18.1	1496	20	AAW81030	Melanoma associate
34	267.5	18.1	1496	21	AAU70469	Human p53 target m
35	267.5	18.1	1496	24	ABU03498	Angiogenesis-assoc
36	267.5	18.1	1498	22	ABW11587	Human peroxidasin
37	265.5	18.0	1463	23	AAO21660	Human secreted pro
38	260.5	17.7	937	22	AAU78714	Human protein SEQ
39	260.5	17.7	952	22	AAU78715	Human protein SEQ
40	260.5	17.7	1267	24	AAE32108	Human cytoskeleton
41	260.5	17.7	1359	24	AAE32109	Human cytoskeleton
42	260.5	17.7	1370	24	ABJ19347	NOVX related prote
43	259	17.6	1527	22	ABW57771	Drosophila melanog
44	250.5	17.0	3931	24	ABU07377	Human protein NOV9
45	240	16.3	1026	23	ABW53276	Human polypeptide

ALIGNMENTS

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ID ABP62033 standard; Protein; 303 AA.
AC ABP62033;
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XX
DT 12-NOV-2002 (first entry)
DE Human secreted protein SEQ ID NO 86.

Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnery;
antiparkinsonian; antiskickling; antianemic; antitubercular; cancer;
antihemagic; hepatotropic; cerebroprotective; antinflammatory;
antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
antiparasitic; cardiant; immune disorder; cardiovascular disorder;
neurological disease; infection; nephrotropic; gene therapy; vaccine.

Homo sapiens.

WO200257420-A2.

25-JUL-2002.

17-JAN-2002; 2002WO-US01109.

18-JAN-2001; 2001US-262066P.

(HUMA-) HUMAN GENOME SCI INC.

Moore PA, Ruben SM, LaFleur DW, Shi Y, Rosen CA, Olsen H;

Ebner R, Brewer LA;

```
XX WPI; 2002-599716/64.
DR N-PSDB; ABQ92573.
XX
XX New polynucleotides and polypeptides useful for diagnosing, prognosing,
PT treating or preventing e.g. neurodegenerative, central nervous system,
PT autoimmune, respiratory, reproductive, or inflammatory diseases or
PT disorders
XX
XX Claim 11; Fig 1; 785pp; English.
XX
XX The invention relates to novel genes (ABQ92553-ABQ92607) and proteins
CC (ABP62013-ABP62153) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
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XX Sequence 303 AA;
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XX Query Match 99.6%; Score 1469; DB 23; Length 303;
XX Best Local Similarity 100.0%; Pred. No. 1.5e-121;
XX Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX 208 VATNSAGHRESRAARVSIQEPDYTEPVELLAVRIQLENVTLNPDPAEGPKPPAVWLX 267
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XX 241 WKVSGPXLPLNLTTPCSGPRLPREARELRGRRNTG 276
XX 268 WKVSGPXLPLNLTTPCSGPRLPREARELRGRRNTG 303
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XX RESULT 2
XX AAY12934
XX ID AAY12934 standard; Protein; 304 AA.
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XX AC AAY12934;
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XX 17-JUN-1999 (first entry)
XX
XX Amino acid sequence of a human secreted peptide.
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XX Human secreted protein; cancer; immune disorder; infection;
XX inflammatory disorder; skin disorder; tumour; atherosclerosis;
XX restenosis; autoimmune disorder; Alzheimer's disease;
XX peripheral neuropathy; trauma; spinal cord injury; allergy;
XX hematopoietic disorder; skeletal disorder; neurological disorder;
XX arthritic disorder; asthma; immunodeficiency disease; AIDS;
XX transplant rejection; ss.
XX
XX Homo sapiens.
XX
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XX Key Location/Qualifiers
XX Peptide 1...27
XX Protein /note= "signal peptide"
XX /note= "secreted protein"
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XX WO9911293-A1.
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XX 11-MAR-1999.
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XX 03-SEP-1998; 98WO-US18360.
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XX 12-SEP-1997; 97US-0058974.
XX 05-SEP-1997; 97US-0057626.
XX 05-SEP-1997; 97US-0057663.
XX 05-SEP-1997; 97US-0057669.
XX 12-SEP-1997; 97US-0058666.
XX 12-SEP-1997; 97US-0058667.
XX 12-SEP-1997; 97US-0058973.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Brewer LA, Ebner R, Lafleur DW, Moore PA, Olsen HS;
XX Rosen GA, Ruben SM, Shi Y;
XX
XX WPI; 1999-204988/17.
XX N-PSDB; AAX51721.
XX
XX New isolated human genes and the secreted polypeptides they encode
XX - useful for diagnosis and treatment of e.g. neurological disorders,
XX tumours, immune disorders, inflammation or haematological disorders
XX
XX Claim 11; Page 190-191; 215pp; English.
XX
XX AAY12914-68 represent human secreted proteins. The polypeptides and
XX their corresponding polynucleotides are useful for preventing,
XX treating or ameliorating medical conditions, e.g. by protein or gene
XX therapy. Pathological conditions can also be diagnosed by determining the
XX the amount of the new polypeptides in a sample or by determining the
XX presence of mutations in the new polynucleotides. Specific uses are
XX described for each polynucleotide, based on which tissues they are
XX most highly expressed in, and include developing products for the
XX diagnosis or treatment of cancer, immune disorders, infection,
XX inflammatory disorders, skin disorders, tumours, atherosclerosis,
XX restenosis, autoimmune disorders, Alzheimer's disease, peripheral
XX neuropathies, trauma, spinal cord injuries, allergy, hematopoietic
XX disorders, skeletal disorders, neurological disorders, arthritic
XX disorders, asthma, immunodeficiency diseases, AIDS and transplant
XX rejection. The polypeptides are also useful for identifying their
XX binding partners.
XX
XX Sequence 304 AA;
XX
XX Query Match 99.6%; Score 1469; DB 20; Length 304;
XX Best Local Similarity 100.0%; Pred. No. 1.5e-121;
XX Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX 1 QDSPPPQILVHPDQLFQGGPFARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHLLPDGT 60
XX 28 QDSPPPQILVHPDQLFQGGPFARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHLLPDGT 87
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XX 61 LLLLOPPARGHAHDGQALSTDLGVYTCEASNRIGTAVSRGARLSVAVLREDFOIQPRDMV 120
XX 88 LLLLOPPARGHAHDGQALSTDLGVYTCEASNRIGTAVSRGARLSVAVLREDFOIQPRDMV 147
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XX 121 AVVGEQFTLECGPPWGHPEPTVSWWKGKPLALQPGHRTVSGSLLMARAEKSDXTYMC 180
XX 148 AVVGEQFTLECGPPWGHPEPTVSWWKGKPLALQPGHRTVSGSLLMARAEKSDXTYMC 207
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XX 208 VATNSAGHRESRAARVSIQEPDYTEPVELLAVRIQLENVTLNPDPAEGPKPPAVWLX 267
XX
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Db 239 VATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLLNPDPAEGFKPRPAVWLS 298
 QY 241 WKVSGP 246
 Db 299 WKVSGP 304

RESULT 4
 ID AAY41716 standard; Protein; 985 AA.
 XX AAY41716
 AC AAY41716;
 DT 07-DEC-1999 (first entry)
 XX Human PRO860 protein sequence.
 DE Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
 KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
 KW secreted protein; transmembrane protein.
 XX Homo sapiens.
 OS WO9946281-A2.
 XX 16-SEP-1999.
 XX 08-MAR-1999; 99WO-US05028.
 XX 10-MAR-1998; 98US-0077450.
 PR 11-MAR-1998; 98US-0077632.
 PR 11-MAR-1998; 98US-0077641.
 PR 11-MAR-1998; 98US-0077643.
 PR 12-MAR-1998; 98US-0077791.
 PR 13-MAR-1998; 98US-0078004.
 PR 17-MAR-1998; 98US-0040220.
 PR 20-MAR-1998; 98US-0078886.
 PR 20-MAR-1998; 98US-0078910.
 PR 20-MAR-1998; 98US-0078936.
 PR 20-MAR-1998; 98US-0078933.
 PR 25-MAR-1998; 98US-0079294.
 PR 26-MAR-1998; 98US-0079656.
 PR 27-MAR-1998; 98US-0079664.
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 PR 27-MAR-1998; 98US-0079728.
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 PR 31-MAR-1998; 98US-0080105.
 PR 31-MAR-1998; 98US-0080107.
 PR 31-MAR-1998; 98US-0080165.
 PR 31-MAR-1998; 98US-0080194.
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 PR 01-APR-1998; 98US-0080333.
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 PR 08-APR-1998; 98US-0081049.
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 PR 21-APR-1998; 98US-0082568.
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 PR 22-MAY-1998; 98US-0086392.
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 PR 22-MAY-1998; 98US-0086486.
 PR 28-MAY-1998; 98US-0087098.
 PR 28-MAY-1998; 98US-0087106.
 PR 30-JUL-1998; 98US-0087208.
 PR 11-SEP-1998; 98US-0094651.
 XX 98US-0100038.
 PA (GETH) GENENTECH INC.
 XX Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
 PI WPI; 1999-551358/46.
 XX N-PSDB; AAZ34069.
 DR
 DR
 XX
 PT New secreted and transmembrane polypeptides and their polynucleotides,
 PT useful for treating blood coagulation disorders, cancers and cellular
 PT adhesion disorders -
 XX
 PS Claim 12; Fig 77; 530pp; English.
 XX
 CC The present invention describes secreted and transmembrane polypeptides
 CC and their polynucleotides. The nucleotide sequences are useful as
 CC sources of probes, primers, for chromosome mapping, and for generation
 CC of antisense sequences. They can also be used to create transgenic
 CC animals. The proteins can be used to treat a variety of diseases and
 CC disorders, depending on their function. Diseases that may be treated
 CC include blood coagulation disorders, cancers and cellular adhesion
 CC disorders. They may also be used to raise antibodies. AAZ33891 to
 CC AAZ34338, and AA41685 to AA41774 represent polynucleotide and
 CC polypeptide sequence given in the exemplification of the present
 CC invention.
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 SQ Sequence 985 AA;
 Query Match 88.9%; Score 1311; DB 20; Length 985;

Best Local Similarity 98.8%; Pred. No. 5.7e-107;	
Matches 243; Conservative 1; Mismatches 2; Indels 0; Gaps 0;	
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Db	6 QDPPQLVHPQDQLFQPGPARMSCQASGPPPTIRWLLNGQLSMVPPDPHLLPDGT 65
Qy	61 LLLQLPPARGHAHQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLRDFQIQPRDMV 120
Db	66 LLLQLPPARGHAHQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLRDFQIQPRDMV 125
Qy	121 AVVGEQFTLSCGPPWGHPEPTVSWKDGKPLALQGRHTVSGGSLLMARAESDXTYMC 180
Db	126 AVVGEQFTLSCGPPWGHPEPTVSWKDGKPLALQGRHTVSGGSLLMARAESDXTYMC 185
Qy	181 VATNSAGHRSEARARVSIQEPQDYTEPVELLAVRIQLENTVLLNPPDPAEGPKRPAYWLX 240
Db	186 VATNSAGHRSEARARVSIQEPQDYTEPVELLAVRIQLENTVLLNPPDPAEGPKRPAYWLX 245
Qy	241 WKVSGP 246
Db	246 WKVSGP 251
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AAB44272	
ID	AAB44272 standard; Protein; 985 AA.
XX	AAB44272;
AC	08-FEB-2001 (first entry)
DT	Human PRO860 (UNQ421) protein sequence SEQ ID NO:211.
DE	Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;
KW	expressed sequence tag; detection; cancer.
KW	
XX	Homo sapiens.
OS	WC2000053756-A2.
PN	14-SEP-2000.
XX	18-FEB-2000; 2000WO-US04341.
XX	08-MAR-1999; 99WO-US05028.
PR	12-MAR-1999; 99US-0123957.
PR	29-MAR-1999; 99US-0126773.
PR	21-APR-1999; 99US-0130232.
PR	28-APR-1999; 99US-0131445.
PR	14-MAY-1999; 99US-0134287.
PR	23-JUN-1999; 99US-0141037.
PR	26-JUL-1999; 99US-0145698.
PR	29-OCT-1999; 99US-0162506.
PR	30-NOV-1999; 99WO-US28313.
PR	02-DEC-1999; 99WO-US28551.
PR	02-DEC-1999; 99WO-US28565.
PR	16-DEC-1999; 99WO-US30095.
PR	30-DEC-1999; 99WO-US31243.
PR	05-JAN-2000; 99WO-US31274.
PR	06-JAN-2000; 2000WO-US00219.
PR	06-JAN-2000; 2000WO-US00277.
PR	06-JAN-2000; 2000WO-US00376.
XX	(GETH) GENENTECH INC.
XX	Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI	Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI	Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI	Klajavin LJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;
PI	Shelton DJ, Stewart TA, Tumas D, Williams PM, Wood WI;
XX	WPI; 2000-611443/58.

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PR 07-OCT-1998; 98WO-US211141.
PR 20-NOV-1998; 98WO-US24855.
PR 05-JAN-1999; 99WO-US00106.
PR 08-MAR-1999; 99WO-US05028.
PR 10-MAR-1999; 99WO-US05190.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 30-NOV-1999; 99WO-US28313.
PR 02-DEC-1999; 99WO-US28551.
PR 16-DEC-1999; 99WO-US28565.
PR 30-DEC-1999; 99WO-US30095.
PR 30-DEC-1999; 99WO-US31243.
PR 05-JAN-2000; 99WO-US1274.
PR 06-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03365.
PR 18-FEB-2000; 2000WO-US04341.
PR 24-FEB-2000; 2000WO-US05004.
PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 24-AUG-2000; 2000WO-US23328.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 22-MAR-2001; 2001WO-US09552.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 17-OCT-1997; 97US-062250P.
PR 03-NOV-1997; 97US-064249P.
PR 13-NOV-1997; 97US-065311P.
PR 21-NOV-1997; 97US-066364P.
PR 10-MAR-1998; 98US-077450P.
PR 11-MAR-1998; 98US-077632P.
PR 11-MAR-1998; 98US-077641P.
PR 11-MAR-1998; 98US-077649P.
PR 12-MAR-1998; 98US-077791P.
PR 13-MAR-1998; 98US-078004P.
PR 20-MAR-1998; 98US-078886P.
PR 20-MAR-1998; 98US-078910P.
PR 20-MAR-1998; 98US-078936P.
PR 20-MAR-1998; 98US-078939P.
PR 25-MAR-1998; 98US-079294P.
PR 26-MAR-1998; 98US-079656P.
PR 27-MAR-1998; 98US-079663P.
PR 27-MAR-1998; 98US-079664P.
PR 27-MAR-1998; 98US-079689P.
PR 27-MAR-1998; 98US-079728P.
PR 27-MAR-1998; 98US-079786P.
PR 30-MAR-1998; 98US-079920P.
PR 30-MAR-1998; 98US-079923P.
PR 26-MAY-1981; 81US-0267213.
PR 17-MAR-1998; 98US-0040220.
PR 26-JUN-1998; 98US-0105413.
PR 07-OCT-1998; 98US-0168978.
PR 02-NOV-1998; 98US-0184216.
PR 06-NOV-1998; 98US-0187368.
PR 07-DEC-1998; 98US-0202054.
PR 22-DEC-1998; 98US-0218517.
PR 05-MAR-1999; 99US-0254465.
PR 10-MAR-1999; 99US-0265686.
PR 12-APR-1999; 99US-0284291.
PR 14-MAY-1999; 99US-0311832.

PR 14-MAY-1999; 99US-0380137.
PR 25-AUG-1999; 99US-0380138.
PR 25-AUG-1999; 99US-0380142.
PR 08-NOV-2000; 2000US-0709238.
PR 27-NOV-2000; 2000US-0723749.
PR 20-DEC-2000; 2000US-0747259.
PR 22-MAR-2001; 2001US-0816744.
PR 22-MAR-2001; 2001US-0816920.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 01-JUN-2001; 2001US-0872035.
PR 05-JUN-2001; 2001US-0874503.
PR 14-JUN-2001; 2001US-0882636.
PR 19-JUN-2001; 2001US-0886342.
PR 30-JUL-2001; 2001US-0918585.
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi A, Baker KP, Botstein D, Desnoyers L, Eaton D;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kijavini IJ, Kuo SS, Napier MA, Pan J, Paoni NP, Roy MA;
PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
XX WPI; 2003-288163/28.
DR N-PSDB; ABX92441.
XX
XX Novel secreted and transmembrane polypeptides and polynucleotides
PT encoding them useful for treating cancer, kidney diseases, bone,
PT cartilage disorders and immune deficiencies -
XX
XX Claim 12; Fig 77; 459pp; English.
XX
XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The
CC PRO polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for
CC linking bioactive molecules to cells expressing PRO polypeptides,
CC for modulating biological activities of cells expressing PRO
CC polypeptides, and for identifying agonists or antagonists. The
CC bioactive molecule maybe a toxin, radiolabel or antibody, and causes
CC apoptosis or death of the cell. The PRO polypeptides are useful for
CC treating immune disorders, diabetes or hyper- or hypo-insulinaemia,
CC cardiac insufficiency, nervous system disorders, kidney disorders,
CC bone and cartilage disorders or arthritis, tumours, and wound healing.
CC The polynucleotide sequences encoding PRO polypeptides are useful as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of antisense RNA and DNA, in the preparation of PRO polypeptides, for
CC generating transgenic animals or knockout animals, for the genetic
CC analysis of individuals with genetic disorders, and in gene therapy.
CC ABU61071-ABU61164 represent the human PRO polypeptides of the
CC invention.
CC Note: The sequence data for this patent, was obtained in electronic
CC format directly from the USPTO web site at
CC seqdata.uspto.gov/psipsDIDentry.html.
XX
XX Sequence 985 AA;
SQ
Query Match 88.9%; Score 1311; DB 24; Length 985;
Best Local Similarity 98.8%; Pred. No. 5,7e-107;
Matches 243; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 QDSPPQILVHPQDLFOGPGPARMSCASCOPPTIRWLNGQPLSVPPDPHLLPDGT 60
Db 6 QDSPPQILVHPQDLFOGPGPARMSCASCOPPTIRWLNGQPLSVPPDPHLLPDGT 65
Qy 61 LLLQLPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRCARLSVAVLRDFQIQPRDMV 120
Db 66 LLLQLPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRCARLSVAVLRDFQIQPRDMV 125
Qy 121 AVVGEQFTLECGPPWGHPEPTVSNWKGKPLAQPGHRTVSGGSLLMARAEKSDGYTMC 180
Db 126 AVVGEQFTLECGPPWGHPEPTVSNWKGKPLAQPGHRTVSGGSLLMARAEKSDGYTMC 185
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[illegible]

RESULT 7	
ABB97310	
ID	ABB97310 standard; Protein; 1007 AA.
XX	
XX	
.AC	ABB97310;
XX	
DT	27-JUN-2002 (first entry)
XX	
DE	Novel human protein SEQ ID NO: 578.
XX	
KW	Human; antianaemic; vulnery; antiinflammatory; immunomodulator;
KW	antiinfertility; cerebroprotective; cytosatic; rheumatic; gene therapy;
KW	neuroprotective; antiparkinsonian; protein therapy; EST;
KW	expressed sequence tag.

XX Homo sapiens.
XX
PN WO200223660-A2.

PD 21-MAR-2002.

PF 10-SEP-2001; 2001WO-US26015.

PR 11-SEP-2000; 2000US-0659671.

PA (HYSE-) HYSEQ INC.

Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;

DR WPI; 2002-292408/33.

[illegible]

PT encoded polypeptide such as cancer and multiple sclerosis -

PS Example 2; SEQ ID NO 578; 509pp; English.

The present invention provides the protein and coding sequences of 444 novel human proteins. These were isolated from expressed sequences tags (ESTs). They can be used to stimulate cell growth, to regulate haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth e.g. in burn treatment, to regulate the immune system e.g. to treat multiple sclerosis, to regulate activin or inhibin e.g. to treat infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke and cancer, to screen for drugs, to treat inflammatory conditions e.g. rheumatoid arthritis, and to treat nervous system disorders e.g. Parkinson's disease. The present sequence is a protein of the invention.

Sequence 1007 AA:

Query Match 88.9%: Score 1311: DB 23: Length 1007:

Best local similarity 50.00, P-Val: 3.0e-107,
Matches 243; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy	1	QDSPPOILVHPDQLFGPGPARMSCRASGQPPTIRWLLNGQPLSMVPDPHILLPDGT	60
		:	
Db	28	QDSPPOILVHPDQLFGPGPARMSCRASGQPPTIRWLLNGQPLSMVPDPHILLPDGT	87

Qy	61 LLLLOPPARGHAHQALSTDLGVVYTCESNRLGTAVSRGARLSVAVLREDFIQPRDMV 120
D_b	88 LLLLOPPARGHAHQALSTDLGVVYTCESNRLGTAVSRGARLSVAVLREDFIQPRDMV 147

QY	121	AVVGEQFTLECGP	PMWGHPEPTV	WMWCKGKPLAL	QGRHTVSGSL	LMARAEKSD	EYTYMC	180
DB	148	AVVGEQFTLECGP	PMWGHPEPTV	WMWCKGKPLAQ	QGRHTVSGSL	LMARAEKSD	EYTYMC	207
QY	181	VATNSAGHRESRA	ARVSIQEPQDY	TEPVVELLA	AVRIQLENTV	LLNPDPAEG	KPRPAWLX	240
DB	208	VATNSAGHRESRA	ARVSIQEPQDY	TEPVVELLA	AVRIQLENTV	LLNPDPAEG	KPRPAWLX	267
QY	241	WKVSGP	246					
DB	268	WKVSGP	273					

RESULT 8

AAU99419

ID AAU99419 standard; Protein; 1104 AA.

AC AAU99419;

DT 07-OCT-2002 .(first entry)

Human ECSM4 protein.

Human; endothelial cell-specific molecule 4; ECSM4; neovasculature;
imaging vascular endothelium; proliferative disease; cancer;
poorly; diabetic retinopathy; atherosclerosis; menorrhagia;
endothelial damage; tumour neovasculature; cardiac disease;
endometriosis; hypoxic condition; angiogenesis; cytostatic;
cardiant.

OS Homo sapiens.

WO200236771-A2

PD 10-MAY-2002.

06-NOV-2001: 2001WO-GB04906.

PR 06-NOV-2000: 2000US-245566P.

FR 07-MAX-2001; 2001US-27366ZF.
XX

XX
XX
FBI / MEDICAL CANCELS TECHNOLOGY DIV.
(THUR / 11:00 AM)

XX
XX
BICKELL N, HUMPHREYS D,

DR WF1; 2002-308120/34.
DR N-PSDB: ABK87137.

PT Novel endothelial cell-specific molecule polypeptide 1 or 4, useful for
AA imaging, diagnosing and treating a condition involving vascular
PT endothelium e.g. cancer, cardiac disease, endometriosiis, diabetes -
PT

PS Claim 53; Fig 12; 248pp; English.

The present invention relates to endothelial cell-specific molecule 4 (ECSM4), and the polynucleotide sequences encoding it. The ECSM4 proteins are useful for imaging vascular endothelium in the body of an individual, and for diagnosing and treating a proliferative disease or condition involving the vascular endothelium (preferably, neovasculature) such as cancer, psoriasis, diabetic retinopathy, atherosclerosis or menorrhagia. The ECSM4 proteins are also useful in the manufacture of diagnostic or prognostic agent for such conditions. The proteins are also useful for detecting endothelial damage or activation, detecting a tumour or tumour neovasculature, cardiac disease, or endotheliosis by detecting the amount of ECSM4 present in a sample. The polynucleotide sequences encoding ECSM4 are useful in gene therapy for treating a hypoxic condition such as cancer, cardiac disease, endometriosis or atherosclerosis and in the manufacture of medicaments for treating the above disease. The sequences are useful for modulating angiogenesis in an individual. The present sequence represents human ECSM4 protein.

Sequence 1104 AA;

Query Match 88.9%; Score 1311; DB 23; Length 1104;
Best Local Similarity 98.8%; Pred. No. 6.5e-107;
Matches 243; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QDSPPQILVHPDQQLFQGGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHLLPDGT 60
Db 28 QDSPPQILVHPDQQLFQGGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHLLPDGT 87

Qy 61 LLLLOPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLRDFQIQPRDMV 120
Db 88 LLLLOPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLRDFQIQPRDMV 147

Qy 121 AVVGEQFTLECGPPWGHPEPTVSWKDGKPLALQPGRHTVSGSLLMARAESDXTYMC 180
Db 148 AVVGEQFTLECGPPWGHPEPTVSWKDGKPLALQPGRHTVSGSLLMARAESDXTYMC 207

Qy 181 VATNSAGHRESRAARVSIQEPQDYTEPVELLAIVRIQLENVTLLNPDPAEGPKPPAVWLX 240
Db 208 VATNSAGHRESRAARVSIQEPQDYTEPVELLAIVRIQLENVTLLNPDPAEGPKPPAVWLX 267

Qy 241 WKVSGP 246
Db 268 WKVSGP 273

RESULT 9
AAB95515
ID AAB95515 standard; Protein; 792 AA.

XX AC AAB95515;
XX DT 26-JUN-2001 (first entry)
XX DE Human protein sequence SEQ ID NO:18085.
XX KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.
XX OS Homo sapiens.
XX XX EP1074617-A2.
XX PD 07-FEB-2001.
XX PF 28-JUL-2000; 2000EP-0116126.
XX PR 29-JUL-1999; 99JP-0248036.
XX PR 27-AUG-1999; 99JP-0300253.
XX PR 11-JAN-2000; 2000JP-0118776.
XX PR 02-MAY-2000; 2000JP-0183767.
XX PR 09-JUN-2000; 2000JP-0241899.
XX PA (HELI-) HELIX RES INST.
XX PA Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
XX PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX XX WPI; 2001-318749/34.
XX XX Primer sets for synthesizing polynucleotides, particularly the 5602
XX PT full-length cDNAs defined in the specification, and for the detection
XX PT and/or diagnosis of the abnormality of the proteins encoded by the
XX PT full-length cDNAs -
XX XX Claim 8; SEQ ID 18085; 2537pp + CD ROM; English.
XX PS The present invention describes primer sets for synthesizing 5602
XX CC full-length cDNAs defined in the specification. Where a primer set
XX CC comprises: (a) an oligo-dr primer and an oligonucleotide complementary
XX CC to the complementary strand of a polynucleotide which comprises one of
XX CC the 5602 nucleotide sequences defined in the specification, where the
XX CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
XX CC of an oligonucleotide comprising a sequence complementary to the

CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence and the oligonucleotide is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.

XX Sequence 792 AA;

Query Match 88.3%; Score 1303; DB 22; Length 792;
Best Local Similarity 98.4%; Pred. No. 2.2e-106;
Matches 242; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QDSPPQILVHPDQQLFQGGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHLLPDGT 60
Db 28 QDSPPQILVHPDQQLFQGGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHLLPDGT 87

Qy 61 LLLLOPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLRDFQIQPRDMV 120
Db 88 LLLLOPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLRDFQIQPRDMV 147

Qy 121 AVVGEQFTLECGPPWGHPEPTVSWKDGKPLALQPGRHTVSGSLLMARAESDXTYMC 180
Db 148 AVVGEQFTLECGPPWGHPEPTVSWKDGKPLALQPGRHTVSGSLLMARAESDXTYMC 207

Qy 181 VATNSAGHRESRAARVSIQEPQDYTEPVELLAIVRIQLENVTLLNPDPAEGPKPPAVWLX 240
Db 208 VATNSAGHRESRAARVSIQEPQDYTEPVELLAIVRIQLENVTLLNPDPAEGPKPPAVWLX 267

Qy 241 WKVSGP 246
Db 268 WKVSGP 273

RESULT 10
AAG67430
ID AAG67430 standard; Protein; 792 AA.

XX AC AAG67430;
XX DT 26-NOV-2001 (first entry)
XX DE Amino acid sequence of a human protein kinase/protein phosphatase.
XX XX Human; protein kinase; protein phosphatase; signal transduction;
XX KW intracellular signalling pathway.
XX OS Homo sapiens.
XX XX WO200109345-A1.
XX PD 08-FEB-2001.
XX PF 28-JUL-2000; 2000WO-JP05060.
XX PR 29-JUL-1999; 99JP-0248036.
XX PR 18-OCT-1999; 99US-0159590.
XX PR 11-JAN-2000; 2000JP-0118776.
XX PR 17-FEB-2000; 2000US-0183322.
XX PR 02-MAY-2000; 2000JP-0183767.
XX XX (HELI-) HELIX RES INST.
XX PA Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
XX PI

PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S;
XX Senoo C, Nezu J;
DR WPI: 2001-564736/63.
DR N-PSDB; AAH78073.

XX New genes encoding protein kinase and protein phosphatase, useful* for
PT identifying modulators which can be used to treat human or animal
PT disorders associated with the expression or function of these enzymes -
XX.

PS Claim 2; Page 175-180; 336pp; Japanese.

XX The present sequence represents a human protein kinase/protein
CC phosphatase. The polypeptides are expected to participate in signal
CC transduction in cells. The kinase phosphatases are connected with
CC intracellular signalling pathways. Antisense oligonucleotides and
CC compounds identified by screening (agonists or antagonists) can be
CC used to treat human or animal disorders associated with the expression
CC or function of the protein. In addition, the polypeptides may be used
CC as target molecules for drug development.

XX Sequence 792 AA;

Query Match 88.3%; Score 1303; DB 22; Length 792;
Best Local Similarity 98.4%; Pred. No. 2.2e-106;
Matches 242; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 QDSPPQILVHPQDQLFQGGPARMSCRASGQPPPTIRWLLNQPLSMVPPDPHLLPDGT 60
DB 28 QDSPPQILVHPQDQLFQGGPARMSCRASGQPPPTIRWLLNQPLSMVPPDPHLLPDGT 87
QY 61 LLLLOPPARGHADGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLRDFQIOPRDMV 120
DB 88 LLLLOPPARGHADGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLRDFQIOPRDMV 147
QY 121 AVVGEQFTLECGPPMGHPPTVSWWKGKPLALQPGRTVSGSLLMARAESDXTYMC 180
DB 148 AVVGEQFTLECGPPMGHPPTVSWWKGKPLALQPGRTVSGSLLMARAESDXTYMC 207
QY 181 VATNSAGHRESRAARVSIQEPDYTEPVVELLAVRIQLENVTLNPDPAEGPKPRPAVWLX 240
DB 208 VATNSAGHRESRAARVSIQEPDYTEPVVELLAVRIQLENVTLNPDPAEGPKPRPAVWLX 267
QY 241 WKVSGP 246
DB 268 WKVSGP 273

RESULT 11
AAU99420
ID AAU99420 standard; Protein; 1015 AA.

XX AAU99420;

XX 07-OCT-2002 (first entry)

XX Mouse ECSM4 protein #1.

XX Mouse; endothelial cell-specific molecule 4; ECSM4; neovasculature;
KW imaging vascular endothelium; proliferative disease; cancer;
KW psoriasis; diabetic retinopathy; atherosclerosis; hemorrhagia;
KW endothelial damage; tumour neovasculature; cardiac disease;
KW endometriosis; hypoxic condition; angiogenesis; cytostatic;
KW cardiant.

XX Mus sp.

XX WO200236771-A2.

XX 10-MAY-2002.

XX 06-NOV-2001; 2001WO-GB04906.

XX

PR 06-NOV-2000; 2000US-245566P.
PR 07-MAR-2001; 2001US-273662P.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.

XX Bicknell R, Huminiacki L;

XX WPI; 2002-508120/54.

XX N-PSDB; ABK87138.

PT Novel endothelial cell-specific molecule polypeptide 1 or 4, useful for
PT imaging, diagnosing and treating a condition involving vascular
PT endothelium e.g. cancer, cardiac disease, endometriosis, diabetes -
XX Disclosure; Fig 13; 248pp; English.

XX The present invention relates to endothelial cell-specific molecule 4
CC (ECSM4), and the polynucleotide sequences encoding it. The ECSM4
CC proteins are useful for imaging vascular endothelium in the body of
CC an individual, and for diagnosing and treating a proliferative
CC disease or condition involving the vascular endothelium (preferably,
CC neovasculature) such as cancer, psoriasis, diabetic retinopathy,
CC atherosclerosis or hemorrhagia. The ECSM4 proteins are also useful in
CC the manufacture of diagnostic or prognostic agent for such conditions.
CC The proteins are also useful for detecting endothelial damage or
CC activation, detecting a tumour or tumour neovasculature, cardiac
CC disease, or endometriosis by detecting the amount of ECSM4 present in
CC a sample. The polynucleotide sequences encoding ECSM4 are useful in
CC gene therapy for treating a hypoxic condition such as cancer, cardiac
CC disease, endometriosis or atherosclerosis and in the manufacture of
CC medicaments for treating the above disease. The sequences are useful
CC for modulating angiogenesis in an individual. The present sequence
CC represents a mouse ECSM4 protein.

XX Sequence 1015 AA;

Query Match 69.8%; Score 1029.5; DB 23; Length 1015;
Best Local Similarity 78.5%; Pred. No. 4.3e-82;
Matches 193; Conservative 20; Mismatches 32; Indels 1; Gaps 1;

QY 2 DSSPQILVHPQDQLFQGGPARMSCRASGQPPPTIRWLLNQPLSMVPPDPHLLPDGT 61
DB 39 DSSPQILVHPQDQLFQGGPARMSCRASGQPPPTIRWLLNQPLSMATPDLHYLLPDGT 98
QY 62 LLLLOPPARGHADGQ-ALSTDLGVYTCEASNRLGTAVSRGARLSVAVLRDFQIOPRDMV 120
DB 99 LLLHRPSVQGRPDQDQNLISAILGVYTCEASNRLGTAVSRGARLSVAVLRDFQIOPRDTV 158
QY 121 AVVGEQFTLECGPPMGHPPTVSWWKGKPLALQPGRTVSGSLLMARAESDXTYMC 180
DB 159 AVVGESLVLECGPPMGYPKPSVSWWKGKPLVLPQGRVTVSGDSLMSVRAEKNDSTYMC 218
QY 181 VATNSAGHRESRAARVSIQEPDYTEPVVELLAVRIQLENVTLNPDPAEGPKPRPAVWLX 240
DB 219 MATNNAGQRESRAARVSIQESQDHKEHLELLAVRIQLENVTLNPDPAEGPKPRPAVWLX 278
QY 241 WKVSGP 246
DB 279 WKVSGP 284

RESULT 12

AAU00500
ID AAU00500 standard; Protein; 934 AA.

XX AAU00500;

XX 18-JUL-2001 (first entry)

XX Human TANGO 330 form 1 protein.

XX Human; TANGO 315; clone jthaa060g22; TANGO 330; TANGO 437; TANGO 480;
KW cellular process regulator; gene therapy; adrenal gland; cancer;

KW	Roundabout; adrenal cortex; hypoadrenalism; hyperadrenalism; neoplasia;
KW	cell proliferative disorder; neurological disorder; Alzheimer's disease.
XX	Homo sapiens.
XX	
XX	
PH	Key Location/Qualifiers
FT	Domain 1..393
FT	/label= Extracellular_domain
FT	Misc-difference 1
FT	/note= "Alternatively this residue is Asp due to species variation"
FT	Misc-difference 2
FT	/note= "Alternatively this residue is Ser due to species variation"
FT	Misc-difference 3
FT	/note= "Alternatively this residue is Val due to species variation"
FT	Modified-site 29..34
FT	/note= "N-myristylation site"
FT	Modified-site 37..42
FT	/note= "N-myristylation site"
FT	Modified-site 44..46
FT	/note= "Protein kinase C phosphorylation site"
FT	Modified-site 48..53
FT	/note= "N-myristylation site"
FT	Misc-difference 53
FT	/note= "Alternatively this residue is Lys due to species variation"
FT	Modified-site 54..59
FT	/note= "N-myristylation site"
FT	Domain 78..136
FT	/label= Ig-like_domain
FT	Modified-site 126..132
FT	/note= "Tyrosine kinase phosphorylation site"
FT	Modified-site 130..135
FT	/note= "N-myristylation site"
FT	Modified-site 151..154
FT	/note= "Casein kinase II phosphorylation site"
FT	Modified-site 173..176
FT	/note= "Aen is N-glycosylated"
FT	Modified-site 194..196
FT	/note= "Protein kinase C phosphorylation site"
FT	Modified-site 221..226
FT	/note= "N-myristylation site"
FT	Modified-site 239..244
FT	/note= "N-myristylation site"
FT	Modified-site 254..256
FT	/note= "Protein kinase C phosphorylation site"
FT	Modified-site 282..284
FT	/note= "Protein kinase C phosphorylation site"
FT	Modified-site 287..290
FT	/note= "Aen is N-glycosylated"
FT	Modified-site 304..309
FT	/note= "N-myristylation site"
FT	Modified-site 316..319
FT	/note= "Aen is N-glycosylated"
FT	Modified-site 323..326
FT	/note= "Aen is N-glycosylated"
FT	Modified-site 331..334
FT	/note= "Casein kinase II phosphorylation site"
FT	Modified-site 352..357
FT	/note= "N-myristylation site"
FT	Modified-site 391..393
FT	/note= "Protein kinase C phosphorylation site"
FT	Domain 394..417
FT	/label= Transmembrane_domain
FT	Modified-site 411..416
FT	/note= "N-myristylation site"
FT	Domain 418..934
FT	/label= Cytoplasmic_domain
FT	Modified-site 434..437
FT	/note= "Casein kinase II phosphorylation site"
FT	Modified-site 455..457

Db 178 DVMVAVGEPAVMECOPPRGHPEPTISWKXGSPLEDDKDERITIRGGKLMITYTRKSDAGK 237
Qy 178 YMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRI 215
Db 238 YVCVGTNNVGERESEVAELTVLERPSFVKRPSNLATV 275

Search completed: January 30, 2004, 15:54:43
Job time : 36.7513 secs

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OM protein - protein search, using sw model

Run on: January 30, 2004, 15:53:19 ; Search time 13.8238 Seconds
(without alignments)
844.758 Million cell updates/sec

Title: US-10-047-021-86_COPY_28_303
Perfect score: 1475
Sequence: 1 QDSPQILVHPDQLFQGP.....SGPRLPREARELGGRRNTG 276

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/prodata/1/1aa/5B-COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A-COMB.pep:*
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5: /cgn2_6/prodata/1/1aa/PCTUS-COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	446.5	30.3	1651	US-09-540-245A-18	Sequence 18, Appl
2	395.5	26.8	1395	US-09-540-245A-15	Sequence 15, Appl
3	354.5	24.0	1297	US-09-540-245A-17	Sequence 17, Appl
4	345	23.4	1381	US-09-540-245A-16	Sequence 16, Appl
5	251	17.0	630	US-08-752-307B-14	Sequence 14, Appl
6	251	17.0	630	US-09-707-802-14	Sequence 14, Appl
7	251	17.0	630	US-09-991-326-14	Sequence 14, Appl
8	228	15.5	607	US-08-752-307B-12	Sequence 12, Appl
9	228	15.5	607	US-09-707-802-12	Sequence 12, Appl
10	228	15.5	607	US-09-991-326-12	Sequence 12, Appl
11	219	14.8	596	US-08-752-307B-13	Sequence 13, Appl
12	219	14.8	596	US-09-707-802-13	Sequence 13, Appl
13	219	14.8	596	US-09-991-326-13	Sequence 13, Appl
14	218.5	14.8	1501	US-08-447-464-3	Sequence 3, Appl
15	218.5	14.8	1501	US-08-716-679-3	Sequence 3, Appl
16	206.5	14.0	1911	US-08-348-006B-5	Sequence 5, Appl
17	206.5	14.0	1911	US-08-800-825A-5	Sequence 5, Appl
18	206.5	14.0	1911	US-09-158-657-5	Sequence 5, Appl
19	206.5	14.0	1911	PCT-US94-10166-5	Sequence 5, Appl
20	206	14.0	1447	US-09-041-886-25	Sequence 25, Appl
21	206	14.0	1447	PCT-US94-05277-2	Sequence 2, Appl
22	198.5	13.5	615	US-08-752-307B-9	Sequence 9, Appl
23	198.5	13.5	615	US-09-707-802-9	Sequence 9, Appl
24	198.5	13.5	615	US-09-991-326-9	Sequence 9, Appl
25	194.5	13.2	612	US-08-752-307B-11	Sequence 11, Appl
26	194.5	13.2	612	US-09-707-802-11	Sequence 11, Appl
27	194.5	13.2	612	US-09-991-326-11	Sequence 11, Appl

28	194.5	13.2	1268	4	US-08-506-296B-28	Sequence 28, Appl
29	192	13.0	1091	3	US-08-986-485-5	Sequence 5, Appl
30	191	12.9	1260	4	US-08-506-296B-21	Sequence 21, Appl
31	189	12.8	946	5	PCT-US95-08493-13	Sequence 13, Appl
32	188.5	12.8	1101	3	US-08-986-485-2	Sequence 2, Appl
33	186	12.6	416	4	US-09-638-649-1	Sequence 1, Appl
34	185	12.5	611	2	US-08-752-307B-10	Sequence 10, Appl
35	185	12.5	611	4	US-09-707-802-10	Sequence 10, Appl
36	185	12.5	611	4	US-09-991-326-10	Sequence 10, Appl
37	185	12.5	1253	4	US-08-506-296B-14	Sequence 14, Appl
38	175.5	11.9	1209	4	US-09-130-158A-2	Sequence 2, Appl
39	175	11.9	462	2	US-08-752-307B-7	Sequence 7, Appl
40	175	11.9	462	4	US-09-707-802-7	Sequence 7, Appl
41	175	11.9	462	4	US-09-991-326-7	Sequence 7, Appl
42	175	11.9	465	2	US-08-752-307B-5	Sequence 5, Appl
43	175	11.9	465	4	US-09-707-802-5	Sequence 5, Appl
44	175	11.9	465	4	US-09-991-326-5	Sequence 5, Appl
45	175	11.9	1266	4	US-08-506-296B-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-09-540-245A-18
; Sequence 18, Application US/09540245A
; Patent No. 6270984
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey
; APPLICANT: Kid, Thomas
; APPLICANT: Brose, Katja
; APPLICANT: Tessier-Lavigne, Marc
; TITLE OF INVENTION: Modulating Robo: Ligand Interactions
; FILE REFERENCE: B98-031-3
; CURRENT APPLICATION NUMBER: US/09/540,245A
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 60/065,544
; PRIOR FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: 60/081,057
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 18
; LENGTH: 1651
; TYPE: PRT
; ORGANISM: human
US-09-540-245A-18

Query Match 30.3%; Score 446.5; DB 3; Length 1651;
Best Local Similarity 41.7%; Pred. No. 7.7e-36;
Matches 91; Conservative 31; Mismatches 87; Indels 9; Gaps 2;

QY 1 QDSPQILVHPDQLFQGPGRMSCRASGQPPPIRMLNLCOPLSMWPPDPHH---LLP 57
DB 64 EDFPPIRVEHPSDLIVSGEPATLNCAGRPPTIETWYKGERVETDKDPRSHRMLLP 123
QY 58 DGTLLLOPPARGHAHDGQALSTDLGVVTCASNRLGTAVSRGARLSVAVLRDEFQIQPR 117
DB 124 SGLSFLR-----IVHGKSRPDEGVTVCVARNYLGAVSNASLEVAILLRDFRQPS 177
QY 118 DMVAVVGQFTLECPMPWGHPEPTVSWWKGKPLALQFGRHTVSGGSLIMARAESDXT 177
DB 178 DMVAVGPAVMCEQPPRGHPEPTISWKGKPLDGDKDERITIRGKLMITTRKSDACK 237
QY 178 YNCVATNSAGHRESRAARVSTQEPDYTEPVELLAVRI 215
DB 238 YVCVTNNVGERSESEVAELTVLERPSFVKRPSNLAVTV 275

RESULT 2
US-09-540-245A-15
; Sequence 15, Application US/09540245A
; Patent No. 6270984

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; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey
; APPLICANT: Kid, Thomas
; APPLICANT: Brose, Katja
; APPLICANT: Tessier-Lavigne, Marc
; TITLE OF INVENTION: Modulating Robo: Ligand Interactions
; FILE REFERENCE: B98-031-3
; CURRENT APPLICATION NUMBER: US/09/540,245A
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 60/065,544
; PRIOR FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: 60/081,057
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-540-245A-15

Query Match 26.8%; Score 395.5; DB 3; Length 1395;
Best Local Similarity 37.1%; Pred. No. 8.1e-31;
Matches 92; Conservative 35; Mismatches 100; Indels 21; Gaps 6;

Qy 1 QDSPPQILVHPDQDLFOGPGPARMSCRASGPPPTIRLLNGQPLSMVPPDPHLL-LPDG 59
Db 52 QYQSPRIIEHTDVLVKNKEPATLNCVKVEGPEPTIEWFKDGEVSTNEKSHRVQFKD 111
Qy 60 TLLILQPPARGHAHDGQALSTDLGVYTCESNRGLTAVSRGARSVAVLREDFOIQPRDM 119
Db 112 ALFFVTRTQWQKEQDG-----GEYWCXKRVQAVSRHASLQIAVLRRDPRVEPKDT 164
Qy 120 VAVVGEQTLSCGPPWGHPEPTVSWKDGKPL-----ALQGRHT-----VSGSLLMARAE 171
Db 165 RVAKGETALLCGPPKGPPEPTLWIKDGVPLDLKAMSGASSRVRIVDGNLLISNVE 224
Qy 172 KSDEXTVMCVATNSAGHRESRAARVSIQ-EPQDYTEPVELLAVRIQLENVTLNPDPAEG 230
Db 225 PIDEGNYKICIAQNLVGTRESSYAKLIVQVKPYFWKEPKD-----QVMLYGTATFHCVS 280
Qy 231 PKRPAVW 238
Db 281 DPPKVLW 288

RESULT 3
US-09-540-245A-17
; Sequence 17, Application US/09540245A
; Patent No. 6270984
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey
; APPLICANT: Kid, Thomas
; APPLICANT: Brose, Katja
; APPLICANT: Tessier-Lavigne, Marc
; TITLE OF INVENTION: Modulating Robo: Ligand Interactions
; FILE REFERENCE: B98-031-3
; CURRENT APPLICATION NUMBER: US/09/540,245A
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 60/065,544
; PRIOR FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: 60/081,057
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-540-245A-17

Query Match 24.0%; Score 354.5; DB 3; Length 1297;
Best Local Similarity 34.0%; Pred. No. 9.7e-27;
Matches 91; Conservative 31; Mismatches 102; Indels 46; Gaps 8;

Qy 5 PQILVHPDQDLFOGPGPARMSCRASGPPPTIRLLNGQPLSMVPPDPHLLPDGTL 64
Db 4 PRIIEHPMDTTPVKNDPFTFCNQAEQGNPTFTIQWFKDGRKLTDTGSHRIMLPAGGLPFL 63
Qy 65 QPPARGHAHDGQALSTDLGVYTCESNRGLTAVSRGARSVAVLREDFOIQPRDMVAVG 124
Db 64 KV-----IHSRR--ESDAGTYWCEAKNEFGVARSNATLQVAVLRDEFRLPEPANTRVAQ 116
Qy 125 EQFTLECGPPWGHPEPTVSWKDGKPLAQGR--HTVSGSLLMARAEKSDEXTVMCVA 182
Db 117 EVALMECCAPRGSPFQISWRKNGQTLNLVGNKRIRIVDGNLAIQARQSDDDGRYQCVV 176
Qy 183 TNSAGHRESRAARVS-----IQEPDYTEPVELLAV-----RIQLENVTLNPDPAEGPK 232
Db 177 KVVVGTRESATAFLKVHVRPFPLIRGPQNTAVVSSVVFQCR-----GGD 222
Qy 233 PRPAVWLXWVSGPXRLPNLTPCSPGRLP 262
Db 223 PLPDV--LWR-----RTASGGNMP 239
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Matches 96; Conservative 44; Mismatches 101; Indels 41; Gaps 11;

Qy 5 PQILVHPDQDLFOGPGPARMSCRASGPPPT--IRWLLNGQPL--SMVPPDPHLLPD-G 59
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Qy 60 TLLILQPPARGHAHDGQALSTDLGVYTCESNRGLTAVSRGARSVAVLREDFOIQPRDM 119
Db 87 SLFLLLKVNKGKNGKD-----SDAGAYYCVASNEHEGEVKSNEGSLKLAWLREDFVRPRTV 141
Qy 120 VAVVGEQTLSCGPPWGHPEPTVSWKDGKPLALQP--GRHTV--SGSLLMARAEKSDXT 177
Db 142 QALGGENAVLECSPPRGFPFVWSWRKDKELRIQDMPRYTLHSDGNLIIDPVDSDSGT 201
Qy 178 YMCVATNSAGHRESRAARVSI-----QEPDYTEPVELLAVRIQLENVTLNPDPAEG 230
Db 202 YQCVANNMVGERSVNSPARLSVFKEPKFEQEPKQMT-----VDVGAVALFDCRVVTGD 252
Qy 231 PKRPAVWLXWVSGPXRLPNLTPCSPGRLPRLPREARELRGOR 272
Db 253 PQPQ-----ITWK-----RKNEPMPVTRAVIAKDNRGRIER 284

RESULT 4
US-09-540-245A-16
; Sequence 16, Application US/09540245A
; Patent No. 6270984
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey
; APPLICANT: Kid, Thomas
; APPLICANT: Brose, Katja
; APPLICANT: Tessier-Lavigne, Marc
; TITLE OF INVENTION: Modulating Robo: Ligand Interactions
; FILE REFERENCE: B98-031-3
; CURRENT APPLICATION NUMBER: US/09/540,245A
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 60/065,544
; PRIOR FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: 60/081,057
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 1381
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-540-245A-16

Query Match 23.4%; Score 345; DB 3; Length 1381;
Best Local Similarity 33.7%; Pred. No. 9.6e-26;
Matches 91; Conservative 31; Mismatches 102; Indels 46; Gaps 8;

Qy 5 PQILVHPDQDLFOGPGPARMSCRASGPPPTIRLLNGQPLSMVPPDPHLLPDGTL 64
Db 4 PRIIEHPMDTTPVKNDPFTFCNQAEQGNPTFTIQWFKDGRKLTDTGSHRIMLPAGGLPFL 63
Qy 65 QPPARGHAHDGQALSTDLGVYTCESNRGLTAVSRGARSVAVLREDFOIQPRDMVAVG 124
Db 64 KV-----IHSRR--ESDAGTYWCEAKNEFGVARSNATLQVAVLRDEFRLPEPANTRVAQ 116
Qy 125 EQFTLECGPPWGHPEPTVSWKDGKPLAQGR--HTVSGSLLMARAEKSDEXTVMCVA 182
Db 117 EVALMECCAPRGSPFQISWRKNGQTLNLVGNKRIRIVDGNLAIQARQSDDDGRYQCVV 176
Qy 183 TNSAGHRESRAARVS-----IQEPDYTEPVELLAV-----RIQLENVTLNPDPAEGPK 232
Db 177 KVVVGTRESATAFLKVHVRPFPLIRGPQNTAVVSSVVFQCR-----GGD 222
Qy 233 PRPAVWLXWVSGPXRLPNLTPCSPGRLP 262
Db 223 PLPDV--LWR-----RTASGGNMP 239
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RESULT 5
US-08-752-307B-14
; Sequence 14, Application US/08752307B
; Patent No. 5952171
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.
; APPLICANT: Gearing, David P.
; APPLICANT: Levinson, Douglas A.
; TITLE OF INVENTION: METHOD FOR IDENTIFYING GENES
; TITLE OF INVENTION: ENCODING NOVEL SECRETED OR MEMBRANE-ASSOCIATED PROTEIN
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/752,307B
; FILING DATE: 19-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 09404/020001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 630 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-752-307B-14

Query Match 17.0%; Score 251; DB 2; Length 630;
Best Local Similarity 34.5%; Pred. No. 8.9e-17;
Matches 71; Conservative 34; Mismatches 71; Indels 30; Gaps 11;

Qy 5 PQILVHPQDOLFQPG-PAVMSCRASGPPPTIRMLNGOPLSMVPPDPHLLPDGTLLL 63
Db 355 PYWLDEPQN-LILAPGEGRLVCRANGPKPSIQMLVNGEPIEGSPNPSREVAGDTIVF 413
Qy 64 LQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLRDFQIQPR----- 117
Db 414 -----RDTQIGSS--AVYQCNASNEHGYLE--ANAFVSVL----DVPPIILAPRN 455
Qy 118 DMVAVVGQFT-LECGPWGHPEPTVSWKDGKPLALQPGHRTV-SGGSLLMARAEKSD 175
Db 456 QLIKVIQYNRTRLD-C-PFFGSPITLRFKNGQGNMLDGGNYKAHENGSLMSMARKEDQ 514
Qy 176 XYTCMVATNSAGHSRAARVSIQEP 201
Db 515 GIYTCVATNILGKVEAQ-VRLVKDP 539

RESULT 6
US-09-707-802-14
; Sequence 14, Application US/09707802
; Patent No. 6391586
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.

; Gearing, David P.
; Levinson, Douglas A.
; TITLE OF INVENTION: METHOD FOR IDENTIFYING GENES
; TITLE OF INVENTION: ENCODING NOVEL SECRETED OR MEMBRANE-ASSOCIATED PROTEIN
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/707,802
; FILING DATE: 07-No. 6391586-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/752,307
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 09404/020001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 630 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-707-802-14

Query Match 17.0%; Score 251; DB 4; Length 630;
Best Local Similarity 34.5%; Pred. No. 8.9e-17;
Matches 71; Conservative 34; Mismatches 71; Indels 30; Gaps 11;

Qy 5 PQILVHPQDOLFQPG-PAVMSCRASGPPPTIRMLNGOPLSMVPPDPHLLPDGTLLL 63
Db 355 PYWLDEPQN-LILAPGEGRLVCRANGPKPSIQMLVNGEPIEGSPNPSREVAGDTIVF 413
Qy 64 LQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLRDFQIQPR----- 117
Db 414 -----RDTQIGSS--AVYQCNASNEHGYLE--ANAFVSVL----DVPPIILAPRN 455
Qy 118 DMVAVVGQFT-LECGPWGHPEPTVSWKDGKPLALQPGHRTV-SGGSLLMARAEKSD 175
Db 456 QLIKVIQYNRTRLD-C-PFFGSPITLRFKNGQGNMLDGGNYKAHENGSLMSMARKEDQ 514
Qy 176 XYTCMVATNSAGHSRAARVSIQEP 201
Db 515 GIYTCVATNILGKVEAQ-VRLVKDP 539

RESULT 7
US-09-991-326-14
; Sequence 14, Application US/09991326
; Patent No. 6395872
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.
; Gearing, David P.
; Levinson, Douglas A.
; TITLE OF INVENTION: METHOD FOR IDENTIFYING GENES
; TITLE OF INVENTION: ENCODING NOVEL SECRETED OR MEMBRANE-ASSOCIATED PROTEIN
; NUMBER OF SEQUENCES: 14

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Fish & Richardson, P.C.
;; STREET: 225 Franklin Street
;; CITY: Boston
;; STATE: MA
;; COUNTRY: US
;; ZIP: 02110-2804
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: Windows95
;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/991.326
;; FILING DATE: 21-NOV-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/752.307
;; FILING DATE: 19-NOV-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Meiklejohn, Ph.D., Anita L.
;; REGISTRATION NUMBER: 35,283
;; REFERENCE/DOCKET NUMBER: 09404/020002
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-542-5070
;; TELEFAX: 617-542-8906
;; TELEX: 200154
;; INFORMATION FOR SEQ ID NO: 14:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 630 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-991-326-14

Query Match 17.0%; Score 251; DB 4; Length 630;
Best Local Similarity 34.5%; Pred. No. 8.9e-17;
Matches 71; Conservative 34; Mismatches 71; Indels 30; Gaps 11;

QY 5 PQILVHPDQQLFQPGP-PARMSCRASQPPPTIRWLLNGQPLSMVPPDPHLLPDGTL 63
Db 355 PYWLDEPQN-LILAPGEDGRIVCRANGNPKPSIQWLVNGEPIEGSPNPSPREVAGDTIVF 413
QY 64 LQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLRDFOIQPR----- 117
Db 414 -----RTQIGSS--AVTQCNASNEHYLL---ANAFVSL-----DVPPRILAPRN 455
QY 118 DMVAVVGQFT-LEGCPWPGHPEPTVSWKDGKPLALQPGRHTV-SGSLMARAEKSDS 175
Db 456 QLIRKVIQYNRRLDC-PPFGSPITPLRWFKNQGNMLDGNYKAHENGSLMSMARKEDQ 514
QY 176 XYMCVATNSAGHRESRAARVSIQEP 201
Db 515 GIYTCVATNIIKRVKVEAQ-VRLVKDP 539

RESULT 8
US-08-752-307B-12
; Sequence 12, Application US/08752307B
; Patent No. 5952171
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.
; APPLICANT: Gearing, David P.
; APPLICANT: Levinson, Douglas A.
; TITLE OF INVENTION: METHOD FOR IDENTIFYING GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US

;; ZIP: 02110-2804
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: Windows95
;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/752.307B
;; FILING DATE: 19-NOV-1996
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Meiklejohn, Ph.D., Anita L.
;; REGISTRATION NUMBER: 35,283
;; REFERENCE/DOCKET NUMBER: 09404/020001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-542-5070
;; TELEFAX: 617-542-8906
;; TELEX: 200154
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 607 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-752-307B-12

Query Match 15.5%; Score 228; DB 2; Length 607;
Best Local Similarity 29.5%; Pred. No. 1.7e-14;
Matches 79; Conservative 38; Mismatches 99; Indels 52; Gaps 13;

QY 1 QDSPPQILVHPDQQLFQPGP-PARMSCRASQPPPTIRWLLNGQPLSMVPPDPHLLPDGT 60
Db 40 EDQPLSVL-EPPESTEE--QVLLACRARASPPATYRWKMGKTEMKLEPGSRHQLV-GGN 94
QY 61 LLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLRDFOIQPRDMV 120
Db 95 LVIMNP-----TKAQDAGVYQCLASNPVGTVVSRRAILRFGFLQB-FSKEEDPV 143
QY 121 -AVVGEQFTLECGPPWGHPEPTVSWKDGKPLAL-QPGRHTVS--GGSLMARAEKSDX 176
Db 144 KAHEGWMGLPCNPAPHYPCGLSYRWLLNEFPNFIPTDGRHFVSTQTTGNLYIARTNASDLG 203
QY 177 TYMCVATNSAGHRE-----SRAARVSIQ-----EPQDYTEPVELLAVRIQLE 218
Db 204 NYSCLATS---HMDFTSKVSFKAQLNLAEDTRLFAPSIRKARFPAETVALVQGVQVTL 260
QY 219 NVTLIPDPAEGPKPRPAVWLXW-KVSG 245
Db 261 CFAFGNVPVR-----IKWRKVDG 278

RESULT 9
US-09-707-802-12
; Sequence 12, Application US/09707802
; Patent No. 6391586
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.
; APPLICANT: Gearing, David P.
; APPLICANT: Levinson, Douglas A.
; TITLE OF INVENTION: METHOD FOR IDENTIFYING GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/707,802
FILING DATE: 07-NOV-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/752,307
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 09404/020001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 607 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-707-802-12

Query Match 15.5%; Score 228; DB 4; Length 607;
Best Local Similarity 29.5%; Pred. No. 1.7e-14;
Matches 79; Conservative 38; Mismatches 99; Indels 52; Gaps 13;
QY 1 QDSPPOILVHPDQQLFQGGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHLLPDGT 60
DB 40 EDQPLSVL-FPEESTEE---QVLLACRARASPPATYRWKMGTEMKLEPGSRHQLV-GGN 94
QY 61 LLLQPPARGHAHDQALSTDLGVYTCASNRLGTAVSARGARLSVAVLRDFQIQPRDMV 120
DB 95 LVIMNP-----TKAQDAGVYQCLASNPVGTWVSREAILRFGFLQE-FSKEERDPV 143
QY 121 -AVVGEQFTLEGCPGWGHEPPTVSMWKGKPLAL-OPGRHTVS---GGSLLMARAEKSDX 176
DB 144 KAHEGWVLPNCPNPPAHYPGLSYRWLLNEFPNFIPTDGRHFVSQTGNLYIARTNASDLG 203
QY 177 TYMCVATNSAGHRE-----SRAARVSIQ-----EPQDYTEPVELLAVRIQLE 218
DB 204 NVSCLATS---HMDFTKSVFSKFAQLNLAEDTRLFAPSIRKARPPAETVALVGQOVTL 260
QY 219 NVTLLNPDPAEGPKRPAVWLXW-KVSG 245
DB 261 CFAFGNPVPR-----IKWRKVDG 278

RESULT 10
US-09-991-326-12
Sequence 12, Application US/09991326
Patent No. 6395872
GENERAL INFORMATION:
APPLICANT: McCarthy, Sean A.
Gearing, David P.
Levinson, Douglas A.
TITLE OF INVENTION: METHOD FOR IDENTIFYING GENES
ENCODING NOVEL SECRETED OR MEMBRANE-ASSOCIATED PROTEIN
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95

COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/991,326
FILING DATE: 21-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/752,307
FILING DATE: 19-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 09404/020002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 607 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-991-326-12
Query Match 15.5%; Score 228; DB 4; Length 607;
Best Local Similarity 29.5%; Pred. No. 1.7e-14;
Matches 79; Conservative 38; Mismatches 99; Indels 52; Gaps 13;
QY 1 QDSPPOILVHPDQQLFQGGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHLLPDGT 60
DB 40 EDQPLSVL-FPEESTEE---QVLLACRARASPPATYRWKMGTEMKLEPGSRHQLV-GGN 94
QY 61 LLLQPPARGHAHDQALSTDLGVYTCASNRLGTAVSARGARLSVAVLRDFQIQPRDMV 120
DB 95 LVIMNP-----TKAQDAGVYQCLASNPVGTWVSREAILRFGFLQE-FSKEERDPV 143
QY 121 -AVVGEQFTLEGCPGWGHEPPTVSMWKGKPLAL-OPGRHTVS---GGSLLMARAEKSDX 176
DB 144 KAHEGWVLPNCPNPPAHYPGLSYRWLLNEFPNFIPTDGRHFVSQTGNLYIARTNASDLG 203
QY 177 TYMCVATNSAGHRE-----SRAARVSIQ-----EPQDYTEPVELLAVRIQLE 218
DB 204 NVSCLATS---HMDFTKSVFSKFAQLNLAEDTRLFAPSIRKARPPAETVALVGQOVTL 260
QY 219 NVTLLNPDPAEGPKRPAVWLXW-KVSG 245
DB 261 CFAFGNPVPR-----IKWRKVDG 278

RESULT 11
US-08-752-307B-13
Sequence 13, Application US/08752307B
Patent No. 5952171
GENERAL INFORMATION:
APPLICANT: McCarthy, Sean A.
Gearing, David P.
Levinson, Douglas A.
TITLE OF INVENTION: METHOD FOR IDENTIFYING GENES
ENCODING NOVEL SECRETED OR MEMBRANE-ASSOCIATED PROTEIN
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95

SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752.307B
FILING DATE: 19-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 09404/020001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 596 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-752-307B-13

Query Match 14.8%; Score 219; DB 2; Length 596;
Best Local Similarity 28.2%; Pred. No. 1.4e-13;
Matches 80; Conservative 39; Mismatches 119; Indels 46; Gaps 12;
QY 5 PQILVHPDQQLFQGGPAR---MSCRASGQPPPTIRWLLNGQPLSMVPPDPHLLPDGTL 61
DB 25 PVFVKEPSNIFPVGSEDKKTILNCEARGNPSPHYRWQLNGSDID-TSLDHYRYKLNGNL 83
QY 62 LLLQPPARGHAHDGQALSTDGLVYTCEASNLGTAVSGARLSVAVLREDFOIQPRDWA 121
DB 84 IVINPNR-----NWDTSYQCFATNSLGTIVSREAKLQFAYL-ENFKSMRGRVS 132
QY 122 V-VGEQFTLECGPWGHPPTVSW-WKDGKPLALQPGRHVTS--GGSLLMARAEKSDEXT 177
DB 133 VREGGVLLCGPPHSGELSYAVWFNEYPSFVEEDSRFRVSQETGHLIYIAKVPSPDVG 192
QY 178 YMCVATN-----SAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENV 220
DB 193 YTCVVTSTVNARVLGSPTLVLRSDGVMGEYEPKIELQFPE--TLPA-ARGSTVKLECF 249
QY 221 TLLNPDP-----AEGKPRPAVWLXWKVSGPXRLNLTRECSG 258
DB 250 ALGNPVPQINWRRSDG-MPFTTKIKLRFNGVLEIPNFQEDTG 292

RESULT 12
US-09-707-802-13
Sequence 13, Application US/09707802
Patent No. 6391586
GENERAL INFORMATION:
APPLICANT: McCarthy, Sean A.
Gearing, David P.
Levinson, Douglas A.
TITLE OF INVENTION: METHOD FOR IDENTIFYING GENES
ENCODING NOVEL SECRETED OR MEMBRANE-ASSOCIATED PROTEIN
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/707,802
FILING DATE: 07-No. 6391586-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/752,307
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 09404/020001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 596 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-707-802-13

Query Match 14.8%; Score 219; DB 4; Length 596;
Best Local Similarity 28.2%; Pred. No. 1.4e-13;
Matches 80; Conservative 39; Mismatches 119; Indels 46; Gaps 12;
QY 5 PQILVHPDQQLFQGGPAR---MSCRASGQPPPTIRWLLNGQPLSMVPPDPHLLPDGTL 61
DB 25 PVFVKEPSNIFPVGSEDKKTILNCEARGNPSPHYRWQLNGSDID-TSLDHYRYKLNGNL 83
QY 62 LLLQPPARGHAHDGQALSTDGLVYTCEASNLGTAVSGARLSVAVLREDFOIQPRDWA 121
DB 84 IVINPNR-----NWDTSYQCFATNSLGTIVSREAKLQFAYL-ENFKSMRGRVS 132
QY 122 V-VGEQFTLECGPWGHPPTVSW-WKDGKPLALQPGRHVTS--GGSLLMARAEKSDEXT 177
DB 133 VREGGVLLCGPPHSGELSYAVWFNEYPSFVEEDSRFRVSQETGHLIYIAKVPSPDVG 192
QY 178 YMCVATN-----SAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENV 220
DB 193 YTCVVTSTVNARVLGSPTLVLRSDGVMGEYEPKIELQFPE--TLPA-ARGSTVKLECF 249
QY 221 TLLNPDP-----AEGKPRPAVWLXWKVSGPXRLNLTRECSG 258
DB 250 ALGNPVPQINWRRSDG-MPFTTKIKLRFNGVLEIPNFQEDTG 292

RESULT 13
US-09-991-326-13
Sequence 13, Application US/09991326
Patent No. 6395872
GENERAL INFORMATION:
APPLICANT: McCarthy, Sean A.
Gearing, David P.
Levinson, Douglas A.
TITLE OF INVENTION: METHOD FOR IDENTIFYING GENES
ENCODING NOVEL SECRETED OR MEMBRANE-ASSOCIATED PROTEIN
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/991,326

;; FILING DATE: 21-NOV-1993
;; APPLICATION DATA:
;; APPLICATION NUMBER: 08/752,307
;; FILING DATE: 19-NOV-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Melkiohn, Ph.D., Anita L.
;; REGISTRATION NUMBER: 35,283
;; REFERENCE/DOCKET NUMBER: 09404/020002
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-542-5070
;; TELEFAX: 617-542-8906
;; TELEX: 200154
;; INFORMATION FOR SEQ ID NO: 13:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 596 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-991-326-13

Query Match 14.8%; Score 219; DB 4; Length 596;
Best Local Similarity 28.2%; Pred. No. 1.4e-13;
Matches 80; Conservative 39; Mismatches 119; Indels 46; Gaps 12;

QY 5 PQILVHPDQLFQGGPARGHAGDQALST--MSCRASGQPPPTIRWLLNGQPLSNVPPDPHLLPDGTL 61
DB 25 PVFVKPEPNSIFPVGSEDKITLNCARGNPSPHYRWQLNGSDID-TSLDHYRYKLNGNL 83
QY 62 LLLQPPARGHAGDQALSTDLGVYTCASNRLGTAVSRGARSVAVLREDFOIQPRDMVA 121
DB 84 IIVINPR-----NWDTSYQCFATNSLGTIVSREAKLQFAYL-ENFKSRMRSRVS 132
QY 122 V-VGEQFTLECGPPHGHPEPTVSW-WKDGKPLALQPGHRTVS--CGSLMARAESDEXT 177
DB 133 VREGQGVLLCGPPHSGELSYAWVFNEPSPFVEDSRFRVSQETGHLIYIAKVEPSDVGN 192
QY 178 YMCVATN-----SAGHRESRAARVSIOEPDYTEPVVELLAVRIQLENV 220
DB 193 YTCVTSITVNARVLGSPPTPLVLRDGVNGVEPKIELOFPE--TLPA-AGKSTVKLRCF 249
QY 221 TLLNDDP-----ASGPKPRPAWLKWKVSGPXRLPNLTRPCSG 258
DB 250 ALGNVPVQINWRRSDG-MPFPFKIKLRKFGVLEIPNFQOEDTG 292

RESULT 14
US-08-447-464-3
; Sequence 3, Application US/08447464
; Patent No. 5840842
; GENERAL INFORMATION:
; APPLICANT: Schllessinger, Joseph
; APPLICANT: Yan, Hai
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PROTEIN
; TITLE OF INVENTION: PHOSPHOTYROSINE PHOSPHATASE-SIGMA
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,464
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: 08/130,570
;; FILING DATE: 01-OCT-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mistrock, S. Leslie
;; REGISTRATION NUMBER: 18,872
;; REFERENCE/DOCKET NUMBER: 7683-043
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212-790-9090
;; TELEFAX: 212-869-8864/9741
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1501 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-447-464-3

Query Match 14.8%; Score 218.5; DB 2; Length 1501;
Best Local Similarity 30.9%; Pred. No. 5.6e-13;
Matches 67; Conservative 37; Mismatches 74; Indels 39; Gaps 11;

QY 2 DSPQILVHPDQLFQGGPARGHAGDQALST--MSCRASGQPPPTIRW-----LNGQPLSNVPPDPHLL 56
DB 30 EEPFRFTREPDKQIGVSGVASFVCQATGDKPKPRVTNNKGGKVNRSQRFETIDFDE---- 85
QY 57 PDGTLILLQPPARGHAGDQALST--DLGVYTCASNRLGTAVSRGARSVAVLREDFOI 114
DB 86 SSGAVLRIQP-----LRTPRDENVEYCAQNSVG-EITVHAKLT--VLRED-QL 130
QY 115 QPRDMVAVVGRQF-----TLECGPPHGHPEPTVSWWKDGKPL--ALQPGR-HTVSG 162
DB 131 PPGFNIDMGQPLKVVETRTATMLCAAS-GNPDEITWFKDPLPVDPSASNGRIKQLRS 189
QY 163 GSLMARAESDEXTCYMCVATNSAGHRESRAARVSIQ 199
DB 190 GALQTESSEETDQGYECVATNSAGVRYSSPANLYVR 226

RESULT 15
US-08-716-679-3
; Sequence 3, Application US/08716679
; Patent No. 5846800
; GENERAL INFORMATION:
; APPLICANT: Schllessinger, Joseph
; APPLICANT: Yan, Hai
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PROTEIN
; TITLE OF INVENTION: PHOSPHOTYROSINE PHOSPHATASE-SIGMA
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/716,679
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/130,570
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7683-043
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-790-9090
 ; TELEFAX: 212-869-8864/9741
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1501 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-716-679-3

Query Match 14.8%; Score 218.5; DB 2; Length 1501;
 Best Local Similarity 30.9%; Pred. No. 5.6e-13;
 Matches 67; Conservative 37; Mismatches 74; Indels 39; Gaps 11;

Qy	2	DSPQILVHPDQLFQGGPARMSCRASGQPPPTIRM-----LNGQPLSMVPPDPHLL	56
Db	30	EEPRFIREPKDQIGVSGVASFVCATGDKPRVTWNKGGKVSQRFETIDFDE----	85
Qy	57	PDGTLILLQPPARGHAHDGQALST--DLGVYTCASNELGTAVSRGARLSVAVLREDFOI	114
Db	86	SSGAVLRIOF-----LRTPRDENVYECVAQNSVG-EITVHAKLT--VLRED-QL	130
Qy	115	QPRDMVAVVGEQF-----TLECGPPMGHPPTVSMWKDGKPL--ALQGR-HTVSG	162
Db	131	PPGFNIDMGPLKXVVERTRTATMLCAAS-GNPDPEITWFKDFLPVDPASNGRIKQLRS	189
Qy	163	GSLMARAEKSDEXTYMCVATNSAGHRESRAARVSIQ	199
Db	190	GALQIESSEETDQGYECVATNSAGVRYSSPANLYVR	226

Search completed: January 30, 2004, 15:57:51
 Job time : 13.8238 secs


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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (203)
; OTHER INFORMATION: Xaa equals any amino acid
; NAME/KEY: SITE
; LOCATION: (267)
; OTHER INFORMATION: Xaa equals any amino acid
; NAME/KEY: SITE
; LOCATION: (274)
; OTHER INFORMATION: Xaa equals any amino acid
US-10-047-021-86

Query Match          99.6%; Score 1469; DB 12; Length 303;
Best Local Similarity 100.0%; Pred. No. 7.2e-114;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDSPPQILVHPQDQLFQGGPARMSCRASGQPPPTIRWLLNGQLPSMVPPDPHLLPDGT 60
DB 28 QDSPPQILVHPQDQLFQGGPARMSCRASGQPPPTIRWLLNGQLPSMVPPDPHLLPDGT 87
QY 61 LLLQPPARGHAHDGQALSTDLGVYTCEASNRGLGTAVSRGARLSVAVLRDFQIQPRDMV 120
DB 88 LLLQPPARGHAHDGQALSTDLGVYTCEASNRGLGTAVSRGARLSVAVLRDFQIQPRDMV 147
QY 121 AVVGEQFTLECGPWGHPPTVSWKDGKPLALQPGRHVTSGSLLMARAEKSDEXTYMC 180
DB 148 AVVGEQFTLECGPWGHPPTVSWKDGKPLALQPGRHVTSGSLLMARAEKSDEXTYMC 207
QY 181 VATNSAGHRESRAARVSIQEQDYTEPVVELLAVRIQLENVTLNPDPAEGPKRPVAVWLX 240
DB 208 VATNSAGHRESRAARVSIQEQDYTEPVVELLAVRIQLENVTLNPDPAEGPKRPVAVWLX 267
QY 241 WKVSGPXRLPNLTRPCSGPRLPREARELRQRRNTG 276
DB 268 WKVSGPXRLPNLTRPCSGPRLPREARELRQRRNTG 303

RESULT 2
US-10-411-224-86
; Sequence 86, Application US/10411224
; Publication No. US20030166906A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 50 Human Secreted Proteins
; FILE REFERENCE: PZ016P1
; CURRENT APPLICATION NUMBER: US/10/411,224
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: US/09/722,329
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/262,109
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: 60/057,626
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/057,663
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/057,669
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/058,667
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/058,974
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/058,973
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/058,666
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/090,112
; PRIOR FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 86
; LENGTH: 304

; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (203)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (267)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (274)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-411-224-86

Query Match          99.6%; Score 1469; DB 12; Length 304;
Best Local Similarity 100.0%; Pred. No. 7.2e-114;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDSPPQILVHPQDQLFQGGPARMSCRASGQPPPTIRWLLNGQLPSMVPPDPHLLPDGT 60
DB 28 QDSPPQILVHPQDQLFQGGPARMSCRASGQPPPTIRWLLNGQLPSMVPPDPHLLPDGT 87
QY 61 LLLQPPARGHAHDGQALSTDLGVYTCEASNRGLGTAVSRGARLSVAVLRDFQIQPRDMV 120
DB 88 LLLQPPARGHAHDGQALSTDLGVYTCEASNRGLGTAVSRGARLSVAVLRDFQIQPRDMV 147
QY 121 AVVGEQFTLECGPWGHPPTVSWKDGKPLALQPGRHVTSGSLLMARAEKSDEXTYMC 180
DB 148 AVVGEQFTLECGPWGHPPTVSWKDGKPLALQPGRHVTSGSLLMARAEKSDEXTYMC 207
QY 181 VATNSAGHRESRAARVSIQEQDYTEPVVELLAVRIQLENVTLNPDPAEGPKRPVAVWLX 240
DB 208 VATNSAGHRESRAARVSIQEQDYTEPVVELLAVRIQLENVTLNPDPAEGPKRPVAVWLX 267
QY 241 WKVSGPXRLPNLTRPCSGPRLPREARELRQRRNTG 276
DB 268 WKVSGPXRLPNLTRPCSGPRLPREARELRQRRNTG 303

RESULT 3
US-09-796-753-158
; Sequence 158, Application US/09796753
; Publication No. US20030027998A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-227-999
; CURRENT APPLICATION NUMBER: US/09/796,753
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/183,175
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 09/223,094
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/223,546
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/224,246
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/259,388
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/122,458
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: 09/312,359
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/336,536
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 09/342,687
; PRIOR FILING DATE: 1999-06-29
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PRIOR APPLICATION NUMBER: 09/345,464
 PRIOR FILING DATE: 1999-06-30
 PRIOR APPLICATION NUMBER: 09/365,164
 PRIOR FILING DATE: 1999-07-30
 PRIOR APPLICATION NUMBER: 09/399,723
 PRIOR FILING DATE: 1999-09-20
 PRIOR APPLICATION NUMBER: 09/409,634
 PRIOR FILING DATE: 1999-09-30
 PRIOR APPLICATION NUMBER: 09/471,179
 PRIOR FILING DATE: 1999-12-23
 PRIOR APPLICATION NUMBER: 09/474,071
 PRIOR FILING DATE: 1999-12-29
 PRIOR APPLICATION NUMBER: 09/474,072
 PRIOR FILING DATE: 1999-12-29
 PRIOR APPLICATION NUMBER: 09/514,010
 PRIOR FILING DATE: 2000-02-25
 PRIOR APPLICATION NUMBER: 09/516,745
 PRIOR FILING DATE: 2000-03-01
 PRIOR APPLICATION NUMBER: 09/572,002
 PRIOR FILING DATE: 2000-05-14
 PRIOR APPLICATION NUMBER: 09/597,993
 PRIOR FILING DATE: 2000-06-19
 PRIOR APPLICATION NUMBER: 09/599,596
 PRIOR FILING DATE: 2000-06-22
 PRIOR APPLICATION NUMBER: 09/630,334
 PRIOR FILING DATE: 2000-07-31
 PRIOR APPLICATION NUMBER: 09/606,565
 PRIOR FILING DATE: 2000-06-29
 PRIOR APPLICATION NUMBER: 09/606,317
 PRIOR FILING DATE: 2000-06-29
 PRIOR APPLICATION NUMBER: 09/665,666
 PRIOR FILING DATE: 2000-09-20
 PRIOR APPLICATION NUMBER: 09/677,751
 PRIOR FILING DATE: 2000-09-30
 NUMBER OF SEQ ID NOS: 162
 SEQ ID NO 158
 LENGTH: 480
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-796-753-158

Query Match 88.9%; Score 1311; DB 11; Length 480;
 Best Local Similarity 98.8%; Pred. No. 1.6e-100;
 Matches 243; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

 QY 1 QDSPPQILVHPDQLFQGGPARMSCRASGQPPPTIRLLNGQPLSMVPPDPHLLPDGT 60
 DB 59 QDSPPQILVHPDQLFQGGPARMSCRASGQPPPTIRLLNGQPLSMVPPDPHLLPDGT 118

 QY 61 LLLQPPARGHAHDGQALSTDLGVVTCBASNLGLTAVSRGARLSVAVLRDPFIQIPDMV 120
 DB 119 LLLQPPARGHAHDGQALSTDLGVVTCBASNLGLTAVSRGARLSVAVLRDPFIQIPDMV 178

 QY 121 AVVGQFTLECGPPNGHPPTVSWWKGKPLALQPGRTVSGGSLLMARAEKSDXTYMC 180
 DB 179 AVVGQFTLECGPPNGHPPTVSWWKGKPLALQPGRTVSGGSLLMARAEKSDGTMYC 238

 QY 181 VATNSAGHRESRAARVSTQEPDYTPVELLAVRIQLENVTLNDDPAEGKPPRAVWLX 240
 DB 239 VATNSAGHRESRAARVSTQEPDYTPVELLAVRIQLENVTLNDDPAEGKPPRAVWLS 298

 QY 241 WKVSGP 246
 DB 299 WKVSGP 304

RESULT 4
 US-09-978-295A-211
 Sequence 211, Application US/09978295A
 Patent No. US20020156006A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth J.
 APPLICANT: Kllavin, Ivar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James;
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: ROY, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2630P1C11
 CURRENT APPLICATION NUMBER: US/09/978,295A
 CURRENT FILING DATE: 2001-10-15
 PRIOR APPLICATION NUMBER: 09/918585
 PRIOR FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/064249
 PRIOR FILING DATE: 1997-11-03
 PRIOR APPLICATION NUMBER: 60/065311
 PRIOR FILING DATE: 1997-11-13
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 PRIOR FILING DATE: 1998-03-12
 PRIOR APPLICATION NUMBER: 60/078004
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 ; PRIOR APPLICATION NUMBER: 60/085579
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 ; PRIOR APPLICATION NUMBER: 60/085580
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085573
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085704
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 88.9%; Score 1311; DB 10; Length 985;

Best Local Similarity 98.8%; Fred. No. 3.7e-100; Matches 243; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy	1	QDPPQILVHPQDLFOGPGFARMSCRASGPPPTIRWLLNQPLSMVPPDPHLLPDGT	60
Db	6	QDPPQILVHPQDLFOGPGFARMSCRASGPPPTIRWLLNQPLSMVPPDPHLLPDGT	65
Qy	61	LLLLQPPARGHADGQALSTDLGVYTCEASNRGLTAVSRGARLSVAVLREDFQIQPRDMV	120
Db	66	LLLLQPPARGHADGQALSTDLGVYTCEASNRGLTAVSRGARLSVAVLREDFQIQPRDMV	125
Qy	121	AVVGEQFTLECGPPWGHPEPTVSWKDGKPLALOPGHTVSGSLLMARAEKSDXTYMC	180
Db	126	AVVGEQFTLECGPPWGHPEPTVSWKDGKPLALOPGHTVSGSLLMARAEKSDXTYMC	185
Qy	181	VATNSAGHRESRAARVSIQBPQDYTERVELLAVRIQLENVTLLNPDPAEGPKPAPVWLX	240
Db	186	VATNSAGHRESRAARVSIQBPQDYTERVELLAVRIQLENVTLLNPDPAEGPKPAPVWLX	245
Qy	241	WKVSGP	246
Db	246	WKVSGP	251

RESULT 5
US-09-978-697-211
; Sequence 211, Application US/09978697
; Patent No. US20020169284A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC27
; CURRENT APPLICATION NUMBER: US/09/978,697
; PRIOR FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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1 PRIOR FILING DATE: 1998-04-29
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11 PRIOR FILING DATE: 1998-04-29
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29 PRIOR FILING DATE: 1998-05-07
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56 PRIOR APPLICATION NUMBER: 60/085704
57 PRIOR FILING DATE: 1998-05-15
58 PRIOR APPLICATION NUMBER: 60/085697

Query Match 88.9%; Score 1311; DB 10; Length 985;
Best Local Similarity 98.8%; Pred. No. 3.7e-100;
Matches 243; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 QDSPPQILVHQQDQLFQGGPARNMCRASGQPPPTIRWLLNGQPLSMVPPDPHLLPDGT 60
Db 6 QDSPPQILVHQQDQLFQGGPARNMCRASGQPPPTIRWLLNGQPLSMVPPDPHLLPDGT 65
Qy 61 LLLQPPARGHAHQDQALSTDLGVYTCEASNRGLGTAVSRGRLSVAVLRDFQIQPRDMV 120
Db 66 LLLQPPARGHAHQDQALSTDLGVYTCEASNRGLGTAVSRGRLSVAVLRDFQIQPRDMV 125
Qy 121 AVVEQFTLECGPPWGHPEPTVSWWKGKPLALQPGRHVTSGSLLMARAEKSDXTYMC 180

Db 126 AVVEQFTLECGPPWGHPEPTVSWWKGKPLALQPGRHVTSGSLLMARAEKSDXTYMC 185
Qy 181 VATNSAGHRESRAARVSIQEPDYTEPVELLAVRIQLENTLLNPDPAGPKPRPAVWLX 240
Db 186 VATNSAGHRESRAARVSIQEPDYTEPVELLAVRIQLENTLLNPDPAGPKPRPAVWLX 245
Qy 241 WKVSGP 246
Db 246 WKVSGP 251

RESULT 6

US-09-378-192A-211
Sequence 211, Application US/09978192A
Patent No. US20020177553A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C9
CURRENT APPLICATION NUMBER: US/09/978,192A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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;; PRIOR FILING DATE: 1998-05-15
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;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 88.9%; Score 1311; DB 10; Length 985;
Best Local Similarity 98.8%; Pred.No.3.7e-100;
Matches 243; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 QDSPPQILVHPDQDLFQGGPGPARMSCRASGQPPPTIRLLNGQPLSMVPPDPHLLPDCT 60

Db 6 QDSPPQILVHQDQLFCQGGPARMSCQASQGPPTIRMLNGQPLSMVPPDPHLLPDGT 65
Qy 61 LLLLOPPARGHAHQDQALSTDLGVYTCASNRLGTAVSRGARLSVAVLREDFQIQPRDMV 120
Db 66 LLLLOPPARGHAHQDQALSTDLGVYTCASNRLGTAVSRGARLSVAVLREDFQIQPRDMV 125
Qy 121 AVVGQFTLECGPPMGHPPTVSMWKDGKPLALOPGRHTVSGGSLLMARAEKSDEXTVMC 180
Db 126 AVVGQFTLECGPPMGHPPTVSMWKDGKPLALOPGRHTVSGGSLLMARAEKSDEXTVMC 185
Qy 181 VATSAGHRESRAARVSIQEQDYTEPVVELLAVRIQLENNVLLNPDPAEGKPRPAVWLX 240
Db 186 VATSAGHRESRAARVSIQEQDYTEPVVELLAVRIQLENNVLLNPDPAEGKPRPAVWLS 245
Qy 241 WKVSGP 246
Db 246 WKVSGP 251

RESULT 7

US-09-999-832A-211
; Sequence 211, Application US/09999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PLC63
; CURRENT APPLICATION NUMBER: US/09/999,832A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
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Query Match      88.9%; Score 1311; DB 10; Length 985;
Best Local Similarity 98.8%; Pred No. 3.7e-100;
Matches 243; Conservative 1; Mismatches 2; Indels 0; Gaps 0

Qy 1 QDSPPPQILVHPDQLFQPGCPARMSCRASQPPPTIRWLLNGQPLSMVPPDPHLLPDGT 60
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Qy 61 LLLLOPPARGHANDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPRDMV 120
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Qy 121 AVVGEQFTLECGPPWGHPEFTVSWKDGKPLALQPGRHTVSGGSLLMARAEKSDEXTYMC 180
Db 126 AVVGEQFTLECGPPWGHPEFTVSWKDGKPLALQPGRHTVSGGSLLMARAEKSDEXTYMC 185
Qy 181 VATNSAGHRESRAARVSIQPDQYTEPVELLAVRIQLENVTLLNPDPAEGPKRPVAVLX 240
Db 186 VATNSAGHRESRAARVSIQPDQYTEPVELLAVRIQLENVTLLNPDPAEGPKRPVAVLX 245
Qy 241 WKVSGP 246
Db 246 WKVSGP 251

RESULT 8
US-09-978-189-211
; Sequence 211, Application US/09978189
; Publication No. US20030004102A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C7
; CURRENT APPLICATION NUMBER: US/09/978,189
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
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;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 88.9%; Score 1311; DB 11; Length 985;
Best Local Similarity 98.8%; Pred. No. 3.7e-100;
Matches 243; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QDSPPQILVHPQDQLFOGPGPARMSCRASGQPPPTIRMLLNGQPLSMVPPDPHLLPDGT 60
DB 6 QDSPPQILVHPQDQLFOGPGPARMSCRASGQPPPTIRMLLNGQPLSMVPPDPHLLPDGT 65
QY 61 LLLLOPPARGHAHDGQALSTDGLVYTCEASNRLGTAVSRGARLSVAVLRDFQIQPRDMV 120
DB 66 LLLLOPPARGHAHDGQALSTDGLVYTCEASNRLGTAVSRGARLSVAVLRDFQIQPRDMV 125
QY 121 AVVGEQFTLECGPPMGHPPTVSWKDGKPLALQPGRHTVSGSLLMARAESDXTYMC 180
DB 126 AVVGEQFTLECGPPMGHPPTVSWKDGKPLALQPGRHTVSGSLLMARAESDXTYMC 185
QY 181 VATNSAGHRESRAARVSIQEPDYTEPVVELLAVRIQLENVTLNPDPAEGPKPRPAVWLX 240
DB 186 VATNSAGHRESRAARVSIQEPDYTEPVVELLAVRIQLENVTLNPDPAEGPKPRPAVWLX 245
QY 241 WKVSGP 246
DB 246 WKVSGP 251

RESULT 9
US-09-978-608A-211
; Sequence 211, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC22

;; CURRENT APPLICATION NUMBER: US/09/978.608A
;; CURRENT FILING DATE: 2001-10-16
;; NUMBER OF SEQ ID NOS: 624
;; PRIOR Application removed - See File Wrapper or Palm
;; SEQ ID NO 211
;; LENGTH: 985
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-978-608A-211

Query Match 88.9%; Score 1311; DB 11; Length 985;
Best Local Similarity 98.8%; Pred. No. 3.7e-100;
Matches 243; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY 121 AVVGEQFTLECGPPMGHPPTVSWKDGKPLALQPGRHTVSGSLLMARAESDXTYMC 180
DB 126 AVVGEQFTLECGPPMGHPPTVSWKDGKPLALQPGRHTVSGSLLMARAESDXTYMC 185
QY 181 VATNSAGHRESRAARVSIQEPDYTEPVVELLAVRIQLENVTLNPDPAEGPKPRPAVWLX 240
DB 186 VATNSAGHRESRAARVSIQEPDYTEPVVELLAVRIQLENVTLNPDPAEGPKPRPAVWLX 245
QY 241 WKVSGP 246
DB 246 WKVSGP 251

RESULT 10
US-09-978-585A-211
; Sequence 211, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC15
; CURRENT APPLICATION NUMBER: US/09/978.585A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624

;; PRIOR FILING DATE: 1998-04-08
;; PRIOR APPLICATION NUMBER: 60/081049
;; PRIOR FILING DATE: 1998-04-08
;; PRIOR APPLICATION NUMBER: 60/081071
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;; PRIOR APPLICATION NUMBER: 60/081195
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;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

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Pred. No.: 2,9e-136 Length: 3716
Score: 1550.00 Matches: 292
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Best Local Similarity: 98.32% Mismatches: 3
Query Match: 96.39% Indels: 1
DB: 10 Gaps: 0

US-10-047-021-86 (1-303) x US-09-978-295A-210 (1-3716)

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Db 1 GGAGGAGACAGCCCTCTGGGGGCGAGGGGTTCCCTGCTCTGCTCTCATATG 60
Qy 24 GlyGlyMetAlaGlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPhe 43
Db 61 GGAGGATGGCTCAGGACTCCCGCCCCAGATCTTAGTCCACCCAGGACCATGTC 120
Qy 44 GlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIle 63
Db 121 CAGGGCCCTGGCCCTGCCAGGATGAGCTGCCAAGCCTCAGGCGCAGCCACCTCCCATC 180
Qy 64 ArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisLeuLeu 83
Db 181 CGCTGGTTGCTGAATGGGACGCCCCCTGAGCATGGTGCCCCAGACCCACACCTCTCG 240
Qy 84 ProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGln 103
Db 241 CCTGATGGACCCCTTCTGCTACTACAGCCCTTCCCGGGGACATGCCACGATGCCAG 300
Qy 104 AlaLeuSerThrAspLeuGlyValTrpThrCysGluAlaSerAsnArgLeuGlyThrAla 123
Db 301 GCCCTGTCCACAGACCTGGGTGTACACATGTGAGGCGCAGCAACCGGCTTGGCAGCGCA 360
Qy 124 ValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAppPheGlnIleGlnPro 143
Db 361 GTCAGCAGAGCGCTCGGCTCTCTGTGCTCTCTCCGGGAGGATTTCCAGATCCAGCT 420
Qy 144 ArgAspMetValAlaValGlyGlnPheThrLeuGluCysGlyProProTrpGly 163
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Qy 164 HisProGluProThrValSerTrpTrpAspGlyLysProLeuAlaLeuGlnProGly 183
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; PRIOR FILING DATE: 1997-09-12
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; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: US 60/058,973
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: US 60/058,666
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: US 60/090,112
; PRIOR FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (637)..(637)
; OTHER INFORMATION: n equals a,t,g, or c
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; LOCATION: (850)..(850)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-047-021-31

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Score: 1602.00 Matches: 303
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.63% Indels: 0
DB: 12 Gaps: 0

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Db 91 CTCATCATGGGAGGCGATGGCTCAGGACTCCCGGGCCAGATCTTAGTCCACCCCGGAG 150
Qy 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60
Db 151 CAGCTGTTCCAGGGCCCTGGCCCTGCCAGGATGAGCTCCGAGCTCAGGCGCAGCCACCT 210
Qy 61 ProThrIleArgTTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80
Db 211 CCCACCATCCGCTGCTGCTGAATGGGCGAGCCCTGAGCATGGTGTGCCCGGAGCCACAC 270
Qy 81 HisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100
Db 271 CACCTCTGCTGATGGGAGCCCTTCTGTGTACAGCCCTCTGCGGGGAGCATGCCAC 330
Qy 101 AspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeu 120
Db 331 GATGGCCAGGCCCTGTCACAGACCTGGGTGTCTACACATGTGAGCCCGAGCAACCGGCTT 390
Qy 121 GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln 140
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Qy 141 IleGlnProArgAspMetValAlaValValGlyGlnGlnPheThrLeuGluCysGlyPro 160
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Db 691 GCCCGGGTTTCCATCCAGGAGCCCGGAGCTACAGGAGCTGTGGAGCTTCTGGCTGTG 750
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Db 811 AGACCGGCGGTGTGGCTCACTCGAARGTCACTGGCGCTTGGCGCTTCCCAATCTTACA 870
Qy 281 ArgProCysSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArgArg 300
Db 871 CGGCTTGTTCAGGACCCAGACTGCCCGGGAGGCCAGGAGCTCCCTGGCAGAGGAGG 930
Qy 301 AsnThrGly 303
Db 931 AACACAGGA 939

RESULT 2
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; Sequence 31, Application US/10411224
; Publication No. US20030166906A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 50 Human Secreted Proteins
; FILE REFERENCE: P2016P1
; CURRENT APPLICATION NUMBER: US/10/411,224
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: US/09/722,329
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/262,109
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: 60/057,626
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/057,663
; PRIOR FILING DATE: 1997-09-05
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; PRIOR APPLICATION NUMBER: 60/058,666
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/090,112
; PRIOR FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 1346
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (637)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (850)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-411-224-31
Alignment Scores:
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

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Title: US-10-047-021-86

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Delop 6.0 , Delext 7.0

Searched: 2434939 seqs, 1822278265 residues

Total number of hits satisfying chosen parameters: 4869878

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database : Published Applications NA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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ALIGNMENTS

RESULT 1

US-10-047-021-31
; Sequence 31, Application US/10047021
; Publication No. US20040002591A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 50 Human Secreted Proteins
; FILE REFERENCE: P2016P2
; CURRENT APPLICATION NUMBER: US/10/047,021
; CURRENT FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: US 60/262,066
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 09/722,329
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/262,109
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: PCT/US98/18360
; PRIOR FILING DATE: 1998-09-03
; PRIOR APPLICATION NUMBER: US 60/057,626
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/057,663
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/057,669
; PRIOR FILING DATE: 1997-09-05

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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/904,991
FILING DATE: June 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Minnich, Richard J.
REGISTRATION NUMBER: 24,175
REFERENCE/DOCKET NUMBER: CWR 2 149-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 861-5582
TELEFAX: (216) 241-1666
TELEX: (216) 980162
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3774
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: irrelevant
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Homo Sapiens
INDIVIDUAL ISOLATE: 17-18 week fetus
IMMEDIATE SOURCE:
LIBRARY: Stratagene cDNA Library 936206
CLONE: synthesis of 4 clones
PUBLICATION INFORMATION:
AUTHORS: Hlavin, Mary Louise
AUTHORS: Lemmon, Vance
TITLE: Molecular structure and functional
TITLE: testing of human L1CAM: an
TITLE: interspecies comparison.
JOURNAL: GENOMICS
VOLUME: 11
ISSUE:
PAGES: 416-423
DATE: 1991
RELEVANT RESIDUES IN SEQ ID NO: 1 TO 3774
US-08-341-843B-1

Alignment Scores:
Pred. No.: 3,516-07 Length: 3774
Score: 199.00 Matches: 88
Percent Similarity: 36.67% Conservative: 33
Best Local Similarity: 26.67% Mismatches: 107
Query Match: 12.38% Indels: 102
DB: 2 Gaps: 19

US-10-047-021-86 (1-303) x US-08-341-843B-1 (1-3774)

QY	26	MetAlaGlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGly	45
DB	109	ATCAGGAACAGTCTCCACGGCGCTGTGTGTCTTCCACAGATGACATC	159
QY	46	ProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTrp	65
DB	160	-----AGCCTCAAGTGTGAGCGCAGTGGCAAGCCCGAAGTGCAGTTCGGCTGG	207
QY	66	LeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAsp	85
DB	208	ACGAGGATGGTGTC-----CACTTCAAACCCCAAG	237
QY	86	GlyThrLeu-----LeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGln	103
DB	238	GAAGAGCTGGGTGTGACCGGTGTACCAAGTCGCCC-----CACTCTGGCTCC	282
QY	104	AlaLeuSerThrAsp-----LeuGlyValThrCys	114
DB	283	TTCACATCAGGGCAACACAGCACTTGTCTGACAGGTTCCAGGGCATCTACCGCTGC	342
QY	115	GluAlaSerAsnArgLeuGlyThrAlaValSerArgGlyAlaArgLeuSerValAlaVal	134

DB	343	TTTCCAGCAATAAGCTGGGCACCCCATGTCCTCCATGAGATCCGGCTC	390
QY	135	LeuArgGluAspPheGlnIleGlnProArgAspMetValAlaValVal	150
DB	391	ATGCGCGAGGGTGCCTCCCAAGTGGCCAAAGAGACAGTGAAGCCCTGGAGGTGAGGAA	450
QY	151	GlyGluGlnPheThrLeuGluCysGlyProTrpTrpGlyHisProGlyProThrValSer	170
DB	451	GGGAGTCAAGTGTCTTGCCTTGCACCCCTCC-----CCAAGTGCAGAGCCTCTCCGGATC	507
QY	171	TrpTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrValSerGly	189
DB	508	TACTGGATGAACAGCAAGATCTTCACATCAAGCAGGACGAGCGGGTGCACATGGGCCAG	567
QY	190	--GlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu***Thr--TyrMetCys	207
DB	568	AACGGCAACCTCTACTTTGCCAATGTGCTCACTCCCGCAACCACTAGACTATCTGTC	627
QY	208	ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu	227
DB	628	-----CACGCCACTTCCCGAGGCACCGAGGACCATCATTCAGAAG	666
QY	228	ProGlnAspTyrThrGluProValGluLeuAlaValArgIleGlnLeuGluAsnVal	247
DB	667	-----GAACCCATTGACCTC-----CGGTCAAGGCCACCAAC	699
QY	248	ThrLeuLeuAsnProAspPro-AlaGluGlyProLysProArgProAlaVal	264
DB	700	AGCATGATTGACAGGAAGCGCGCTGCTCTTCCCACTCCAGCACTCCAGCAGCCACTGTGTG	759
QY	265	-----TrpLeu***TrpLysValSerGlyPro***ArgLeuPro--	277
DB	760	GCCTTGCAGGGGAGCCATTGG---TCCTGGAGTGCATCG---CCGAGGGCTTTCCACAG	813
QY	277	-----	277
DB	814	CCCACCATCAAAATGGCTGCGCCCGAGTGGCCCATGTCAGCTGACCGTGTCACTTACCAG	873
QY	278	-AsnLeuThrArgProCysSer-GlyPro-----ArgLeuProA	290
DB	874	AACCACAACAGACCTGTCAGCTGCTGAAAGTGGCGAGGAGATGATGGCGAGTACCGC	933
QY	290	rgGluAlaArgGluLeuArgGlyGln	298
DB	934	TGCCTGGCCGAGAACTCACTGGGCAG	959

Search completed: January 31, 2004, 15:30:45
Job time : 83.4611 secs

Qy 265 -----TrrLeu***TrrLysValSerGlyPro***ArgLeuPro-- 277
Db 786 GCCTTGACGGGGCAGCCATCG---TCCTGGAGTGCATCG---CCGAGGGCTTTCCACG 839
Qy 277 ----- 277
Db 840 CCCACCATCAATGGCTGCGCCCGCAGTGGCCCATGCCAGCTGACCGTGTCCACTACCCAG 899
Qy 278 -AsnLeuThrArgProCysSer-GlyPro-----ArgLeuProA 290
Db 900 AACCAACAAGACCTCGACTGCTGAAAGTGGCGGAGGAGTATGGCGAGTACCGC 959
Qy 290 rgGluAlaArgGluLeuArgGlyGln 298
Db 960 TGCCTGGCGGAGAACTCACTGGGCAG 985
RESULT 14
US-09-638-649-2
; Sequence 2, Application US/09638649
; Patent No. 6563015
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Yan, Shi Du
; TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED
; TITLE OF INVENTION: GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 0575/62175
; CURRENT APPLICATION NUMBER: US/09/638,649
; CURRENT FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1426
; TYPE: DNA
; ORGANISM: Bos Taurus
US-09-638-649-2
Alignment Scores:
Pred. No.: 1,028-07 Length: 1426
Score: 199.00 Matches: 89
Percent Similarity: 38.63% Conservative: 35
Best Local Similarity: 27.73% Mismatches: 122
Query Match: 12.38% Indels: 76
Gaps: 4
US-10-047-021-86 (1-303) x US-09-638-649-2 (1-1426)
Qy 32 ProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGly---ProGlyProAlaArg 50
Db 376 CCAGAAAT---GTTGATCTGCTCTGCACTCATGGTGTGTCCTCCCAATAAGTGGG 432
Qy 51 MetSerCysArgAlaSerGlyGlnProProProThrIleArgTrrLeuLeuAsnGlyGln 70
Db 433 ACATGTGTGTCGAGGGGGGTACCTCGACGGGACTCTTAACCTGCTCTTGGATGGGAA 492
Qy 71 ProLeuSerMetValProProAspProHisLeuLeuProAspGlyThrLeuLeuLeu 90
Db 493 ACT-----CTGATCTCTGATGGCAAGAGGTGTCA 522
Qy 91 LeuGlnProProAlaArgGlyHisAlaHisAspGlyGln---AlaLeuSerThrAspLeu 109
Db 523 GTGAAGGAAGAGACCAAGACAGACACCAAGACAGGGCTTTTCAGCTCCATTCCGAGCTG 582
Qy 110 GlyVal-----TyrThrCysGluAlaSer--- 117
Db 583 ATGTGACCCAGCTCGGGGAGGAGCTCTCCACCCCACTTCTCTCTGTAGCTTCCACCT 642
Qy 118 -----AsnArgLeuGlyThrAlaVal----- 124
Db 643 GGCCTTCCCGCGCGCGAGCCCTGCACACGGCCCTCCATCCAGCTCAGGCTGTGAGTAG 702
Qy 125 -----SerArgGlyAlaArgLeuSerValAlaValLeuArgGlu---AspPheGln 140

Db 703 CACGAGGTGGGAGGGCCCCAACGTCGACGCTGTGCTCACTGAAGGAAGTCCAGTTGGTG 762
Qy 141 IleGlnProArgAspMetValAlaValValGlyGlnPheThrLeuGluCysGlyPro 160
Db 763 GTAGAGCCCAAGAGGGGAGCAGTAGCTCTCGTGGTGTACTGTGACCTTGACCTGTGAAGCC 822
Qy 161 ProTrrPglyHisProGluProThrValSerTrrTrrLysAspGlyLysProLeuAlaLeu 180
Db 823 CCC---GCCAGCCCCCACTCAATCCACTGGATCAAGATGGCAGGCCCTCCCTT 879
Qy 181 GlnProGlyArgHisThrValSerGlySerLeuLeuMetAlaArgAlaGlyLysSer 200
Db 880 CCCCCCT-----GGCCCCATGCTGCTCTCTCCAGAGGTAGGGCCCTGAG 921
Qy 201 AspGlu***ThrTyrMetCysValAlaThrAsn---SerAlaGlyHisArgGluSerArg 219
Db 922 GACGAGGAACTACATGTTGTGTGGCCACCATCCCATGCGCCAGGAGGAGCCGT 981
Qy 220 AlaAlaArgValSerIleGlnGluProGlnAspTrrThrGluProValGluLeuAla 239
Db 982 GCTGTACGCTCAGCATCATCGAA-----ACAGCGAGGAGGGGACGACTGCA 1029
Qy 240 ValArgIleGlnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLys 259
Db 1030 GGCTCTGTGAAGGGCGGGCTGGAACCCCTAGC-CCTGACCTGGGGATCTCTGGGAGG 1088
Qy 260 Pro-----ArgProAlaValTrr-----Leu***TrrLysValSer----- 271
Db 1089 CCTGGGACACATGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1148
Qy 272 -----GlyPro***ArgLeu-----ProAsnLeuThr 280
Db 1149 AGGACAGAGGAGGAGGTCCCGGAAACACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1208
Qy 281 ArgProCysSerGlyProArgLeuProArgGlu-----AlaArgGluLeuArgGlyGln 298
Db 1209 GAACGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1268
Qy 299 Arg 299
Db 1269 CGG 1271
RESULT 15
US-08-341-843B-1
; Sequence 1, Application US/08341843B
; Patent No. 5872225
; GENERAL INFORMATION:
; APPLICANT: Lemmon, Vance
; TITLE OF INVENTION: A Method for Characterizing the
; TITLE OF INVENTION: Nucleotide Sequence of LicAM and
; Patent No. 5872225
; TITLE OF INVENTION: the Nucleotide Sequence
; TITLE OF INVENTION: Characterized Thereby
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fay, Sharpe, Beall, Fagan,
; ADDRESSEE: Minnich & McKee
; STREET: 1100 Superior Avenue
; STREET: Suite 700
; CITY: Cleveland
; STATE: Ohio
; COUNTRY: U.S.A.
; ZIP: 44114-2518
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; MEDIUM TYPE: storable
; COMPUTER: Compaq Prolinea 5100e
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/341,843B
; FILING DATE: No. 5872225ember 18, 1994

Db 550 TGCAGT---ACCATGGGGAATCCAAACACGAGCCATTCATGTTCAAGATGAAACTGCA 606
Qy 178 LeuAlaLeu---GlnProGlyArgHisThrValSerGlyGlySerLeuLeuMetAlaArg 196
Db 607 CTGAAAATGACGAGCTCGAAGCTTCTGCTTGTAGTCTGGGAACCTTAAGAATTGCAAT 666
Qy 197 AlaGluLysSerAspGlu***ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArg 216
Db 667 GTTCAGCTTGAAGATGACGAGAAATATCGATGTTTGGCAAGAAACAGCCTGGGCTTCGAG 726
Qy 217 GluSerArgAlaAlaArgValSerIleGln 226
Db 727 TATTCAGATCTGCGGCTCTGGAAGTGCAG 756

RESULT 13

US-08-427-497E-6

Sequence 6, Application US/08427497E

Patent No. 5969124

GENERAL INFORMATION:

APPLICANT: Lemmon, Vance

TITLE OF INVENTION: A Method for Characterizing the

TITLE OF INVENTION: Nucleotide Sequence of L1CAM and

Patent No. 5969124

TITLE OF INVENTION: the Nucleotide Sequence

TITLE OF INVENTION: Characterized Thereby

NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fay, Sharpe, Beall, Fagan,

ADDRESSEE: Minnich & McKee

STREET: 1100 Superior Avenue

CITY: Cleveland

STATE: Ohio

COUNTRY: U.S.A.

ZIP: 44114-2518

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb

MEDIUM TYPE: storable

COMPUTER: Compaq Prolinea 5100e

OPERATING SYSTEM: DOS 5.0

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/427,497E

FILING DATE: April 24, 1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/904,991

FILING DATE: June 26, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Minnich, Richard J.

REGISTRATION NUMBER: 24,175

REFERENCE/DOCKET NUMBER: CWR 2 149-3-1

TELEPHONE: (216) 861-5582

TELEFAX: (216) 241-1666

TELEX: (216) 980162

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 1042

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: nucleic acids

HYPOTHETICAL: irrelevant

ANTI-SENSE: no

ORIGINAL SOURCE:

ORGANISM: homo sapiens

INDIVIDUAL ISOLATE: 17-18 week fetus

IMMEDIATE SOURCE:

LIBRARY: Stratagene cDNA Library 936206

CLONE: C2

PUBLICATION INFORMATION:

AUTHORS: Hlavin, Mary Louise

AUTHORS: Lemmon, Vance
TITLE: Molecular structure and functional testing of
human L1CAM: an interspecies comparison.
JOURNAL: GENOMICS
VOLUME: 11
ISSUE:
PAGES: 416-423
DATE: 1991
RELEVANT RESIDUES IN SEQ ID NO: -26 to 1016
US-08-427-497E-6

Alignment Scores:

Pred. No.: 6,84e-08 Length: 1042

Score: 199.00 Matches: 88

Percent Similarity: 26.67% Conservative: 33

Best Local Similarity: 26.67% Mismatches: 107

Query Match: 12.38% Indels: 102

DB: 2 Gaps: 19

US-10-047-021-86 (1-303) x US-08-427-497E-6 (1-1042)

Qy	26	MetAlaGlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGly	45
Db	135	ATCAGCGAACAAGTCTCCACGGCGCTGTTGTTCTTCCCCACAGATGACATC	185
Qy	46	ProGlyProAlaArgMetSerCysArgAlaSerGlnProProThrIleArgTrp	65
Db	186	-----AGCCTCAAGTGTAGCCAGTGCAGCCCGGAGAGTGCAGTCCGCTGG	233
Qy	66	LeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAsp	85
Db	234	ACGAGGGATGTGTC-----CACTTCAAAACCCCAAG	263
Qy	86	GlyThrLeu-----LeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGln	103
Db	264	GAAGAGCTGGGTGTGACCGTGTACCGTGTGCGCC-----CACTCTGGCTCC	308
Qy	104	AlaLeuSerThrAsp-----LeuGlyValTyrThrCys	114
Db	309	TTCACCATCACGGGCAACACAGCAACTTCTGCTCAGAGTTCCAGGGGCATCTACCGCTGC	368
Qy	115	GluAlaSerAsnArgLeuGlyThrAlaValSerArgGlyAlaArgLeuSerValAlaVal	134
Db	369	TTTGCCAGCAATAAGCTGGGCAACCGCATGTCCCATGAGATCCGGCTC-----	416
Qy	135	LeuArgGluAspPheGlnIleGlnProArgAspMetValAlaVal-----	150
Db	417	ATGCGCGAGGTGCCCCCAAGTGGCCAAAGGAGACAGTGAAGCCGTGGAGGTGAGGAA	476
Qy	151	GlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluProThrValSer	170
Db	477	GGGAGTCAAGTGTGCTGCTTGAACCTTCC-----CCAAAGTGAGAGCCCTCTCCGGATC	533
Qy	171	TrpTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrValSerGly---	189
Db	534	TACTGGATGAACACAGATCTTCACATCAGCAGGAGCGGGTACAGTGGGCCAG	593
Qy	190	---GlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu***Thr---TyrMetCys	207
Db	594	AACGGCAACCTCTACTTTGCCAATGTGCTCACCTCCGACACCACTCAGACTACATCTGC	653
Qy	208	ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu	227
Db	654	-----CAGCCCACTTCCAGGACACGAGACCATTCATTCAGAAAG	692
Qy	228	ProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluAsnVal	247
Db	693	-----GAACCATTTGACCTC-----CGGTCAGAGCCCAACAC---	725
Qy	248	ThrLeuLeuAsnProAspPro-AlaGluGlyProLysProArgProAlaVal-----	264
Db	726	AGCATGATTGACAGGAAGCGCGCTGCTCTTCCCACTCCAACTCCAGCAGCACCTGCTGTG	785

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Best Local Similarity: 27.98% Mismatches: 97
Query Match: 12.81% Indels: 42
DB: 5 Gaps: 11

US-10-047-021-86 (1-303) x PCT-US94-05277-1 (1-4608)

Qy 51 MetSerCysArgAlaSerGlyGlnProProThrIleArgTyrLeuLeuAsnGlyGln 70
Db 475 CTCAAGTGTGAAGTCATTGGGAGCCCATGCCAATCCACTGCCAGAGAACCAACAA 534
Qy 71 ProLeuSerMetValProProAspProHis---HisLeuLeuProAspGlyThrLeuLeu 89
Db 535 GACCTGACTCAATCCCAAGGAGTCCCGAGTGGTGTCTTGGCCCTCTGGAGCATTCGAG 594
Qy 90 Leu-----LeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 107
Db 595 ATCAGCCGACTCCACCG-----GGG 615
Qy 108 AspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArg--- 126
Db 616 GACATTGGAATTTACCGATGCTCAGCTCGAAT-----CCAGCCAGCTCAAGAAC 666
Qy 127 GlyAlaArgLeuSerValAlaValLeuArgGluAsp-----Phe 139
Db 667 GGAATGAAGCAGAGTCAAGATTTTATCAGATCCAGGACTGCATAGACAGCTGTATTTT 726
Qy 140 GlnIleGlnProArgAspMetValAlaValGlyGluGlnPheThrLeuGluCysGly 159
Db 727 CTGCAAGACCATCAATGTATGATGACCATTAAGGAAGAAGATGCTGCTCGAATGTGT 786
Qy 160 ProProTrpGlyHisProGluProProThrValSerTrpTrpLysAspGlyLysProLeuAla 179
Db 787 GTTCTCT---GGCTATCTCCACCAAGTTTACCTGTTACGAGCGAGGAAGTCATCCAA 843
Qy 180 LeuGlnProGlyArgHisThrValSerGlyGlySer---LeuLeuMetAlaArgAlaGlu 198
Db 844 CTCAGGTCTAAAGATATTCTTTATGTTGGTGGAGCAACTTGTCTATCTCCAATGTGACA 903
Qy 199 LysSerAspGlu**ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSer 218
Db 904 GATGATGACAGTGGATGATATACCTGTTGTTCATATATAAATGAGAAATATAGTGCC 963
Qy 219 ArgAlaAlaArgValSerIleGlnGluProGlnAspTyrThrGluProValIleGluLeu 238
Db 964 TCTGCAGAGCTCACAGTCTGTGTTCCGCCATGTTTAAATCATCTCTTCCAACTGTAT 1023
Qy 239 Ala-----ValArgIleGlnLeuGluAsnValThrLeuLeuAsnProAspProAla 255
Db 1024 GCCTATGAAGCATGGATATTGAGTTTGAATGTACAGTC-----1062
Qy 256 GluGlyProLysProArgProAlaValTrpLeu**TrpLysValSerGlyPro**Arg 275
Db 1063 ---TCTGAAGCCCTGTGCCACTGTG-----AATTGGATGAAGATGGAGATGTGTC 1113
Qy 276 LeuProAsn 278
Db 1114 ATTCCTACT 1122

RESULT 12
PCT-US95-08493-12
Sequence 12, Application PC/TUS9508493
GENERAL INFORMATION:
APPLICANT: Wood, Clive
APPLICANT: Caruso, Anthony
TITLE OF INVENTION: Novel mlk Receptor Tyrosine Kinases
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESS: LEGAL AFFAIRS
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
```

```
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08493
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: GI5234A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 3398 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 121..2961
PCT-US95-08493-12

Alignment Scores:
Pred. No.: 1.91e-07 Length: 3398
Score: 201.50 Matches: 66
Percent Similarity: 43.91% Conservative: 35
Best Local Similarity: 28.70% Mismatches: 86
Query Match: 12.53% Indels: 43
DB: 5 Gaps: 12

US-10-047-021-86 (1-303) x PCT-US95-08493-12 (1-3398)
Qy 15 LeuProGlnIleLeuLeuLeuLeuLeuMet-----GlyGlyMetAlaGln-----Asp 29
Db 142 ATTCACCTCTGTGATGATCTCTCTGTGACAACTGGGGCTCAGCTGACGGAACTCTTCCC 201
Qy 30 SerProGlnIleLeu-----ValHisProGlnAspGlnLeuPheGlnGlyProGly 47
Db 202 AAAGCTCCACAGATCACCAGTCCCTTGAGACAGATGCTGCTGTGAG-----GAA 255
Qy 48 ProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTrpLeuLeu 67
Db 256 GAAGCTTCTTTCATGTGTGCAGTGTTCATATCCAGCGGCGAGAGATTACCTGGACCCGC 315
Qy 68 AsnGlyGlnProLeuSerMetValProAspProHisHisLeuLeuProAspGlyThr 87
Db 316 AATAACATTCCTAAGAA-----CCCTTTGACACTCGCTACAGTACAAAGAA----- 363
Qy 88 LeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSer--- 106
Db 364 -----AATGCCAGATATTAAACATC 384
Qy 107 -----ThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGly 121
Db 385 CTCAGCGTTGAAGACACAGACAAATGGGTGTACTGTCTGACCCGCCAACACGCGATGGG 444
Qy 122 ---ThrAlaValSerArgGlyAla-----ArgLeuSerValAlaValLeuArgGlu 137
Db 445 AGCTCTGCTCAAAGCTGTGGTCCCTCCAGTCAAAATGAAGCCAAAGATCATTCGG--- 501
Qy 138 AspPheGlnIleGlnProArgAspMetValAlaValValGlyGluGlnPheThrLeuGlu 157
Db 502 -----CCACCCTGATGTGCAGACATGCTGGGATCGGATCGAAGTTGTGTACT 549
Qy 158 CysGlyProProTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLysPro 177
Db -----
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
FILING DATE:
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2626
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 4608 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 1..4342

US-09-041-886-24

Alignment Scores:
Pred. No.: 1.2e-07 Length: 4608
Score: 206.00 Matches: 68
Percent Similarity: 42.80% Conservativity: 36
Best Local Similarity: 27.98% Mismatches: 97
Query Match: 12.81% Indels: 42
DB: 3 Gaps: 11

US-10-047-021-86 (1-303) x US-09-041-886-24 (1-4608)

QY 51 MetSerCysArgAlaSerGlyGlnProProThrIleArgTyrLeuLeuAsnGlyGln 70
DB 475 CTCAGTGTGAAGTATGGGAGGCCATCCACAACTCCATGCGAAGAACCAACA 534
QY 71 ProLeuSerMetValProProAspProHis---HisLeuLeuProAspGlyThrLeuLeu 89
DB 535 GACCTGACTCCAAATCCAGGTGACTCCCGAGTGGTGTCTGCCCTCTGGAGCATTCGAG 594
QY 90 Leu-----LeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 107
DB 595 ATCAGCCGACTCCAAACCG-----GGG 615
QY 108 AspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArg--- 126
DB 616 GACATTGGAATTTACCGATGCTCAGCTCGAAT-----CCAGCCAGCTCAGAACA 666
QY 127 GlyAlaArgLeuSerValAlaValLeuArgGluAsp-----Phe 139
DB 667 GGAATGGAAGCAGAGAGTCAAGATTTATCAGATCCAGGACTGCATAGACAGCTGTATTT 726
QY 140 GlnIleGlnProArgAspMetValAlaValGlyGluGlnPheThrLeuGluCysGly 159
DB 727 CTGCAAGACCACCAATAGTAGTACCCATGAAGGAAAGAGTGTCTCTGGAATTTGT 786
QY 160 ProProTyrGlyHisGluProThrValSerTyrTyrAspGlyLysProLeuAla 179
DB 787 GTTTCCT---GGTATCTCTCCCAAGTTTACCTGGTTACGAGCGGAGGAAGTCAACAA 843
QY 180 LeuGlnProGlyArgHisThrValSerGlyGlySer---LeuLeuMetAlaArgAlaGlu 198
DB 844 CTCAGGTCTAAAGATATTCTTTATTGGTGGAGCAACTTGCTTATCTCCAATGTGACA 903
QY 199 LysSerAspGlu***ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSer 218
DB 904 GATGATGACAGTGGAGTACCTGTGTGTGCACATATATAAAATGAGAATATTAGTGCC 963
QY 219 ArgAlaAlaArgValSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeu 238

Db 964 TCTGACAGCTCAGACTCTGGTTCCGCCATGTTTAAATCATCTCTCCCAACCTGTAT 1023
QY 239 Ala-----ValArgIleGlnLeuGluAsnValThrLeuLeuAsnProAspProAla 255
DB 1024 GCCTATGAAGCATGATATTGAGTTTGAATGTACAGTC-----1062
QY 256 GluGlyProLysProArgProAlaValTrpLeu**TrpLysValSerGlyPro***Arg 275
DB 1063 ---TCTGGAAGCCTGTGCCACCTGTG-----AATTGGATGAGAGATGGAGATGGTGC 1113
QY 276 LeuProAsn 278
DB 1114 ATTCCTAGT 1122

RESULT 11

PCT-US94-05277-1

Sequence 1, Application PC/TUS9405277

GENERAL INFORMATION:

APPLICANT: Bruskin, Arthur

APPLICANT: Jarosz, David E.

APPLICANT: Johnson, Karen

APPLICANT: Kinzler, Kenneth W.

APPLICANT: Vogelstein, Bert

APPLICANT: Zabrecky, James R.

TITLE OF INVENTION: Antibodies Specific for DCC Gene Product

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner, Birch, McKie & Beckett

STREET: 1001 G Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20001

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/05277

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Kagan, Sarah A. 32,141

REGISTRATION NUMBER: 32,141

REFERENCE/DOCKET NUMBER: 01107.42709

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202.508.9100

TELEFAX: 202.508.9299

TELEX: 197430 BMB UT

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 4608 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: CDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORGANISM: Homo sapiens

POSITION IN GENOME: 18q21

CHROMOSOME/SEGMENT: 18q21

FEATURE:

NAME/KEY: CDS

LOCATION: 1..4342

PCT-US94-05277-1

Alignment Scores:

Pred. No.: 1.2e-07 Length: 4608

Score: 206.00 Matches: 68

Percent Similarity: 42.80% Conservativity: 36


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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
PCT-US94-10166-6

Alignment Scores:
Pred. No.: 8.31e-11 Length: 6000
Score: 246.00 Matches: 94
Percent Similarity: 44.13% Conservative: 45
Best Local Similarity: 29.84% Mismatches: 101
Query Match: 15.30% Indels: 77
DB: 5 Gaps: 17

US-10-047-021-86 (1-303) x PCT-US94-10166-6 (1-6000)

Qy 2 GlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeu 21
Db 38 GGCCTGCGATGCTGTGTGTTGTTGCCATGCGC-----CTCCTTGTGTCTG 88
Qy 22 IleMetGlyGlyMetAlaGlnAspSerProGlnIleLeuValHisProGlnAspGln 41
Db 89 CTCGTGGAGCTGTGCAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 148
Qy 42 LeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 61
Db 149 ATCGCGGTGTGCGGCGGTGTGCTCTTTCGTGTGTGTCAGGCGAGGCGTGCACCA 208
Qy 62 ThrIleArgTTP-----LeuLeuGlnGlyGlnProLeuSerMetValPro 76
Db 209 CGAGTGACCTGGAAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 268
Qy 77 ProAspProHisLeuLeuProAspGlyThrLeuLeuLeuGlnProProAlaArg 96
Db 269 TTTGATGAG-----AGTCAGGCGAGTGTGTGAGATCCAGCG----- 307
Qy 97 GlyHisAlaHisAspGlyGlnAlaLeuSerThr-----AspLeuGlyValThrCys 114
Db 308 -----CTGAGGACACCGCGGAGTGAAGAGTGTACGAGTGT 343
Qy 115 GluAlaSerAsnArgLeuGlyThrAlaValSerGlyAlaArgLeuSerValAlaVal 134
Db 344 GTGGCCCAAGATCGGTTGGG---GAGATCACAGTCCATGCCAAGCTTACT-----GTC 394
Qy 135 LeuArgGluAsp-----PheGlnIleGlnProArgAspMet 146
Db 395 CTCGAGAGGACAGCTCCCTCTGGCTTCCCAACATCGACATGGGCCACAGTTGAAG 454
Qy 147 ValAlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGlu 166
Db 455 GTGGTGGAGCGGACACGACGACACCACTGCTCTGTGCAGCCAGC---GGCAACCCCTGAC 511
Qy 167 ProThrValSerTrpTrpIleAspGlyIysProLeu-----AlaLeuGlnProGlyArg 184
Db 512 CTGTAGATCACTGCTTCAAGGACTTCTGCTGTCGATCTCTGTCGAGCAGCAATGGACGC 571
Qy 185 ---HisThrValSerGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu*** 203
Db 572 ATCAACACAGCTCGATCAGGAGCCCTGCGATTTGAAGCAGTGAAGAAACCGACCGGC 631
Qy 204 ThrTrpMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgVal 223
Db 632 AATATGATGTGTGCGCCACCAACAGCGCGCGGTGCGC----- 670
Qy 224 SerIleGlnGluProGlnAspTrpThrGluProValGluLeuLeuAlaValArgIleGln 243
Db 671 -----TACTCTTCACCTGCGCAACCTCTAC---GTGCGAGTCCGC 706
Qy 244 LeuGluAsnValThrLeuLeuAsnPro-----AspProAlaGluGlyPro 258
Db 707 CG-CGTGGCCCGCGCTTCTCATCTCTGCCCATGATGACCGCATGATGCCAGGGGGCAA 765
Qy 259 LysProArgProAlaValTrpLeu***TrpIysValSerGlyPro***ArgLeuProAsn 278
Db 278
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Db 766 CGTGAACATCA-CCTGCTGG-----CCGTGG----- 791
Qy 279 LeuThrArgProCys-----SerGlyProArgLeuProArg 290
Db 792 ---GCTGCCCATGCCATACGTGAAGTGGATGCAGGGGGCGGAGG 833

RESULT 7
US-08-447-464-2
; Sequence 2, Application US/08447464
; Patent No. 5840842
; GENERAL INFORMATION:
; APPLICANT: Schlusser, Joseph
; APPLICANT: Yan, Hai
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PROTEIN
; TITLE OF INVENTION: PHOSPHOTYROSINE PHOSPHATASE-SIGMA
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/447,464
; APPLICATION NUMBER: 08/130,570
; FILING DATE: 01-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7683-043
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5690 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 833..5338
; US-08-447-464-2

Alignment Scores:
Pred. No.: 3.91e-10 Length: 5690
Score: 237.50 Matches: 72
Percent Similarity: 48.07% Conservative: 40
Best Local Similarity: 30.90% Mismatches: 82
Query Match: 14.77% Indels: 39
DB: 2 Gaps: 11

US-10-047-021-86 (1-303) x US-08-447-464-2 (1-5690)

Qy 13 GlySerLeuProLeuLeuLeuLeuLeuMetGlyGlyMetAlaGlnAspSerProPro 32
Db 872 GGTCTGTGGGGCTCTTCTTGTACTGCTGCCAGAGGGTCTTGGCTGAAGACCC 931
Qy 33 GlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGlyProAlaArgMetSer 52
Db 932 AGATTTATCAGAGAGCCCAAGGATCAGATTGGTGTGTGTCAGAGCGGTGCTCTTCTG 991
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; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; QUERY APPLICATION NUMBER: US/09/158,657
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/800,825
; FILING DATE: 14-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: HAND, J. MARK
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: 18992DA
; TELEPHONE: 732-594-3905
; TELEFAX: 732-594-4720
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6000 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-158-657-6

Alignment Scores:
Pred. No.: 8,31e-11 Length: 6000
Score: 246.00 Matches: 94
Percent Similarity: 44.13% Conservative: 45
Best Local Similarity: 29.84% Mismatches: 101
Query Match: 15.30% Indels: 77
DB: 3 Gaps: 17

US-10-047-021-86 (1-303) x US-09-158-657-6 (1-6000)

QY 2 GlySerglyGlyAspSerLeuLeuGlyArgGlySerLeuProLeuLeuLeuLeu 21
Db 38 GGCCTGGCATGGTCTGTGTGGTGGTCCCATGGGC-----CTCTTGTGTCTG 88
QY 22 IleMetGlyMetAlaGlnAspSerProGlnIleLeuValHisProGlnAspGln 41
Db 89 CTCGTGGAGGCTGTGCAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 148
QY 42 LeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 61
Db 149 ATCCGGGTGTCGGGGGTGTGGCTCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 208
QY 62 ThrIleArgTrp-----LeuLeuGlnGlyGlnProLeuSerMetValPro 76
Db 209 CGAGTGACCTGGAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 268
QY 77 ProAspProHisIleLeuLeuProAspGlyThrLeuLeuLeuGlnProProAlaArg 96
Db 269 TTTGATGAG-----AGTCAGGAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 307
QY 97 GlyHisAlaHisAspGlyGlnAlaLeuSerThr-----AspLeuGlyValThrCys 114
Db 308 -----CTGAGGACACCGCGGATGAAACGTGTACAGTGT 343
QY 115 GluAlaSerAsnArgLeuGlyThrAlaValSerArgGlyAlaArgLeuSerValAlaVal 134
Db 344 GTGGCCCAAGACTCGGTTGGG---GAGATCACAGTCCATGCCAAGCTTACT-----GTC 394
QY 135 LeuArgGluAsp-----PheGlnIleGlnProArgAspMet 146
Db 395 CTCGAGAGGAGGACCAAGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 454
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671	Db	-----TACTCTCTCACTGCGCAACCTCTTAC-----GTGGGAGTCCGC	706
244	Qy	LeuGluAsnValThrLeuLeuAsnPro-----AspProAlaGluGlyPro	258
707	Db	: CG-CGTGGCCCGCGCTTCTCCATCTGCCCCATGAGCCAGAGATCATGCCAGGGGGCA	765
259	Qy	LysProArgProAlaValTrpLeu***TrpLysValSerGlyPro***ArgLeuProAsn	278
766	Db	: CGTGAACATCA-CCTGCGTGG-----CCGTGG-----	791
279	Qy	LeuThrArgProCys-----SerGlyProArgLeuProArg	290
792	Db	---GCTCCCCCATGCATACGTGAAGTGGATGCGAGGGGCCGAGG	833

RESULT 4

RESOLUTION 4
US-08-800-825A-6
Sequence 6, Application US/08800825A
Patent No. 5866397
GENERAL INFORMATION:
APPLICANT: RODAN, GIDEON A.
APPLICANT: SCHMIDT, AZRIEL
APPLICANT: RUTLEDGE, SU JANE
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: J. MARK HAND - MERCK & CO., INC.
STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,825A
FILING DATE: 14-FEB-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HAND, J. MARK
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 18992DA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-3905
TELEFAX: 732-594-4720
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 6000 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-800-825A-6

Qy 32 ProGlnIleLeuValHisProGlnAaspGlnLeuPheGlnGlyProGlyProAlaArgMet 51
Db : : : : :
790 CCGCGATCACTCCGAGCCCGAGGACCGAGATGTGACCTCGGGAAACACCGTGTACTTC 849
Qy 52 SerCysArgAlaSerGlyGlnProProProProThrIleArgTrpLeuLeuAasnGlyClnPro 71
Db : : : : :
850 ACCTGCAGAGCGGAGGCAAGCCCAAGCTGAGATCATCTGCTCGGAAACAATAATGAG 909
Qy 72 LeuSerMetValProProAaspProHisIleLeuLeuProAaspGlyThrLeuLeuLeuLeu 91
Db : : : : :
910 CTGACATGAGACAGATCCCGCTAACTGCTGGAGATGGAGCCCTGATGATC--- 966
Qy 92 GlnProProAlaArgGlyHisAlaHisAaspGlyGlnAlaLeuSerThrAaspLeuGlyVal 111
Db : : : : :
967 -----CAGAACACACAGGACAGACACAGGCGTATC 996
Qy 112 TyrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGlyAlaArgLeuSer 131
Db : : : : :
997 TACCAGTGCATGGCAAGAACGTCGCCGAGAGGTGAAGACGCAAGAGGTGACCCCTCAGG 1056
Qy 132 Val-----AlaValLeuArgGluAaspPheGlnIleGlnProArgAaspMetValAlaVal 149
Db : : : : :
1057 TACTTCGGGTCTCCAGCTCGACCCACTTTTGTATCCAGCCACAGATACAGAGGTGTG 1116
Qy 150 ValGlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluProThrVal 169
Db : : : : :
1117 GTTGGGAGAGCGTCACCTGGAGTGCAGGCCACA---GGCCACCCCGCGCGGATC 1173
Qy 170 SerTrpTrpLys---AaspGlyLysProLeuAlaLeuGlnProGlyArgHisThrValSer 188
Db : : : : :
1174 TCCTGCAGAGAGGTGACCGCACACCTTGCAGTTGACCGCGCGGTGAACATCACGGCT 1233
Qy 189 GlyGlySerLeuLeuMetAlaArgAlaGluLysSerAaspGlu**ThrTyrMetCysVal 208
Db : : : : :
1234 TCTGGCGGGCTTATCAGAACCTGTACAGGGGGACGCGGAGATATGCGGTCT 1293
Qy 209 AlaThrAenSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGluPro 228
Db : : : : :
1294 GCGACCAACAACATTTGACAGCGTCCATGCCCGCTTTCATCATCGTCCAGGCTCTTCT 1353
Qy 229 GlnAaspTyrThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluAasnValThr 248
Db : : : : :
1354 CAGTTCACTGTGACGCTCAGGAC-----AGAGTGTGTTATTGAGGGCCAGACC 1401
Qy 249 Leu-Leu-----AenProAaspProAlaGln 256
Db : : : : :
1402 GTGGATTTCCAGTGTGAAGCCAGGCGCAACCGCGCGCTTCATCGCTCGACCAAGGGA 1461
Qy 256 uGly-Pro-----LysProArgProAlaVal----- 264
Db : : : : :
1462 GGGAGCCAGCTCTCGTGGACCGCGGACCTGCTGTCATCGGGAACACTTAGAATC 1521
Qy 265 ---TrpLeu**TrpLysValSerGlyPro**ArgLeuProAasnLeuThrArgProCys 284
Db : : : : :
1522 TCTGTGTGTCCCTCCACGACGAGGCGCAGTACGAATGCCAGGC-----TGTC 1569
Qy 284 erGlyProArgLeuProArgGluAlaArgGluLeuArgGly----- 297
Db : : : : :
1570 AACATCATCGGCTCCCA-----GAAGTGTGTGGCCACCTGACTGTGTCAGGCC 1617
Qy 298 -----GlnArgArgAasnThrGly 303
Db : : : : :
1618 AGAGTCACCCAGTGTGTCAGCATTTCCAGCGACACACACAGTGA 1664

RESULT 2

US-09-016-434-1132
; Sequence 1132, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION

NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1132:
SEQUENCE CHARACTERISTICS:
LENGTH: 4078 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g1407624
US-09-016-434-1132
Alignment Scores:
Pred. No.: 5,09e-11 Length: 4078
Score: 246.00 Matches: 94
Percent Similarity: 44.13% Conservative: 45
Best Local Similarity: 29.84% Mismatches: 101
Query Match: 15.30% Indels: 77
DB: 4 Gaps: 17

US-10-047-021-86 (1-303) x US-09-016-434-1132 (1-4078)

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Db : : : : :
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Qy 22 IleMetGlyGlyMetAlaGlnAaspSerProGlnIleLeuValHisProGlnAaspGln 41
Db : : : : :
89 CTCGTGGAGCTGTGCAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 148
Qy 42 LeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProProPro 61
Db : : : : :
149 ATCGGCGTGTGGGCGGTGTGGCTCTTTCGTGTGTGTCAGGCCACGGGTGACCCCAAGCCA 208
Qy 62 ThrIleArgTrp-----LeuLeuAasnGlyGlnProLeuSerMetValPro 76
Db : : : : :
209 CGAGTGACCTGGAAACAAGAGAGGCAAGAGTCACTCTCAGCGCTTTGACAGCATTCAG 268
Qy 77 ProAaspProHisHisLeuLeuProAaspGlyThrLeuLeuLeuLeuGlnProProAlaArg 96
Db : : : : :
269 TTTCATGAG-----AGTGCAGGCGAGTGTGTGAGGATCCAGCCG----- 307
Qy 97 GlyHisAlaHisAaspGlyGlnAlaLeuSerThr-----AaspLeuGlyValTyrThrCys 114
Db : : : : :
308 -----CTGAGGACACCGCGGGATGAACACGTGTACGAGTGT 343

GenCore version 5.1.1.6
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OM protein - nucleic search, using frame_plus_p2n model
Run on: January 31, 2004, 12:35:25 ; Search time 66.4611 Seconds
(without alignments)
2012.290 Million cell updates/sec

Title: US-10-047-021-86
Perfect score: 1608
Sequence: 1 MGSGDLSLGGKSGSLPLLL.....SGPRLPREARELGGRRNTG 303

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 569978 segs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters: -DEV-xlp
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-Q=/cgn2_1/USPTO.spool_p/US10047021/runat 30012004.145453 24595/app_query.fasta_1.910
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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA.*
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5: /cgn2_6/ptodata/2/ina/PTCUS.COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	276.5	17.2	6814	US-09-484-970B-66	Sequence 66, Appl
2	246	15.3	4078	US-09-016-434-1132	Sequence 1132, Ap
3	246	15.3	6000	US-08-348-006B-6	Sequence 6, Appl
4	246	15.3	6000	US-08-800-825A-6	Sequence 6, Appl
5	246	15.3	6000	US-09-158-657-6	Sequence 6, Appl
6	246	15.3	6000	PCT-US94-10166-6	Sequence 6, Appl
7	237.5	14.8	5690	US-08-447-464-2	Sequence 2, Appl
8	237.5	14.8	5690	US-08-716-679-2	Sequence 2, Appl
9	207	12.9	3888	US-08-506-296B-13	Sequence 13, Appl
10	206	12.8	4608	US-09-041-886-24	Sequence 24, Appl
11	206	12.8	4608	PCT-US94-05277-1	Sequence 1, Appl
12	201.5	12.5	3398	PCT-US95-08493-12	Sequence 12, Appl

13	199	12.4	1042	2	US-08-427-497E-6	Sequence 6, Appl
14	199	12.4	1426	4	US-09-638-649-2	Sequence 2, Appl
15	199	12.4	3774	2	US-08-341-843B-1	Sequence 1, Appl
16	199	12.4	3774	2	US-08-427-497E-1	Sequence 1, Appl
17	199	12.4	3774	2	US-08-427-497E-2	Sequence 2, Appl
18	196.5	12.2	4078	4	US-09-016-434-1120	Sequence 1120, Ap
19	195	12.1	3991	4	US-08-506-296B-3	Sequence 3, Appl
20	194.5	12.1	3943	4	US-08-506-296B-27	Sequence 27, Appl
21	192	11.9	3189	2	US-08-427-497E-3	Sequence 3, Appl
22	191	11.9	3783	4	US-08-506-296B-20	Sequence 20, Appl
23	189	11.8	4843	3	US-08-986-485-1	Sequence 1, Appl
24	185.5	11.5	1391	4	US-09-638-649-4	Sequence 4, Appl
25	182.5	11.3	5824	4	US-09-620-312D-72	Sequence 72, Appl
26	177.5	11.0	3551	4	US-09-620-312D-760	Sequence 760, App
27	175.5	10.9	1493	2	US-08-752-307B-6	Sequence 6, Appl
28	175.5	10.9	1493	4	US-09-707-802-6	Sequence 6, Appl
29	175.5	10.9	1493	4	US-09-991-326-6	Sequence 6, Appl
30	172	10.7	957	2	US-08-633-148-3	Sequence 3, Appl
31	172	10.7	1023	2	US-08-633-148-1	Sequence 1, Appl
32	170.5	10.6	3360	1	US-08-408-093-5	Sequence 5, Appl
33	170.5	10.6	3360	1	US-08-408-420A-5	Sequence 5, Appl
34	170.5	10.6	3360	1	US-08-714-901-5	Sequence 5, Appl
35	170.5	10.6	3360	3	US-08-040-741-5	Sequence 5, Appl
36	170.5	10.6	3453	4	US-09-877-730-7	Sequence 7, Appl
37	169.5	10.5	1143	4	US-09-877-730-3	Sequence 3, Appl
38	169.5	10.5	2715	4	US-09-877-730-5	Sequence 5, Appl
39	169.5	10.5	2958	4	US-09-877-730-9	Sequence 9, Appl
40	169.5	10.5	3210	4	US-09-877-730-1	Sequence 1, Appl
41	169.5	10.5	3874	4	US-09-877-730-31	Sequence 31, Appl
42	167	10.4	3014	2	US-08-808-982-1	Sequence 1, Appl
43	167	10.4	3014	3	US-09-306-902A-1	Sequence 1, Appl
44	166.5	10.4	1967	3	US-09-383-586-22	Sequence 22, Appl
45	165.5	10.3	2610	1	US-08-374-834-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-09-484-970B-66
; Sequence 66, Application US/09484970B
; Patent No. 6426186
; GENERAL INFORMATION:
; APPLICANT: Jones, Karen A.
; APPLICANT: Volkmath, Wayne
; APPLICANT: Walker, Michael G.
; TITLE OF INVENTION: BONE REMODELING GENES
; FILE REFERENCE: PB-0014 US
; CURRENT APPLICATION NUMBER: US/09/484.970B
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PERL Program
; SEQ ID NO 66
; LENGTH: 6814
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6426186 199882.3
; NAME/KEY: unsure
; LOCATION: 1838, 5528
; OTHER INFORMATION: a, t, c, g, or other
US-09-484-970B-66
Alignment Scores:
Pred. No.: 2.96e-13 Length: 6814
Score: 276.50 Matches: 93
Percent Similarity: 38.80% Conservative: 30
Best Local Similarity: 29.34% Mismatches: 125
Query Match: 17.20% Indels: 69
DB: 4 Gaps: 11
US-10-047-021-86 (1-303) x US-09-484-970B-66 (1-6814)

PN W09925833-A1.
XX
PD 27-MAY-1999.
XX
PF 13-NOV-1998; 98WO-US24327.
XX
PR 14-NOV-1997; 97US-0065543.
XX
XX (REGC) UNIV CALIFORNIA.
XX
PI Goodman C, Kid T, Mitchell KJ, Russell C, Tear G;
XX
DR WPI; 1999-338008/28.
XX
XX P-PSDB; MAY13566.
XX
PT Modulation of Robo-Comm polypeptide interactions
XX
PS Disclosure; Page 42-44; 56pp; English.
XX
XX
CC The invention relates to a method for modulating the amount of Comm
CC (commisuresless) polypeptide in contact with a cell expressing active
CC Robo (roundabout) on its surface. The method comprises modulating the
CC effective amount of Comm polypeptide in contact with the cell, where the
CC amount of expressed active Robo is specifically modulated inversely with
CC the modulation of the effective amount of Comm in contact with the cell.
CC The method is used to modulate the amount of active Robo expressed on a
CC cell. The method can be used to screen for agents that modulate Robo:Comm
CC interactions. This is particularly useful for modulating nerve cell
CC function.
XX
SQ Sequence 4956 BP; 1480 A; 1230 C; 1186 G; 1060 T; 0 other;

Alignment Scores:
Pred. No.: 3,09e-19 Length: 4956
Score: 446.50 Matches: 98
Percent Similarity: 54.36% Conservative: 33
Best Local Similarity: 40.66% Mismatches: 95
Query Match: 27.77% Indels: 16
DB: 20 Gaps: 3

US-10-047-021-86 (1-303) x AAX55770 (1-4956)

QY 11 GlyArgGlySerLeuProLeuLeuLeuLeuMetGlyGlyMetAla----- 27
Db 122 GGACGCAATCCCACTCTGATACGATGACAATTCGCTG-GGCTATACAGGCTCCCGT 180
QY 28 -----GlnAspSerProGlnLeuValHisProGlnAspGlnLeuPheGln 44
Db 181 CTTCGTCAGGAAGATTTTCCACCTCGCATTTGTAACACCCCTTCAGACCTGATTGTCTCA 240
QY 45 GlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProProProThrIleArg 64
Db 241 AAAGAGAACCTGCACTTTGAACCTGCAAGCTGAGGCCGCCGCCACACCCTATTGAA 300
QY 65 TrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisHis----- 81
Db 301 TGGTACAAAGGGGAGAGAGTGGAGACAGACAGAAAGATGACCTTCGCTCACCGCAATG 360
QY 82 LeuLeuProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAsp 101
Db 361 TTGCTGCCGAGTGGATCTTTATTTTCTTACGT-----ATAGTACAT 402
QY 102 GlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGly 121
Db 403 GGACGGAAGAGTAGACCTGATGAGAGTCTATGTCTGTGTAGCAAGGAATTACCTTGA 462
QY 122 ThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIle 141
Db 463 GAGGCTGTGAGCCACAATGCATCGCTGGAAGTAGCCATACCTTCGGGATGACTTCAGACAA 522
QY 142 GlnProArgAspMetValAlaValAlaValGlyGlnGlnPheThrLeuGluCysGlyProPro 161
Db 523 AACCCCTCGGATGTCTATGTTGCTAGGAGAGCCCTGCAGTAATGGAATGCCAACCTCCA 582

QY 162 TrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGln 181
Db 583 CGAGGCCATCCTGAGCCACCACCATTTTCATGAAGAAGATGGCTCTCCACTGGATGATAAA 642
QY 182 ProGlyArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAsp 201
Db 643 GATGAAGAATAACTATACGAGGAGGAAGCTCATGATCACTTACACCCCGTAAAGTGAC 702
QY 202 Glu**ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAla 221
Db 703 GCTGGCAATATGTTGTGTGTGTACCAATATGTTGGGAACCTGAGAGTGAAGTAGCC 762
QY 222 ArgValSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaValArg 241
Db 763 GAGCTGACTCTCTAGAGAGACCATCATTTGTGAAGAGAGACCCAGTAACCTTGGCAGTAACT 822
QY 242 Ile 242'
Db 823 GTG 825

Search completed: January 31, 2004, 12:48:08
Job time : 254.772 secs

Db 574 GTGGCTCAGCTGGAAGTCAAGTGGCCCTGCTGCGCTGCCAATCTTACAGCGCTTGT 633
QY 284 erGlyProArgLeuProArgGluAlaArgGluLeuArgGlnArg 299
Db 634 CAGGACCCAGACTGCCCGGGAGGCCAGGAGCTCCGTGGGAGAGG 680

RESULT 14
AAV69278
ID AAV69278 standard; cDNA; 4291 BP.
XX AAV69278;
AC
DT 01-MAR-1999 (first entry)
XX Human T85 cDNA.
XX T85; FMHB-6D4; FMHV-SD4; human; neurological disorder; therapy;
KW diagnosis; ss.
XX Homo sapiens.

Key Location/Qualifiers
CDS 558..3219
FT /*tag= a
FT sig_peptide 558..1017
FT /*tag= b
FT mat_peptide 1018..3216
FT /*tag= b

PN WO9848051-A2.
XX 29-OCT-1998.
XX 17-APR-1998; 98WO-US07714.
XX 10-OCT-1997; 97US-0062017.
XX 18-APR-1997; 97US-0044746.
XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.

PI Holtzman D, McCarthy SA;
DR WPI; 1999-024021/02.
DR P-PSDB; AA83927.
XX New isolated human FTHMA-070 and T85 proteins - used to develop
PT products for the diagnosis and therapy of disorders involving
PT cellular processes, e.g. neuronal development.

PS Claim 24; Fig 3; 127pp; English.

XX This claimed cDNA sequence, the coding region of which is also
CC claimed, codes for novel human T85 (see AA83927), also referred to
CC FMHB-6D4 and FMHB-SD4. The cDNA was identified in a human foetal
CC brain cDNA library using a screen designed to identify genes
CC encoding proteins having a functional signal sequence. T85 nucleic
CC acids and polypeptides of the invention are useful as modulating
CC agents in regulating a variety of cellular processes. They can be
CC used for identifying compounds which bind to or modulate the
CC activity of the polypeptides (claimed). They can also be used in
CC screening assays, detection assays (e.g. chromosomal mapping,
CC tissue typing, forensic biology), predictive medicine (e.g.
CC diagnostic assays, prognostic assays, monitoring clinical trials,
CC and pharmacogenomics), and methods of treatment (e.g. therapeutic
CC and prophylactic) e.g. for neurological disorders.

SQ Sequence 4291 BP; 1154 A; 1011 C; 1045 G; 1081 T; 0 other;

Alignment Scores:
Pred. No.: 1.03e-19 Length: 4291
Score: 453.00 Matches: 98
Percent Similarity: 54.51% Conservative: 35

Best Local Similarity: 40.16% Mismatches: 98
Query Match: 28.17% Indels: 13
DB: 20 Gaps: 3
US-10-047-021-86 (1-303) x AAV69278 (1-4291)
QY 6 AspSerLeuLeuGlyArgGlySerLeuProLeuLeu-LeuLeuLeuLeuMetGly 25
Db 954 GACAATGATTGGGAGCCCGCTCACTTTTACCTGTTGGATTATATCTCTCTGTTGAG 1013
QY 25 Y-----MetalGlnAspSerProGlnLeuValHisProGlnAspGlnLe 42
Db 1014 CTCCCGTCTTCGTTCAGGAAGATTTTCCACCTCGCATGTTGGAACACCTCTCAGACCTGAT 1073
QY 42 uPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProProTh 62
Db 1074 TGTCTCAAAAGGAGAACCTGCACTTTGAACCTGAAAGCTGAAGGCCGCCACCCAC 1133
QY 62 rIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisHis-- 81
Db 1134 TATTGAATGGTACAAAGGGGAGAGAGAGTGGAGACAGACAGATGACCTCGCTCACA 1193
QY 82 -----LeuLeuProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAl 99
Db 1194 CCGAATGTTGCTGCCGAGTGGATCTTTATTTTCTTACGT-----AT 1235
QY 99 aHisAspGlyGlnAlaLeuSerThrAspLeuGlyValThrCysGluAlaSerAsnAr 119
Db 1236 AGTACATGGACGGAAAGTAGACCTGATGAAGGAGTCTATGCTGTGTAGCAAGGAATTA 1295
QY 119 gLeuGlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPh 139
Db 1296 CTTTGGAGAGGCTGTGAGCCACAATGCATCGCTGGAAGTAGCCATCTTCCGGATGACTT 1355
QY 139 eGlnIleGlnProArgAspMetValAlaValAlaValGlyGlnGlnPheThrLeuGluCysGl 159
Db 1356 CAGACAAAACCCCTTCGGATGTTCATGGTTGCAGTAGGAGAGCCTGCAGTAATGAATGCCA 1415
QY 159 yProProTrpGlyHisProGluProThrValSerTrpTrpIysAspGlyIysProLeuAl 179
Db 1416 ACCTCCACGAGGCCATCTGAGCCCACTTTCATGGAAGAAAGATGGCTCTCCACTCGA 1475
QY 179 aLeuGlnProGlyArgHisThrValSerGlyIysSerLeuLeuMetAlaArgAlaGluLy 199
Db 1476 TGATAAGATGAAGAATAACTATACGNGGAGGAAGCTCATGATCACTTACACCCGTAA 1535
QY 199 sSerAspGlu***ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerAr 219
Db 1536 AAGTCAGCGCTGGCAAAATATGTTGTTGGTACCATAATATGTTGGGGAACGTGAGAGTGA 1595
QY 219 gAlaAlaArgValSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAl 239
Db 1596 AGTAGCCGAGCTGACTGTCTTAGAGAGACCAATCATTTGTGAAGAGACCCAGTAACCTGGC 1655
QY 239 aValArgile 242
Db 1656 AGTAACGTGTG 1665
RESULT 15
AAV55770
ID AAV55770 standard; cDNA; 4956 BP.
XX AAV55770;
XX
DT 30-JUL-1999 (first entry)
XX Human Robo 1 polypeptide encoding cDNA.
XX Comm polypeptide; Robo polypeptide; commissureless; roundabout;
KW modulation; nerve cell function; ds.
OS Homo sapiens.
XX

Qy 279 uThrArgProCysSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnAr 299
Dy 876 TACACAGCTCTGTTTCAGGACTCAGAGGTCTCCCGAGGACCAAGGATCTCCATGACAGAG 935
Qy 299 g 239
Dy 936 G 936

RESULT 13
AAS01694
ID AAS01694 standard; cDNA; 3042 BP.
XX AC AAS01694;
XX 18-JUL-2001 (first entry)
XX Human TANGO 330 form 1 cDNA sequence.
XX Human; TANGO 315; clone jthAa060g22; TANGO 330; TANGO 437; TANGO 480;
KW cellular process regulator; gene therapy; adrenal gland; cancer; ss;
KW Roundabout; adrenal cortex; hypoadrenalism; hyperadrenalism; neoplasia;
KW cell proliferative disorder; neurological disorder; Alzheimer's disease.
XX OS Homo sapiens.
XX Key Location/Qualifiers
XX CDS 2..2806
XX /tag= a
XX /partial
XX /product= "TANGO 330 form 1 protein"
XX /note= "The ORF is specifically claimed. This sequence
XX variation replace (4,C)
XX /tag= b
XX variation replace (5,T)
XX /tag= c
XX variation replace (9,T)
XX /tag= d
XX variation replace (159,A)
XX /tag= e
XX WO200123523-A2.
XX 05-APR-2001.
XX 02-OCT-2000; 2000WO-US27202.
XX 30-SEP-1999; 99US-0409634.
XX (MILL-) MILLENNIUM PHARM INC.
XX Kirst S, Wrighton N, Fraser CC;
XX WPI; 2001-235372/24.
XX P-PSDB; AAU00500.
XX Isolated secreted proteins and their encoding nucleic acids are used
XX for diagnosis and treatment of e.g. bacterial and viral infections,
XX autoimmune diseases and inflammatory disorders -
XX Claim 2; Fig 13; 261pp; English.
XX The present sequence encoding for human TANGO 330 form 1 is
XX isolated from cDNA clone jthAa060g22 from a human adrenal gland
XX cDNA library. TANGO 330 is 1 of 4 novel human transmembrane proteins
XX which also includes TANGO 315 (AAU00498-AAU00499), TANGO 437 (AAU00502)
XX and TANGO 480 (AAU00503). The nucleic acids encoding these proteins
XX are useful as modulating agents in regulating a variety of cellular
XX processes and can be used to express the proteins in a host cell in
XX gene therapy applications. Antisense nucleic acid molecules and
XX expression vectors containing the TANGO nucleic acids are also described.
XX Diagnostic assays can be used to detect genetic alterations in the TANGO
XX nucleic acids and to identify compounds that bind to or modulate activity

CC of the TANGO proteins. Anti-TANGO antibodies are used diagnostically to
CC monitor protein levels in tissue as a clinical testing procedure.
CC TANGO 330 shows homology to human Roundabout. TANGO 330 nucleic acids
CC and proteins may be used to diagnose, treat and monitor disorders of the
CC adrenal cortex e.g. hypoadrenalism, hyperadrenalism, and neoplasia. They
CC can also be used to treat cell proliferative disorders (e.g. cancer),
XX and neurological disorders e.g. Alzheimer's disease.
SQ Sequence 3042 BP; 607 A; 1008 C; 859 G; 568 T; 0 other;
Alignment Scores:
Pred. No.: 3.27e-61 Length: 3042
Score: 1104.50 Matches: 222
Percent Similarity: 74.75% Conservative: 0
Best Local Similarity: 74.75% Mismatches: 4
Query Match: 68.69% Indels: 71
DB: Gaps: 1
US-10-047-021-86 (1-303) x AAS01694 (1-3042)
Qy 5 GlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeuLeuMetGly 24
Dy 1 GGAGACAGCCCTCTGGGGGCGAGGGTTCCTGCTCTGCTCTGCTCTGCTCTATC----- 54
Qy 25 GlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAspGlnLeuPheGln 44
Dy 54 ----- 54
Qy 45 GlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProProProThrIleArg 64
Dy 54 ----- 54
Qy 65 TrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuPro 84
Dy 54 ----- 54
Qy 85 AspGlyThrLeuLeuLeuLeuGln-ProProAlaArgGlyHisAlaHisAspGlyGlnAl 104
Dy 55 -----ATGGCCCTCTGCTGGGGGACATGCTCCACAGCGGCTTGGCAGCGGAGT 93
Qy 104 aLeuSerThrAspLeuGlyValThrCysGluAlaSerAsnArgLeuGlyThrAlaVal 124
Dy 94 CCTGTCACAGACTGGGTGCTACACATGTAGGCGCAGCAACCGGCTTGGCAGCGGAGT 153
Qy 124 lSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProAr 144
Dy 154 CAGCAGAGGCGCTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 213
Qy 144 gAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHis 164
Dy 214 GGACATGGTGGCTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCGGCTTGGGCGCA 273
Qy 164 sProGluProThrValSerTrpTrpIlysAspGlyLysProLeuAlaLeuGlnProGlyAr 184
Dy 274 CCCAGAGCCACAGTCTCATGTGTGGAAGATGGGAAACCCCTTGGCCCTTCCAGCCCGAAG 333
Qy 184 gHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu***Th 204
Dy 334 GCACACAGTGTCCGGGGGTCTCTGCTGATGGCAAGAGCAGAGAGAGTAGTACGAGGAGAC 393
Qy 204 rTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSe 224
Dy 394 CTACATGTGTGGCCACCAACAGCGCAGGACATAGGAGAGCGCGCGCGGGTTTC 453
Qy 224 rIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGlnLe 244
Dy 454 CATCCAGAGCCCGCAGGACTACACGGAGCCTGTGGAGCTTCTGGCTGTGGAATTACGCT 513
Qy 244 uGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProIlysProArgProAlaVa 264
Dy 514 GGAAATGTGACACTGTCTGAACCCGGATCTCTGACAGAGGGCCCCAGGCTAGACGGCGGT 573
Qy 264 lTrpLeu***TrpIlysValSerGlyPro***-ArgLeuProAsnLeuThrArgProCysS 284

QY 201 AspGlu***ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAla 220
 |||||
 Db 640 GACGAGGAGGACATACATGTGTGTGGC-ACCAACAGCGCAGGACACAGAGGAGCGCGCA 698
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 QY 221 AlaArgValSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAla 239
 |||||
 Db 699 CC-CGGGTTTNCATTGAGGAGCCCGCANGACTACAGGAACCTGTGGAACTTTTGGCT 754
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RESULT 12

ABK87138
 ID ABK87138 standard; cDNA; 3688 BP.

XX
 AC ABK87138;

XX
 DT 07-OCT-2002 (first entry)

XX
 DE cDNA mouse ECSM4 protein.

XX Mouse; endothelial cell-specific molecule 4; ECSM4; neovasculature;
 KW imaging vascular endothelium; proliferative disease; cancer;
 KW psoriasis; diabetic retinopathy; atherosclerosis; menorrhagia;
 KW endothelial damage; tumour neovasculature; cardiac disease;
 KW endometriosis; hypoxic condition; angiogenesis; cytostatic;
 KW cardiant; gene; ss.

XX Mus sp.

XX Key Location/Qualifiers
 FT CDS 6..3053

FT /*tag= a

FT /note= "ECSM4 #1"

FT 3393..3512

FT /*tag= b

FT /note= "ECSM4 #2"

FT 3579..3683

FT /*tag= c

FT /note= "ECSM4 #3"

XX WO200236771-A2.

XX 10-MAY-2002.

XX 06-NOV-2001; 2001WO-GB04906.

XX 06-NOV-2000; 2000US-245566P.

XX 07-MAR-2001; 2001US-273662P.

XX (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.

XX Bicknell R, Huminiecki L;

XX WPI; 2002-508120/54.

XX P-PSDB; AAU99420, AAU99421, AAU99422.

XX Novel endothelial cell-specific molecule polypeptide 1 or 4, useful for

XX imaging, diagnosing and treating a condition involving vascular

XX endothelium e.g. cancer, cardiac disease, endometriosis, diabetes

XX Disclosure; Fig 13; 248pp; English.

XX The present invention relates to endothelial cell-specific molecule 4

XX (ECSM4), and the polynucleotide sequences encoding it. The ECSM4

XX proteins are useful for imaging vascular endothelium in the body of

XX an individual, and for diagnosing and treating a proliferative

XX disease or condition involving the vascular endothelium (preferably,

XX neovasculature) such as cancer, psoriasis, diabetic retinopathy,

XX atherosclerosis or menorrhagia. The ECSM4 proteins are also useful in

XX the manufacture of diagnostic or prognostic agent for such conditions.

XX The proteins are also useful for detecting endothelial damage or

XX activation, detecting a tumour or tumour neovasculature, cardiac

XX disease, or endometriosis by detecting the amount of ECSM4 present in

XX a sample. The polynucleotide sequences encoding ECSM4 are useful in

XX gene therapy for treating a hypoxic condition such as cancer, cardiac

XX

XX

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XX

CC disease, endometriosis or atherosclerosis and in the manufacture of
 CC medicaments for treating the above disease. The sequences are useful
 CC for modulating angiogenesis in an individual. The present sequence
 CC encodes mouse ECSM4 protein.
 XX
 SQ Sequence 3688 BP; 801 A; 1115 C; 1011 G; 761 T; 0 other;

Alignment Scores:

Pred. No.: 9.94e-64 Length: 3688
 Score: 1145.50 Matches: 223
 Percent Similarity: 82.06% Conservative: 24
 Best Local Similarity: 74.09% Mismatches: 52
 Query Match: 71.24% Indels: 2
 DB: 24 Gaps: 1

US-10-047-021-86 (1-303) x ABK87138 (1-3688)

QY 1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeu 20
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 Db 36 ATGGGCTCTGGAGGAACGGGCTCTCTGGGACGGAGTGGCTCTGCTCTGCTGCTT 95
 |||||
 QY 21 LeuIleMetGlyGlyMetAlaGlnAspSerProGlnIleLeuValHisProGlnAsp 40
 |||||
 Db 96 TTCATCATGGAGGTGAGGCTCTGGATTCTCCACCCAGATCCTAGTTTCACCCCGAGAC 155
 |||||
 QY 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60
 |||||
 Db 156 CAGCTACTTTCAGGGCTCTGGCCAGCCAGATAGGTGCAGATCATTCGGCCAACCACT 215
 |||||
 QY 61 ProThrIleArgTTPLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80
 |||||
 Db 216 CCCACTATCGCTGGCTGCTGAATGGCAGCCCTCAGCATGGCCACCCAGAGCTACAT 275
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 QY 81 HisLeuLeuProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100
 |||||
 Db 276 TACCTTTTGGCGGATGGGACCTCTGTATCATCGGCCCTCTGTCCAGGGACGGCACAA 335
 |||||
 QY 101 AspGlyGln--AlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArg 119
 |||||
 Db 336 GATGACCAAGAACATCTCTCAGCAATCTCTGGTGTCTACACATGTGAGCCAGACACCG 395
 |||||
 QY 120 LeuGlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPhe 139
 |||||
 Db 396 CTGGGCACAGCAGTGAGCGGGTGTAGGCTGTCTGGCTGTCTCCAGAGGAGACTTC 455
 |||||
 QY 140 GlnIleGlnProArgAspMetValAlaValGlnGlnPheThrLeuGluCysGly 159
 |||||
 Db 456 CAGATCCAACTCGGGACACAGTGGCCGTGGTGAGAGAGCTTGGTTCTTTGAGTGGT 515
 |||||
 QY 160 ProProTTPGlyHisProGluProThrValSerTTPTrpLysAspGlyLysProLeuAla 179
 |||||
 Db 516 CTTCCCTGGGGCTACCCAAACCTCTCGTCTCATTGGTGGAAAGACGGGAAACCTCTG 575
 |||||
 QY 180 LeuGlnProGlyArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLys 199
 |||||
 Db 576 CTCCAGCAGGAGGCGCAGATATCTGGGATTCCTCTGATGGTGTCAAGAGCAGAGAG 635
 |||||
 QY 200 SerAspGlu***ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArg 219
 |||||
 Db 636 AATGACTCGGGGACCTATATGTGTATGCCACCAACAATGTGGGCAACCGGAGAGCCGA 695
 |||||
 QY 220 AlaAlaArgValSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAla 239
 |||||
 Db 696 GCAGCCAGGGTGTCTATCCAGGAATCCAGACCAAGGAACATCTAGAGCTCTTGCT 755
 |||||
 QY 240 ValArgIleGlnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLys 259
 |||||
 Db 756 GTTCGCATTGAGCTGGAAATGTGACCTCTAAACCCCGAACCTGTAAAGGTCCCAAG 815
 |||||
 QY 260 ProArgProAlaValTTPLeu***TTPLysValSerGlyPro***ArgLeuProAsnLe 279
 |||||
 Db 816 CTTGGGCCCTCGTGTGGCTCAGCTGGAAGGTGAGCGGCCCTGTGTCACCTGTGAGTCA 875
 |||||

Db 531 CGGACATGGTGGCTGTGGTGGAGCAGTTTACTCTGGAATGTGGCCCTGGGGC 590
Qy 164 HisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGly 183
Db 591 CACCAGAGCCACACAGTCTCATGTGGTGAAGATGGAAACCCCTGGCCCTCCAGCCCGGA 650
Qy 184 ArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu*** 203
Db 651 AGGCACACAGTGTCCGGGGGGTCCCTGCTGTGATGGCAAGAGCAGAGAGTGTACGAGGG 710
Qy 204 ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgVal 223
Db 711 ACCTACATGTGTGGCCACCAACAGCGCAGCAGCATAGCGAGCGCGCAGCCGGGTT 770
Qy 224 SerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGln 243
Db 771 TCCATCCAGGAGCCCCAGGACTACACGAGGCTGTGGAGCTTCTGGCTGTGCGAATTGAG 830
Qy 244 LeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAla 263
Db 831 CTGGAATGTGACACTCTGAACCGGATCTGCGAGAGGGCCCCAAGCCTAGACCGGG 890
Qy 264 ValTrpLeu***TrpLysValSerGlyPro***ArgLeuProAsnLeuThrArgProCys 283
Db 891 GTGTGGCTCAGCTGGAAGGTCACTGGCCCTGTGCGCCTGCGCCCAATCTTACACGGCCTTG 950
Qy 283 sSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArg 299
Db 951 TTCAGGACCCAGACTGCCCCGGAGGCCAGGAGCTCCGTTGGGCAGAGG 999

RESULT 11

AAH08234

ID AAH08234 standard; cDNA; 756 BP.

XX AC AAH08234;

XX DT 26-JUN-2001 (first entry)

XX DE Human cDNA clone (5'-primer) SEQ ID NO:5069.

XX KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

XX OS Homo sapiens.

XX FN EP1074617-A2.

XX PD 07-FEB-2001.

XX PF 28-JUL-2000; 2000EP-0116126.

XX PR 29-JUL-1999; 99JP-0248036.

XX PR 27-AUG-1999; 99JP-0300253.

XX PR 11-JAN-2000; 2000JP-0118776.

XX PR 02-MAY-2000; 2000JP-0183767.

XX PR 09-JUN-2000; 2000JP-0241899.

XX PA (HELI-) HELIX RES INST.

XX PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

XX PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX DR WPI; 2001-318749/34.

XX PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -

XX PS Claim 1; SEQ ID 5069; 2537pp + CD ROM; English.

XX CC The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set

CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesizing polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.

SQ Sequence 756 BP; 147 A; 242 C; 236 G; 128 T; 3 other;

Alignment Scores:

Pred. No.: 2,99e-67 Length: 756
Score: 1190.00 Matches: 232
Percent Similarity: 97.49% Conservative: 1
Best Local Similarity: 97.07% Mismatches: 6
Query Match: 74.00% Indels: 2
DB: 22 Gaps: 0

US-10-047-021-86 (1-303) x AAH08234 (1-756)

Qy 1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeu 20
Db 40 ATGGGCTCTGGAGAGACAGCCTCTCTGGGGGAGGGGTTCCTCGCTCTGCTCTCTG 99
Qy 21 LeuIleMetGlyGlyMetAlaGlnAspSerProGlnIleLeuValHisProGlnAsp 40
Db 100 CTATCATGGAGGATGGCTCAGGACTCCCGGCCCCAGATCTTAGTCCACCCCGAGGAC 159
Qy 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60
Db 160 CAGCTGTTCCAGGGCCCTGGCCCTGCCAGGATGAGTGCACAGCCTCAGGCGCAGCACCT 219
Qy 61 ProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80
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Qy 81 HisLeuLeuProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100
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Qy 101 AspGlyGlnAlaLeuSerThrAspLeuGlyValTrpTrpCysGluAlaSerAsnArgLeu 120
Db 340 GATGGCCAGGCCCTGTCCACAGACCTGGGTGTCTACACATGTGTAGGGCAGCAACCGGCTT 399
Qy 121 GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln 140
Db 400 GGACCGGAGTACAGAGGCGCTCGGCTGTCTGTGGCTGTCTCTCGGGAGGATTTCCAG 459
Qy 141 IleGlnProArgAspMetValAlaValValGlyGlnGlnPheThrLeuGluCysGlyPro 160
Db 460 ATCCAGCCTCGAGACATGGTGGCTGTGGTGGTGAGCAGTTTACTCTGGAATGTGGGCG 519
Qy 161 ProTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeu 180
Db 520 CCCTGGGGCCACCAGAGCCACAGTCTCATGTGGTGAAGATGAGAAACCCCTGGCCCTC 579
Qy 181 GlnProGlyArgHisThrValSerGlySerLeuLeuMetAlaArgAlaGluLysSer 200
Db 580 CAGCCCGGAAGGCACACAGTGTCCGGGGGGTCCCTGCTGTGATGGCAAGAGCAGAGAAGAGT 639

Db 241 CCTGATGGACCCCTTCTGCTACAGCCCTCGCCGGGACATGCCACGATGCCAG 300
Qy 104 AlaLeuSerThrAspLeuGlyValThrCysGluAlaSerAsnArgLeuGlyThrAla 123
Db 301 GCCCTGTCCACAGACTGGGTGTACACATGTAGGCGCAGCAACCGCTTGGCAGCGCA 360
Qy 124 ValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnPro 143
Db 361 GTCAGCAGAGCGCTCGGCTGTCTGTGGCTGTCTCGGGAGGATTTCCAGATCCAGCT 420
Qy 144 ArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGly 163
Db 421 CGGACATGGTGGCTGTGGTGGTGGAGCAGTGTACTCTGGAATGTGGCGCGCTGGGGC 480
Qy 164 HisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGly 183
Db 481 CACCACAGAGCCACAGTCTCATGGTGGAAAGATGGAAACCCCTGGCCCTCCAGCCCGGA 540
Qy 184 ArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu*** 203
Db 541 AGGCACACAGTCTCGGGGGGTCCCTGTGTATGGCAGAGCAGAGAGTGCAGAGGG 600
Qy 204 ThrTyMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgVal 223
Db 601 ACCTACATGTGTGGCCACCAACAGCGCAGGACATAGGAGAGCGCGCAGCCCGGTT 660
Qy 224 SerIleGlnProGlnAspTrpThrGluProValGluLeuAlaValArgIleGln 243
Db 661 TCCATCCAGAGCCCGAGACTACAGGAGCTGTGGAGCTTCTGGCTGTGGGAATTGAG 720
Qy 244 LeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAla 263
Db 721 CTGGAAATGTACACTGTGAACCGGATCTTCAGAGGGCCCAAGCTAGACCGGG 780
Qy 264 ValTrpLeu***TrpLysValSerGlyPro***-ArgLeuProAsnLeuThrArgProCy 283
Db 781 GTGTGGCTCAGCTGGAAGTCACTGGCCCTGTGGCTGTGGCCCAATCTTACAGCGCTTG 840
Qy 283 sSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArg 299
Db 841 TTCAGAGCCAGACTGCCCGGGAGGCCAGGAGCTCCGTGGCGCAGAG 889
RESULT 10
AAS01695
ID AAS01695 standard; cDNA; 3808 BP.
XX AAS01695;
AC AAS01695;
DT 18-JUL-2001 (first entry)
XX Human TANGO 330 form 2 cDNA sequence.
DE Human TANGO 330 form 2 cDNA sequence.
XX Human; TANGO 315; clone Jthx181e12; TANGO 330; TANGO 437; TANGO 480;
KW cellular process regulator; gene therapy; astrocyte; cancer; ss;
KW Roundabout; adrenal cortex; hypoadrenalism; hyperadrenalism; neoplasia;
KW cell proliferative disorder; neurological disorder; Alzheimer's disease.
XX Homo sapiens.
OS Homo sapiens.
XX Key Location/Qualifiers
FT 9..1451
FT CDS /tag= a
FT /product= "TANGO 330 form 2 protein"
FT /note= "The ORF is specifically claimed"
FT sig_peptide 9..68
FT mat_peptide 69..1448
FT /tag= b
FT /tag= c
XX WO200123523-A2.
PN 05-APR-2001.
XX
XX

PF 02-OCT-2000; 2000WO-US27202.
XX
PR 30-SEP-1999; 99US-0409634.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Kirst S, Wrighton N, Fraser CC;
XX
DR WPI; 2001-235372/24.
XX P-PsDB; AAU00501.
PT Isolated secreted proteins and their encoding nucleic acids are used
PT for diagnosis and treatment of e.g. bacterial and viral infections,
PT autoimmune diseases and inflammatory disorders -
XX Claim 2; Fig 14; 261pp; English.
XX
CC The present sequence encoding for human TANGO 330 form 2 is
CC isolated from cDNA clone Jthx181e12 from a human astrocyte cDNA
CC library. TANGO 330 is 1 of 4 novel human transmembrane proteins
CC which also includes TANGO 315 (AAU00498-AAU00499), TANGO 437 (AAU00502)
CC and TANGO 480 (AAU00503). The nucleic acids encoding these proteins
CC are useful as modulating agents in regulating a variety of cellular
CC processes and can be used to express the proteins in a host cell in
CC gene therapy applications. Antisense nucleic acid molecules and
CC expression vectors containing the TANGO nucleic acids are also described.
CC Diagnostic assays can be used to detect genetic alterations in the TANGO
CC nucleic acids and to identify compounds that bind to or modulate activity
CC of the TANGO proteins. Anti-TANGO antibodies are used diagnostically to
CC monitor protein levels in tissue as a clinical testing procedure.
CC TANGO 330 shows homology to human Roundabout. TANGO 330 nucleic acids
CC and proteins may be used to human Roundabout. TANGO 330 disorders of the
CC adrenal cortex e.g. hypoadrenalism, hyperadrenalism, and neoplasia. They
CC can also be used to treat cell proliferative disorders (e.g. cancer),
CC and neurological disorders e.g. Alzheimer's disease.
XX
SQ Sequence 3808 BP; 773 A; 1244 C; 1041 G; 750 T; 0 other;
Alignment Scores:
Pred. No.: 3.14e-83 Length: 3808
Score: 1453.00 Matches: 272
Percent Similarity: 98.56% Conservative: 1
Best Local Similarity: 98.19% Mismatches: 3
Query Match: 90.36% Indels: 1
DB: 22 Gaps: 0
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Qy 24 GlyGlyMetAlaGlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPhe 43
Db 171 GGAGCATGGCTCAGGACTCCCGCCCGCAGATCTTAGTCCACCCCGAGCAGCTGTTC 230
Qy 44 GlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProProProThrIle 63
Db 231 CAGGCGCTCGCCCTGCCAGGATGAGTGCAGGCTTCCAGGCGCAGCCACCTCCACCATC 290
Qy 64 ArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisLeuLeu 83
Db 291 CGCTGGTTGCTGAATGGGCAGCCCTGTAGCATGGTGGCCCGCCAGACCCACACCATCTCTG 350
Qy 84 ProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGln 103
Db 351 CCTGATGGAGCCCTTCTGTCTGTACAGCCCTTCCCGGGGACATGCCACGATGCCAG 410
Qy 104 AlaLeuSerThrAspLeuGlyValThrCysGluAlaSerAsnArgLeuGlyThrAla 123
Db 411 GCCCTGTCCACAGACCTGGGTGTCTACACATGTAGGCGCAGCAACCGCTTGGCAGCGCA 470
Qy 124 ValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnPro 143
Db 471 GTTACAGAGAGCGCTCGGCTGTCTGTGGCTGTCTCGGGAGGATTTCCAGATCCAGCT 530
Qy 144 ArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGly 163

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PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 24-FEB-2000; 2000WO-US05004.
PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 24-AUG-2000; 2000WO-US23328.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 22-MAR-2001; 2001WO-US09552.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 17-OCT-1997; 97US-062250P.
PR 03-NOV-1997; 97US-064249P.
PR 13-NOV-1997; 97US-065311P.
PR 21-NOV-1997; 97US-066364P.
PR 10-MAR-1998; 98US-077450P.
PR 11-MAR-1998; 98US-077632P.
PR 11-MAR-1998; 98US-077641P.
PR 11-MAR-1998; 98US-077649P.
PR 12-MAR-1998; 98US-077751P.
PR 13-MAR-1998; 98US-078004P.
PR 20-MAR-1998; 98US-078886P.
PR 20-MAR-1998; 98US-078910P.
PR 20-MAR-1998; 98US-078936P.
PR 20-MAR-1998; 98US-078939P.
PR 25-MAR-1998; 98US-079234P.
PR 26-MAR-1998; 98US-079656P.
PR 27-MAR-1998; 98US-079663P.
PR 27-MAR-1998; 98US-079664P.
PR 27-MAR-1998; 98US-079689P.
PR 27-MAR-1998; 98US-079728P.
PR 27-MAR-1998; 98US-079786P.
PR 30-MAR-1998; 98US-079920P.
PR 30-MAR-1998; 98US-079923P.
PR 26-MAY-1998; 81US-0267213.
PR 17-MAR-1998; 98US-0040220.
PR 26-JUN-1998; 98US-0105413.
PR 07-OCT-1998; 98US-0168978.
PR 02-NOV-1998; 98US-0184216.
PR 06-NOV-1998; 98US-0187368.
PR 07-DEC-1998; 98US-0202054.
PR 22-DEC-1998; 98US-0218517.
PR 05-MAR-1999; 98US-0254465.
PR 10-MAR-1999; 98US-0265686.
PR 12-APR-1999; 98US-0284291.
PR 14-MAY-1999; 98US-0311832.
PR 14-MAY-1999; 98US-0380137.
PR 25-AUG-1999; 98US-0380138.
PR 25-AUG-1999; 98US-0380142.
PR 08-NOV-2000; 2000US-0709238.
PR 27-NOV-2000; 2000US-0723749.
PR 20-DEC-2000; 2000US-0747259.
PR 22-MAR-2001; 2001US-0816744.
PR 22-MAR-2001; 2001US-0816920.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 01-JUN-2001; 2001US-0872035.
PR 05-JUN-2001; 2001US-0874503.

PR 14-JUN-2001; 2001US-0882636.
PR 19-JUN-2001; 2001US-0886342.
PR 30-JUL-2001; 2001US-0918585.
PR (GETH ) GENENTECH INC.
XX Ahkenazi A, Baker KP, Botstein D, Desnoyers L, Eaton D;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen MB;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kijavini IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;
PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
XX WPI; 2003-288163/28.
DR DR P-PSDB; ABU61102.
XX Novel secreted and transmembrane polypeptides and polynucleotides
PT encoding them useful for treating cancer, kidney diseases, bone,
PT cartilage disorders and immune deficiencies -
XX
PS Claim 2; Fig 76; 459pp; English.
XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The
CC PRO polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for
CC linking bioactive molecules to cells expressing PRO polypeptides,
CC for modulating biological activities of cells expressing PRO
CC polypeptides, and for identifying agonists or antagonists. The
CC bioactive molecule maybe a toxin, radiolabel or antibody, and causes
CC apoptosis or death of the cell. The PRO polypeptides are useful for
CC treating immune disorders, diabetes or hyper- or hypo-insulinaemia,
CC cardiac insufficiency, nervous system disorders, kidney disorders,
CC bone and cartilage disorders or arthritis, tumours, and wound healing.
CC The polynucleotide sequences encoding PRO polypeptides are useful as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of antisense RNA and DNA, in the preparation of PRO polypeptides, for
CC generating transgenic animals or knockout animals, for the genetic
CC analysis of individuals with genetic disorders, and in gene therapy.
CC The present sequence encodes a human PRO polypeptide of the invention.
CC Note: The sequence data for this patent was obtained in electronic
CC format directly from the USPTO web site at
CC seqdata.uspto.gov/patidentry.html.
XX
SQ Sequence 3716 BP; 757 A; 1225 C; 1032 G; 702 T; 0 other;

Alignment Scores:
Pred. No.: 2.14e-89 Length: 3716
Score: 1550.00 Matches: 292
Percent Similarity: 98.65% Conservative: 1
Best Local Similarity: 98.32% Mismatches: 3
Query Match: 96.39% Indels: 1
DB: 25 Gaps: 0

US-10-047-021-86 (1-303) x ABX92441 (1-3716)
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Qy 24 GlyGlyMetAlaGlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPhe 43
Db 61 GGAGGACATGGCTCAGGACTCCCGCCCGCAGATCTAGTCCACCCAGGACAGCTGTTTC 120
Qy 44 GlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIle 63
Db 121 CAGGGCCCTGGCCCTGCCAGATGAGCTGCGACCTCAGGCCAGCCACCTCCACCATC 180
Qy 64 ArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeu 83
Db 181 CGCTGGTGTGATGATGGGACGCCCTGAGCATGTGGTGGCCCGCCAGACCCACCATCTCTG 240
Qy 84 ProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGln 103
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Db 220 |||||CCACCATCCGCTGGTGTGATGAGGAGCCCTCAGCATGGTGCCTCCAGCCACACAC 279
Qy 81 |||||HisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaAargGlyHisAlaHis 100
Db 280 |||||CACCTCTCGCTGATGGGACCTTCTGCTGCTACAGCCCTCCCGGGGACATGCCAC 339
Qy 101 |||||AspGlyGlnAlaLeuSerThrAspLeuGlyValThrCysGluAlaSerAsnArgLeu 120
Db 340 |||||GATGGCCAGGCCCTGTCCACAGACCTGGGTGTCTACATGTGAGGCCAGCAACCGGCTT 399
Qy 121 |||||GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln 140
Db 400 |||||GGCAGGGCAGTCAGCAGAGGCGCTGGCTGTCTGTGGCTGTCTCCGGGAGGATTTCCAG 459
Qy 141 |||||IleGlnProArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyPro 160
Db 460 |||||ATCCAGCCTCGAGACATGTGTGCTGTGGTGTGAGCAGTTTACTCTGGATGTGGCGG 519
Qy 161 |||||ProTrrGlyHisProGluProThrValSerTrrPrrLysAspGlyLysProLeuAlaLeu 180
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Qy 181 |||||GlnProGlyArgHisThrValSerGlyGlySerLeuLeuMetAlaArgNlaGluLysSer 200
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Qy 201 |||||AspGlu***ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAla 220
Db 640 |||||GACGAGGGACCTTACATGTGTGTGGCCACCAAGCCAGGACAGGAGGAGCGCGCA 699
Qy 221 |||||AlaArgValSerIleGlnGluProGlnAspTrrThrGluProValGluLeuLeuAlaVal 240
Db 700 |||||GCCCGGGTTTCCATCCAGGAGCCCGCAGGACTACAGGAGCTGTGGAGCTTCTGGCTGTG 759
Qy 241 |||||ArgIleGlnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysPro 260
Db 760 |||||CGAATTACGCTGGAATAATGTACACTGTGTAACCCGGATCTCTGCAGAGGGCCCAAGCCT 819
Qy 261 |||||ArgProAlaValTrrpleu***TrrLysValSerGlyPro***ArgLeuProAsnLeuTh 280
Db 820 |||||AGACCGCGGTGTGGCTCAGCTGGAAGGTCAGTGGCCCTGCTGGCGCTGCCCAATCTTAC 879
Qy 280 |||||rArgProCysSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArg 299
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RESULT 7
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ID AAZ34069 standard; cdna; 3716 BP.
AC
XX
AC AAZ34069;
XX
DT 07-DEC-1999 (first entry)
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DE Human PRO860 nucleotide sequence.
XX
KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
KW secreted protein; transmembrane protein; ss.
XX
OS Homo sapiens.
XX
PN WO9946281-A2.
XX
PD 16-SEP-1999.
XX
PF 08-MAR-1999; 99WO-US05028.
XX
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PR 10-MAR-1998; 98US-0077450.
PR 11-MAR-1998; 98US-0077632.
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PR 12-MAR-1998; 98US-0077791.
PR 13-MAR-1998; 98US-0078004.
PR 17-MAR-1998; 98US-0040220.
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PR 20-MAR-1998; 98US-0078936.
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PR 25-MAR-1998; 98US-0079294.
PR 26-MAR-1998; 98US-0079656.
PR 27-MAR-1998; 98US-0079663.
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PR 31-MAR-1998; 98US-0080105.
PR 31-MAR-1998; 98US-0080107.
PR 31-MAR-1998; 98US-0080165.
PR 31-MAR-1998; 98US-0080194.
PR 01-APR-1998; 98US-0080327.
PR 01-APR-1998; 98US-0080328.
PR 01-APR-1998; 98US-0080333.
PR 01-APR-1998; 98US-0080334.
PR 08-APR-1998; 98US-0081049.
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PR 09-APR-1998; 98US-0081195.
PR 09-APR-1998; 98US-0081203.
PR 09-APR-1998; 98US-0081229.
PR 15-APR-1998; 98US-0081817.
PR 15-APR-1998; 98US-0081838.
PR 15-APR-1998; 98US-0081952.
PR 15-APR-1998; 98US-0081955.
PR 21-APR-1998; 98US-0082568.
PR 21-APR-1998; 98US-0082569.
PR 22-APR-1998; 98US-0082700.
PR 22-APR-1998; 98US-0082704.
PR 22-APR-1998; 98US-0082804.
PR 23-APR-1998; 98US-0082767.
PR 23-APR-1998; 98US-0082796.
PR 27-APR-1998; 98US-0083336.
PR 28-APR-1998; 98US-0083322.
PR 29-APR-1998; 98US-0083392.
PR 29-APR-1998; 98US-0083495.
PR 29-APR-1998; 98US-0083496.
PR 29-APR-1998; 98US-0083499.
PR 29-APR-1998; 98US-0083500.
PR 29-APR-1998; 98US-0083545.
PR 29-APR-1998; 98US-0083554.
PR 29-APR-1998; 98US-0083558.
PR 29-APR-1998; 98US-0083559.
PR 30-APR-1998; 98US-0083742.
PR 05-MAY-1998; 98US-0084366.
PR 06-MAY-1998; 98US-0084414.
PR 06-MAY-1998; 98US-0084441.
PR 07-MAY-1998; 98US-0084598.
PR 07-MAY-1998; 98US-0084600.
PR 07-MAY-1998; 98US-0084627.
PR 07-MAY-1998; 98US-0084637.
PR 07-MAY-1998; 98US-0084639.
PR 07-MAY-1998; 98US-0084640.
PR 13-MAY-1998; 98US-0084643.
PR 13-MAY-1998; 98US-0085323.
PR 13-MAY-1998; 98US-0085338.
PR 13-MAY-1998; 98US-0085339.
PR 15-MAY-1998; 98US-0085573.
PR 15-MAY-1998; 98US-0085579.
PR 15-MAY-1998; 98US-0085580.
```

```
Pred. No.: 8.83e-90 Length: 4262
Score: 1557.00 Matches: 294
Percent Similarity: 98.33% Conservative: 1
Best Local Similarity: 98.00% Mismatches: 4
Query Match: 96.83% Indels: 1
DB: 22 Gaps: 0

US-10-047-021-86 (1-303) x AAH18180 (1-4262)

QY 1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeu 20
DB 40 ATGGGCTCTGGAGGAGACAGGCTCTGGGGGGCAGGGGTTCCTGCTCTCTCTGCTG 99
QY 21 LeulleMetGlyGlyMetAlaGlnAspSerProGlnLeuLeuValHisProGlnAsp 40
DB 100 CTCATCATGGGAGGATGGCTCAGGACTCCCGGCCAGATCTTAGTCCACCCCGAGGAC 159
QY 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60
DB 160 CAGCTGTTCCAGGGCCCTGGCCCTGCCAGGATGAGTCCCAAGCCTCAGGCGCAGCCACT 219
QY 61 ProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80
DB 220 CCCACATCCGCTGCTGCTGAATGGGAGCCCTCGAGCATGGTCCCGCCAGACCCACAC 279
QY 81 HisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100
DB 280 CACCTCTCTGCTGATGGGACCTTCTGCTGTACAGCCCTGCGCGGGAGCATGCCAC 339
QY 101 AspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeu 120
DB 340 GATGCCAGGCGCTCTCCACAGACCTGGTGTGTACACATGTGAGGCCAGCAACCGGCTT 399
QY 121 GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln 140
DB 400 GGCACGGCAGTCAGCAGAGGGCGCTGGGCTGTCTGTGGCTGCTCCCGGGAGATTCCAG 459
QY 141 IleGlnProArgAspMetValAlaValValGlyGlnGlnPheThrLeuGluCysGlyPro 160
DB 460 ATCCAGCTTCAGACATGGTGGCTGTGGTGGTGAGCAGTTTACTCTGGATGTGGCGG 519
QY 161 ProTrpGlyHisProGluProThrValSerTrpTrpIysAspGlyLysProLeuAlaLeu 180
DB 520 CCCTGGGGCCACCCAGAGCCACAGCTCTCATGGTGAAGATGAGAAACCCCTGGCCCTC 579
QY 181 GlnProGlyArgHisThrValSerGlySerLeuLeuMetAlaArgAlaGluLysSer 200
DB 580 CAGCCCGGAGGACACACAGTGTCCGGGGGTCCTGCTGATGGCAAGAGCAGAGAAGAGT 639
QY 201 AspGlu***ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAla 220
DB 640 GACGAGGGGACCTACATGTGTGGCCACCAACAGCGCAGGACACAGGAGGAGCGCGCA 699
QY 221 AlaArgValSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaVal 240
DB 700 GCCCGGGTTTCCATCCAGGAGCCCGCAGGACTACAGGAGCCTGTGGAGCTTCTGGCTGTG 759
QY 241 ArgIleGlnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysPro 260
DB 760 CGAATTCAGCTGGAATAATGTACATGCTGAACCCCGGATCTTCAGAGGGGCCCCAAGCCT 819
QY 261 ArgProAlaValTrpLeu***TrpLysValSerGlyPro***ArgLeuProAsnLeuTh 280
DB 820 AGACCGCGGGTGTGCTCAGCTGGAGAGGTGCTAGTGGCCCTGTGCGCCTGCCCAATCTTAC 879
QY 280 rArgProCysSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArg 299
DB 880 ACGGCTTTGTTCCAGGACCCAGACTGCCCGGGAGGCCAGGGAGCTCCGTTGGCAGAGG 937

RESULT 6
AAH78073
ID AAH78073 standard; DNA; 4262 BP.
XX
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AAH78073;
26-NOV-2001 (first entry)
Nucleotide sequence of a human protein kinase/protein phosphatase.
Human; protein kinase; protein phosphatase; signal transduction;
intracellular signalling pathway; ss.
Homo sapiens.
Key Location/Qualifiers
CDS 40..2418
FT /*tag= a
FT /product= "protein kinase/protein phosphatase"
XX
XX WO200109345-A1.
XX
XX 08-FEB-2001.
XX
XX 28-JUL-2000; 2000WO-JP05060.
XX
XX 29-JUL-1999; 99JP-0248036.
XX 18-OCT-1999; 99US-0159590.
XX 11-JAN-2000; 2000JP-0118776.
XX 17-FEB-2000; 2000US-0183322.
XX 02-MAY-2000; 2000JP-0183767.
XX
XX (HELI-) HELIX RES INST.
XX
XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S;
XX Senoo C, Nezu J;
XX
XX WPI; 2001-564736/63.
XX P-PSDB; AAG67430.
XX
XX New genes encoding protein kinase and protein phosphatase, useful for
XX identifying modulators which can be used to treat human or animal
XX disorders associated with the expression or function of these enzymes -
XX
XX Claim 1; Page 164-174; 336pp; Japanese.
XX
XX The present sequence encodes a human protein kinase/protein
XX phosphatase. The polypeptides are expected to participate in signal
XX transduction in cells. The kinase phosphatases are connected with
XX intracellular signalling pathways. Antisense oligonucleotides and
XX compounds identified by screening (agonists or antagonists) can be
XX used to treat human or animal disorders associated with the expression
XX or function of the protein. In addition, the polypeptides may be used
XX as target molecules for drug development.
XX
XX Sequence 4262 BP; 873 A; 1333 C; 1209 G; 847 T; 0 other;
XX
XX Alignment Scores:
XX Pred. No.: 8.83e-90 Length: 4262
XX Score: 1557.00 Matches: 294
XX Percent Similarity: 98.33% Conservative: 1
XX Best Local Similarity: 98.00% Mismatches: 4
XX Query Match: 96.83% Indels: 1
XX DB: 22 Gaps: 0
XX
XX US-10-047-021-86 (1-303) x AAH78073 (1-4262)
XX
XX QY 1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeu 20
XX DB 40 ATGGGCTCTGGAGGAGACAGGCTCTGGGGGGCAGGGGTTCCTGCTCTCTCTGCTG 99
XX QY 21 LeulleMetGlyGlyMetAlaGlnAspSerProGlnLeuLeuValHisProGlnAsp 40
XX DB 100 CTCATCATGGGAGGATGGCTCAGGACTCCCGGCCAGATCTTAGTCCACCCCGAGGAC 159
XX QY 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60
XX DB 160 CAGCTGTTCCAGGGCCCTGGCCCTGCCAGGATGAGTCCCAAGCCTCAGGCGCAGCCACT 219
XX QY 61 ProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80
XX DB 220 CCCACATCCGCTGCTGCTGAATGGGAGCCCTCGAGCATGGTCCCGCCAGACCCACAC 279
XX QY 81 HisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100
XX DB 280 CACCTCTCTGCTGATGGGACCTTCTGCTGTACAGCCCTGCGCGGGAGCATGCCAC 339
XX QY 101 AspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeu 120
XX DB 340 GATGCCAGGCGCTCTCCACAGACCTGGTGTGTACACATGTGAGGCCAGCAACCGGCTT 399
XX QY 121 GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln 140
XX DB 400 GGCACGGCAGTCAGCAGAGGGCGCTGGGCTGTCTGTGGCTGCTCCCGGGAGATTCCAG 459
XX QY 141 IleGlnProArgAspMetValAlaValValGlyGlnGlnPheThrLeuGluCysGlyPro 160
XX DB 460 ATCCAGCTTCAGACATGGTGGCTGTGGTGGTGAGCAGTTTACTCTGGATGTGGCGG 519
XX QY 161 ProTrpGlyHisProGluProThrValSerTrpTrpIysAspGlyLysProLeuAlaLeu 180
XX DB 520 CCCTGGGGCCACCCAGAGCCACAGCTCTCATGGTGAAGATGAGAAACCCCTGGCCCTC 579
XX QY 181 GlnProGlyArgHisThrValSerGlySerLeuLeuMetAlaArgAlaGluLysSer 200
XX DB 580 CAGCCCGGAGGACACACAGTGTCCGGGGGTCCTGCTGATGGCAAGAGCAGAGAAGAGT 639
XX QY 201 AspGlu***ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAla 220
XX DB 640 GACGAGGGGACCTACATGTGTGGCCACCAACAGCGCAGGACACAGGAGGAGCGCGCA 699
XX QY 221 AlaArgValSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaVal 240
XX DB 700 GCCCGGGTTTCCATCCAGGAGCCCGCAGGACTACAGGAGCCTGTGGAGCTTCTGGCTGTG 759
XX QY 241 ArgIleGlnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysPro 260
XX DB 760 CGAATTCAGCTGGAATAATGTACATGCTGAACCCCGGATCTTCAGAGGGGCCCCAAGCCT 819
XX QY 261 ArgProAlaValTrpLeu***TrpLysValSerGlyPro***ArgLeuProAsnLeuTh 280
XX DB 820 AGACCGCGGGTGTGCTCAGCTGGAGAGGTGCTAGTGGCCCTGTGCGCCTGCCCAATCTTAC 879
XX QY 280 rArgProCysSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArg 299
XX DB 880 ACGGCTTTGTTCCAGGACCCAGACTGCCCGGGAGGCCAGGGAGCTCCGTTGGCAGAGG 937
```

CC disease, or endometriosis by detecting the amount of ECSM4 present in
CC a sample. The polynucleotide sequences encoding ECSM4 are useful in
CC gene therapy for treating a hypoxic condition such as cancer, cardiac
CC disease, endometriosis or atherosclerosis and in the manufacture of
CC medicaments for treating the above disease. The sequences are useful
CC for modulating angiogenesis in an individual. The present sequence
CC encodes human ECSM4 protein.

XX
SQ Sequence 3715 BP; 725 A; 1239 C; 1053 G; 698 T; 0 other;

Alignment Scores:

Pred. No.: 2,398-90 Length: 3715
Score: 1565.00 Matches: 295
Percent Similarity: 98.67% Conservative: 1
Best Local Similarity: 98.33% Mismatches: 3
Query Match: 97.33% Indels: 1
DB: 24 Gaps: 0

US-10-047-021-86 (1-303) x ABK87137 (1-3715)

QY 1 MetGlySerGlyGlyValSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeu 20
DB 70 ATGGGCTCTGGAGAGACAGCTCTCTGGGGGACAGGGTTCCCTGCTGCTCTCTG 129
QY 21 LeuileMetGlyGlyMetAlaGlnAspSerProGlnIleLeuValHisProGlnAsp 40
DB 130 CTCATCATGGAGGATGCTCAGAGCTCCCGCCAGATCTAGTCCACCCCCAGGAC 189
QY 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnPro 60
DB 190 CAGCTGTTCCAGGGCCCTGGCCCTGCCAGGATGAGTCCCAAGCCCTCAGGCCAGCCT 249
QY 61 ProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80
DB 250 CCCACATCCCTGGTGTGCTGAATGGAGCCCTGAGCATGCTGCCCCAGACCCACAC 309
QY 81 HisLeuLeuProAspGlyThrLeuLeuLeuLeuLeuProAlaArgGlyHisAlaHis 100
DB 310 CACCTCTGCTGATGGGACCTCTGCTGCTACAGCCCTGCGCGGGGACATGCCAC 369
QY 101 AspGlyGlnAlaLeuSerThrAspLeuGlyValThrCysGluAlaSerAsnArgLeu 120
DB 370 GATGCCAGGCCCTGCTCCACAGACCTGGGTGTCTACATGTGAGGCCAGCAACCGGCT 429
QY 121 GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln 140
DB 430 GGACGGGAGTCAGCAGAGGCGCTCGGTGTCTGTGGTGTCTCTCCGGGAGATTTCAG 489
QY 141 IleGlnProArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyPro 160
DB 490 ATCCAGCTCGGACATGCTGCTGTGGTGTGAGCAGTTTACTCTGGATGTGGCGG 549
QY 161 ProTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeu 180
DB 550 CCCTGGGGCCACCGAGGCCACAGTCTCATGGTGAAGATGGGAAACCCCTGGCCCTC 609
QY 181 GlnProGlyArgHisThrValSerGlySerLeuLeuMetAlaArgAlaGluLysSer 200
DB 610 CAGCCCGGAAGGACACAGTGTCCGGGGGGTCCCTGCTGTGGTGAAGAGCAGAGAAGT 669
QY 201 AspGlu***ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAla 220
DB 670 GACGAGGGACCTACTATGTGTGTGGCCACCAACAGCGCAGACATAGGAGAGCGCGCA 729
QY 221 AlaArgValSerIleGlnGluProGlnAspTrpThrGluProValGluLeuLeuAlaVal 240
DB 730 GCCCGGGTTTCCATCCAGAGGCCCGCAGGACTACAGGAGCCTGTGGAGCTTCTGGCTGT 789
QY 241 ArgIleGlnLeuGluAsnValThrLeuLeuLeuLeuProAspProAlaGluGlyProLysPro 260
DB 790 CGAATTACGTGGAAATGTGACACTGCTGAACCCGGATCTTCAGAGGGGCCCAAGCCT 849
QY 261 ArgProAlaValTrpLeu***TrpLysValSerGlyPro***ArgLeuProAsnLeuTh 280

DB 850 AGACGGCGGTGTGGCTCAGCTGGAAGGTCTAGTGGCCCTGCGCCATCTTAC 909
QY 280 rArgProCysSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArg 299
DB 910 ACGGCTTGTTCAGAGACCCAGACTGCCCGGGAGGCCAGGAGCTCCGTGGCAGAGG 967

RESULT 5

AAH18180
ID AAH18180 standard; cDNA; 4262 BP.

XX AC AAH18180;

DT 26-JUN-2001 (first entry)

DE Human cDNA sequence SEQ ID NO:18084.

XX KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

XX OS Homo sapiens.

XX PN EP1074617-A2.

XX PD 07-FEB-2001.

XX PF 28-JUL-2000; 2000EP-0116126.

XX PR 29-JUL-1999; 99JP-0248036.

XX PR 27-AUG-1999; 99JP-0300253.

XX PR 11-JAN-2000; 2000JP-0118776.

XX PR 02-MAY-2000; 2000JP-0183767.

XX PR 09-JUN-2000; 2000JP-0241899.

XX PA (HELI-) HELIX RES INST.

XX PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

XX PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX DR WPI; 2001-318749/34.

XX PS Claim 8; SEQ ID 18084; 2537pp + CD ROM; English.

XX CC The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesizing polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any special methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.

XX SQ Sequence 4262 BP; 873 A; 1333 C; 1209 G; 847 T; 0 other;

Alignment Scores:

XX An isolated polynucleotide for treating diseases associated with its
PT encoded polypeptide such as cancer and multiple sclerosis -
XX
XX Claim 1; SEQ ID NO 134; 509pp; English.
XX
XX The present invention provides the protein and coding sequences of 444
CC novel human proteins. These were isolated from expressed sequences tags
CC (ESTs). They can be used to stimulate cell growth, to regulate
CC haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth
CC e.g. in burn treatment, to regulate the immune system e.g. to treat
CC multiple sclerosis, to regulate activin or inhibin e.g. to treat
CC infertility, to regulate haemostasis or thrombolysis e.g. to treat
CC stroke and cancer, to screen for drugs, to treat inflammatory conditions
CC e.g. rheumatoid arthritis, and to treat nervous system disorders e.g.
CC parkinson's disease. The present sequence is a coding sequence of the
CC invention.

XX
SQ Sequence 3267 BP; 628 A; 1101 C; 927 G; 611 T; 0 other;

Alignment Scores:

Align. No.: 2, 09e-90 Length: 3267
Score: 1565.00 Matches: 295
Percent Similarity: 98.67% Conservative: 1
Best Local Similarity: 98.33% Mismatches: 3
Query Match: 97.33% Indels: 1
DB: 24 Gaps: 0

US-10-047-021-86 (1-303) x ABNS9723 (1-3267)

Qy 1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuLeuLeuLeu 20
Db 35 ATGGGCTCTGGAGGAGACAGCTCTCTGGGGGGAGGGGTTCCTGCTCTGCTCTG 94
Qy 21 LeuLeuMetGlyGlyMetAlaGlnAspSerProProGlnLeuLeuValHisProGlnAsp 40
Db 95 CTCATCATGGGAGGATGGCTCAGGACTCCCGCCGCGCCAGATCTAGTCCACCCCGAGGAC 154
Qy 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60
Db 155 CAGCTGTTCAGGGCCCTGGCCCTGCGAGGATGAGTCCCAAGCCCTCAGGCCAGCCACT 214
Qy 61 ProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80
Db 215 CCCACCATCCCTGGTTCGATGAGGGGAGCCCTGAGCATGGTGCCCGCCAGACCCACAC 274
Qy 81 HisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100
Db 275 CACCTCTCTGCTGATGGAGCCCTTCTGCTGTACAGCCCTGCGCGGGGACATGCCCCAC 334
Qy 101 AspGlyGlnAlaLeuSerThrAspLeuGlyValTyThrCysGluAlaSerAsnArgLeu 120
Db 335 GATGGCCAGGGCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTT 394
Qy 121 GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln 140
Db 395 GGCACGGCAGTCAGCAGAGGGCTCGGTCTGTGGGTCTCTCGGGAGGATTTCCAG 454
Qy 141 IleGlnProArgAspMetValAlaValValGlyGlnGlnPheThrLeuGluCysGlyPro 160
Db 455 ATCCAGCCCTCGGACATGGTGGCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCG 514
Qy 161 ProTrpGlyHisProGluProThrValSerTrpTrpIleAspGlyIleProLeuAlaLeu 180
Db 515 CCCTGGGGCCACCCAGAGCCACAGTCTCATGGTGGAAAGATGGAAACCCCTGGCCCTC 574
Qy 181 GlnProGlyArgHisThrValSerGlySerLeuLeuMetAlaArgAlaGluLysSer 200
Db 575 CAGCCCGGAGGACACACAGTCTCCGGGGGTTCCTGCTGATGGCAAGCAGCAGAGAGAT 634
Qy 201 AspGlu****ThrTyMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAla 220
Db 635 GACGAAGGGACCTCATGTGTGTGGCCACCAACAGCGCAGGACATAGGAGAGCGCGGCA 694

Qy 221 AlaArgValSerIleGlnGluProGlnAspTyThrGluProValGluLeuAlaVal 240
Db 695 GCCGGGTTTCATCCAGGAGGCCAGGACTACACGAGGCTGTGGAGCTTCTGGCTGTG 754
Qy 241 ArgIleGlnLeuGluAenValThrLeuLeuAenProAspProAlaGluGlyProLysPro 260
Db 755 CGAATTCAGCTGGAAAATGTGACACTCTGAACCCGATCTGTCAGAGGGCCCCAAGCCT 814
Qy 261 ArgProAlaValTrpLeu****TrpLysValSerGlyPro****ArgLeuProAenLeuTh 280
Db 815 AGACCGCGGTGTGGCTCAGCTGGAAGGTCACTGGCGCTGCTGCGCTGCCCAATCTTAC 874
Qy 280 rArgProCysSerGlyProArgLeuProArgGluAlaAraGluLeuArgGlyGlnArg 299
Db 875 ACGGCTTGTTCAGGACCCAGACTGCCCCGGAGGCCAGGAGGCTCCGTGGGCGAGAG 932

RESULT 4

ABK87137
ID ABK87137 standard; cDNA; 3715 BP.

XX AC ABK87137;

XX 07-OCT-2002 (first entry)

XX cDNA human ECSM4 protein.

XX Human; endothelial cell-specific molecule 4; ECSM4; neovasculature;
KW imaging vascular endothelium; proliferative disease; cancer;
KW psoriasis; diabetic retinopathy; atherosclerosis; menorrhagia;
KW endothelial damage; tumour neovasculature; cardiac disease;
KW endometriosis; hypoxic condition; angiogenesis; cytostatic;
KW cardiant; gene; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
FH CDS 70..3384
FT /*tag= a
FT /product= "ECSM4"

XX WO200236771-A2.

XX 10-MAY-2002.

XX 06-NOV-2001; 2001WO-GB04906.

XX 06-NOV-2000; 2000US-245566P.

XX 07-MAR-2001; 2001US-273662P.

XX (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.

XX Bicknell R, Huminiecki L;

XX WPI; 2002-508120/54.

XX P-PSDB; AAU99419.

XX Novel endothelial cell-specific molecule polypeptide 1 or 4, useful for
PT imaging, diagnosing and treating a condition involving vascular
PT endothelium e.g. cancer, cardiac disease, endometriosis, diabetes -

XX Disclosure; Fig 12; 248pp; English.

XX The present invention relates to endothelial cell-specific molecule 4
CC (ECSM4), and the polynucleotide sequences encoding it. The ECSM4
CC proteins are useful for imaging vascular endothelium in the body of
CC an individual, and for diagnosing and treating a proliferative
CC disease or condition involving the vascular endothelium (preferably,
CC neovasculature) such as cancer, psoriasis, diabetic retinopathy,
CC atherosclerosis or menorrhagia. The ECSM4 proteins are also useful in
CC the manufacture of diagnostic or prognostic agent for such conditions.
CC The proteins are also useful for detecting endothelial damage or
CC activation, detecting a tumour or tumour neovasculature, cardiac

XX PD 25-JUL-2002.
XX PF 17-JAN-2002; 2002WO-US01109.
XX PR 18-JAN-2001; 2001US-262066P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Moore PA, Ruben SM, LaFleur DW, Shi Y, Rosen CA, Olsen H;
XX PI Ebner R, Brewer LA;
XX DR WPI; 2002-599716/64.
XX DR P-PSDB; ABP62033.
XX PT New polynucleotides and polypeptides useful for diagnosing, prognosing,
XX PT treating or preventing e.g. neurodegenerative, central nervous system,
XX PT autoimmune, respiratory, reproductive, or inflammatory diseases or
XX PT disorders -
XX PS Claim 1; Page 713-714; 785pp; English.
XX CC The invention relates to novel genes (ABQ92553-ABQ92607) and proteins
XX CC (ABP62013-ABP62153) useful for preventing, treating or ameliorating
XX CC medical conditions e.g. by protein or gene therapy. The genes are
XX CC isolated from a range of human tissues disclosed in the specification.
XX CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
XX CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
XX CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
XX CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
XX CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
XX CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
XX CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
XX CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
XX CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
XX CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
XX CC and parasitic infections.
XX SQ Sequence 1346 BP; 318 A; 379 C; 376 G; 267 T; 6 other;

Alignment Scores:
Pred. No.: 3,828-93 Length: 1346
Score: 1602.00 Matches: 303
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.63% Indels: 0
DB: 24 Gaps: 0

US-10-047-021-86 (1-303) x ABQ92573 (1-1346)

QY 1 MetGlySerGlyGlyValSerLeuLeuGlyValGlyArgGlySerLeuProLeuLeuLeu 20
Db 31 ATGGGCTCTGGAGGAGACAGCTCTGGGGGGCAGGGGTCCCTGCTCTGCTGCTGCTG 90
QY 21 LeuLeuMetGlyGlyMetAlaGlnAspSerProGlnIleLeuValHisProGlnAsp 40
Db 91 CTCATCATGGGAGGATGGCTCAGGACTCCCGCCGCCAGATCTAGTCCACCCCGAGAC 150
QY 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60
Db 151 CAGCTGTTCAGGGCCCTGGCCCTCCAGGATGAGTCCGAGGCTCAGGCGCAGCACCT 210
QY 61 ProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80
Db 211 CCCACATCCGCTGGTGTCTGAATGGGAGCCCTCCAGCATGGTGGTCCCGAGACCCACAC 270
QY 81 HisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100
Db 271 CACCTCTCTGCTGATGGACCTCTCTGCTGCTACAGCCCTGCGCGGGGACATGCCAC 330
QY 101 AspGlyGlnAlaLeuSerThrAspLeuGlyValThrCysGluAlaSerAsnArgLeu 120
Db 331 GATGCCAGGGCCCTGTCCACAGACCTGGTGTGTACATGTGAGGCCAGCAACCGGCTT 390

QY 121 GlyThrAlaValSerArgGlyValaArgLeuSerValAlaValLeuArgGluAspPheGln 140
Db 391 GGCACGGCAGTCACAGAGGGCTCGGCTGCTGTGGCTGCTCTCCCGGGAGATTTCCAG 450
QY 141 IleGlnProArgAspMetValAlaValValGlyGluGlnPheThrLeuGlyCysGlyPro 160
Db 451 ATCCAGGCTCGGACATGGTGGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 510
QY 161 ProTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeu 180
Db 511 CCCTGGGGGCCACCCAGAGCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTGGCCCTC 570
QY 181 GlnProGlyArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGlyLysSer 200
Db 571 CAGCCCGGAGGACACACAGTGTCCGGGGGTCCCTGCTGATGGCAAGACAGAGAGT 630
QY 201 AspGlu***ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAla 220
Db 631 GACGAANGGACCTACATGTGTGTGGCCACCAACAGCGCAGGACACAGGAGAGCCGCGCA 690
QY 221 AlaArgValSerIleGlnGluProGlnAspTyrThrGluProValGluLeuAlaVal 240
Db 691 GCCCGGGTTCATCCAGGAGCCCGGAGCTACACGGAGCTGTGGAGCTTCTGGCTGTG 750
QY 241 ArgIleGlnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysPro 260
Db 751 CGAATTCAGCTGGAAATGTGACACTCTGTCNACCCGGATCTGCAGARGGCCCAAGCT 810
QY 261 ArgProAlaValTrpLeu***TrpLysValSerGlyPro***ArgLeuProAsnLeuThr 280
Db 811 AGACCGGGGTGTGGCTCARCTGGAARGTCAGTGGCCCTNTGGCCTGCCCAATCTTACA 870
QY 281 ArgProCysSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArgArg 300
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QY 301 AsnThrGly 303
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RESULT 3
ABN59723
ID ABN59723 standard; cDNA; 3267 BP.
XX AC ABN59723;
XX DT 28-JUN-2002 (first entry)
XX DE Novel human coding sequence SEQ ID NO: 134.
XX KW Human; antianaemic; vulnery; antiinflammatory; immunomodulator;
XX KW antifertility; cerebroprotective; cyostatic; rheumatic; gene therapy;
XX KW neuroprotective; antiparkinsonian; protein therapy; EST;
XX KW expressed sequence tag; gene; ss.
XX OS Homo sapiens.
XX FN WO200222660-A2.
XX PD 21-MAR-2002.
XX PF 10-SEP-2001; 2001WO-US26015.
XX PR 11-SEP-2000; 2000US-0659671.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
XX PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;
XX DR WPI; 2002-292408/33.
XX DR P-PSDB; ABN97310.

and is derived by analysis of the total score distribution.

SUMMARIES

DNA encoding a hum

Human cDNA sequenc

Human PRO860 (UNQ4)
cDNA encoding huma

Human Robo 1 polyp

Human Robo1 cDNA.
Drosophila Robo 1

Drosophila sp. kob
Drosophila melanog

Human neurotropic mi

C. elegans Robo po

C. elegans ROBO CD

Drosophila sp. ROB

Human 5' EST isola

Metastoma associate
Human osteoblast d

Human polynucleoti

**ALL DISORDER;
AIDS;**

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```
QY 227 ----GluProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGlnLeuG1 245
Db 131418 CACAGAGTCACCGGACCAACAGGAGCATCTAGAGCTTCTGGCTGTTCCGAATTCAGCTGGA 131477
QY 245 uAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAlaValTr 265
Db 131478 AAATGTGACCTGTGTAACCCAGAACCTGTAAAGGCCCAAGCCTGGGCCAGCTGTGTG 131537
QY 265 pLeu**TrpLys----- 269
Db 131538 GCTCAGCTGGAAGGTGAGGAGAGACCCCTGAAGACACGGAGAGCTCCCATGACTCCCT 131597
QY 270 -----ValSerGlyPro***-ArgLeuProAsn 278
Db 131598 AGTTCCCTGTCCTTACTCTGACCTCTCCCGAGGTGAGCGGCCCTGCTGCACCTGCCAGT 131657
QY 279 LeuThrArgProCysSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGln 298
Db 131658 CATAACACAGCCCTGTTTCAGGGCGCAGAGGGACCCCGAGGACCCAGGGATCTCCATGGACAG 131717
QY 299 Arg 299
Db 131718 AGG 131720
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Search completed: January 31, 2004, 14:33:31
Job time : 3427.57 secs

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 Weinstock,G. and Gibbs,R.A.
 Direct Submission
 Unpublished
 2 (bases 1 to 250318)
 Worley,K.C.
 Direct Submission
 Submitted (09-FEB-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 250318)
 Rat Genome Sequencing Consortium.
 Direct Submission
 Submitted (15-NOV-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Nov 15, 2002 this sequence version replaced gi:23266067.
 The sequence in this assembly is a combination of BAC based reads
 and whole genome shotgun sequencing reads assembled using Atlas
 (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
 in the feature table below represents a scaffold in the Atlas
 assembly (a 'contig-scaffold'). Within each contig-scaffold,
 individual sequence contigs are ordered and oriented, and separated
 by sized gaps filled with Ns to the estimated size. The sequence
 may extend beyond the ends of the clone and there may be sequence
 contigs within a contig-scaffold that consist entirely of whole
 genome shotgun sequence reads. Both end sequences and whole genome
 shotgun sequence only contigs will be indicated in the feature
 table.
 ----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: http://www.hgsc.bcm.tmc.edu/
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: GRFO
 Center clone name: CH230-85A24
 ----- Summary Statistics
 Assembly program: Phrap; version 0.990329
 Consensus quality: 230810 bases at least Q40
 Consensus quality: 233159 bases at least Q30
 Consensus quality: 234781 bases at least Q20
 Estimated insert size: 236162; sum-of-contigs estimation
 Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

 * NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
 * NOTE: this is a 'working draft' sequence. It currently
 * consists of 1 contigs. Gaps between the contigs
 * are represented as runs of N. The order of the pieces
 * is believed to be correct as given, however the sizes
 * of the gaps between them are based on estimates that have

----- Summary Statistics

Assembly program: Phrap; version 0.990329
Consensus quality: 201827 bases at least Q40
Consensus quality: 204782 bases at least Q30
Consensus quality: 206701 bases at least Q20
Estimated insert size: 209571; sum-of-coverage estimation
Quality coverage: 6x in Q20 bases; sum-of-coverage estimation

- * NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
- * NOTE: this is a 'working draft' sequence. It currently
consists of 1 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces
is believed to be correct as given, however the sizes
of the gaps between them are based on estimates that have
been provided by the submitter.
- * This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.
- * 1 223269: contig of 223269 bp in length.

FEATURES

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1. 223269
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BASE COUNT 59410 a 47952 c 46732 g 54018 t 15157 others

ORIGIN

Alignment Scores:

Pred. No.: 3.12e-36 Length: 223269
Score: 814.50 Matches: 208
Percent Similarity: 37.08% Conservative: 23
Best Local Similarity: 33.39% Mismatches: 49
Query Match: 50.65% Indels: 344
DB: 2 Gaps: 5

US-10-047-021-86 (1-303) x AC120636 (1-223269)

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Db 202698 CTTTCCCTCTTAGGAGGAAGCTCTGGATTCTCCACCACAGATCTAGTTTCATCCCCAG 202639
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256 uGlyProLysProArgProAlaValThrLeu***TrrLys----- 269
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VERSION AC120636.4 GI:25138029
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SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
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Direct Submission
Unpublished
2 (bases 1 to 223269)
Worley, K.C.
Direct Submission
Submitted (09-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 223269)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

Center: Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
Project Information
Center project name: GXDD
Center clone name: CH230-136D4

Web site: <http://www-seq.wi.mit.edu>
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L28797
 Center clone name: 356_D_13

----- Summary Statistics
 Sequencing vector: Plasmid; n/a; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 213654 bases at least Q40
 Consensus quality: 213955 bases at least Q30
 Consensus quality: 214104 bases at least Q20
 Insert size: 210000; agarose-fp
 Insert size: 214159; sum-of-contigs
 Quality coverage: 10.7 in Q20 bases; agarose-fp
 Quality coverage: 10.5 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 5 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 5437: contig of 5437 bp in length
 * 5438 5537: gap of 100 bp
 * 5538 134170: contig of 128633 bp in length
 * 134171 134270: gap of 100 bp
 * 134271 159037: contig of 24767 bp in length
 * 159038 159137: gap of 100 bp
 * 159138 212279: contig of 53142 bp in length
 * 212280 212379: gap of 100 bp
 * 212380 214559: contig of 2180 bp in length.

FEATURES

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BASE COUNT 57879 a 45778 c 47185 g 63317 t 400 others
 ORIGIN

Alignment Scores:

Pred. No.: 5,03e-38 Length: 214559
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 Percent Similarity: 37.99% Conservative: 26
 Best Local Similarity: 33.77% Mismatches: 46
 Query Match: 52.58% Indels: 336
 DB: 2 Gaps: 5

US-10-047-021-86 (1-303) x AC138284 (1-214559)

Qy 20 LeuLeuMetGlyGlyMetAlaGlnAspSerProGlnLeuValHieProGln 39

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Qy 40 AspGlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnPro 59
 Db 188551 GACCAGTACTTTCAGGGCTCTGCCAGCCAGATGAGTGCAGATCATCGGCCAACCA 188492
 Qy 60 ProProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspPro 79
 Db 188491 CCTCCCACTATCGCTGGCTGATGGGAGCCCTCAGCATGGCCACCCAGACCTA 188432
 Qy 80 HisHisLeuLeuProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAla 99
 Db 188431 CATTACCTTTTGGCGGATGGACCTCTGTATCATCGGCCCTCTGTCCAGGGACGGCCA 188372
 Qy 100 HisAspGlyGln---AlaLeuSerThrAspLeuGlyValTyThrCysGluAlaSerAsn 118
 Db 188371 CAAGATGACCAAGAACATCTCTCAGCAATCTGGGTGTCTACACATGTGAGCCAGCAAC 188312
 Qy 119 ArgLeuGlyThrAlaValSerArgGlyAlaArgLeuSerValAla----- 133
 Db 188311 CGGCTGGGCACAGCAGTGCAGCCGGGTGCTAGGCTGTCTGTGGCTGGTGGAGTGGGAG 188252
 Qy 133 ----- 133
 Db 188251 GGTAGGCCAGGGGGAAGCAGAGTTAGGCTGAGATGCTTGTCTCCAGGAAATAGGAGAG 188192
 Qy 133 ----- 133
 Db 188191 TCTGTCTGTGAGGGAGCAGGAGTCTGAGGCTTGGGATGGAGAACTAGTTAACTAG 188132
 Qy 133 ----- 133
 Db 188131 AGATAGAGGGGCAAGGAAGTGGTAGACAGAAATGGGTAAAGCATGTTCCGATAGCCATC 188072
 Qy 133 ----- 133
 Db 188071 CATGTTAGGATGTTAGAAAGACTCAGGGTGGTAGAGTGTCTCTGCTGATTTGCTGAC 188012
 Qy 134 -----ValLeuArgGluAspPheGlnIleGlnProArgAspMetValAlaValVal 150
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 Qy 151 GlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluProThrValSer 170
 Db 187951 GGAGAGAGCTGGTTCCTTGTAGTGTGGTCTCTCCCTGGGGCTACCCAAAACCTCGGTCTCA 187892
 Qy 171 TrpTrpIysAspGlyIysProLeuAlaLeuGlnProGlyArgHis----- 185
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 Qy 186 -----Thr 186
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 Qy 187 -ValSerGlyGlySerLeuLeuMetAlaArgAlaGluIysSerAspGlu***ThrTyMe 206
 Db 187711 GGTATCTGGGATTCCTCTGATGGTGTCAAGACGAGAGAAATGACTCGGGGACTATAT 187652
 Qy 206 tCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleG1 226
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Qy 226 n----- 226
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Qy 226 ----- 226
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Qy 226 ----- 226
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Qy 236 uLeuLeuAlaValArgIleGlnLeuGluAsnValThrLeuLeuAsnProAspProAlaG1 256
Db 10351 GCTTCTGGCTGTTCGATTCAGTTCAGTGGAAATGTGACCTCTGCTAAACCCGCAACCTGTAA 10410
Qy 256 uGlyProLysProArgProAlaValTIPLeu***TIPlys----- 269
Db 10411 AGGTCCCAAGCTGGGCCATCGGTGTGGCTCAGCTGGNAGGTGAGACAGAGGTCCAGAA 10470
Qy 269 ----- 269
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Qy 270 -----ValSerGlyPro***-ArgLeuProAsnLeuThrArgProCysSerGly 285
Db 10531 CTTCTTCCAGGTGAGCGGCCCTGCTGCACCTGCTGAGTCTATACACAGCTCTGTTTCAGGA 10590

Qy 286 ProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArg 299
Db 10591 CTCAGAGTGTCCTCCAGGAGCCAGGATCTCCATGACAGAGG 10632
RESULT 13
AC138284/c
AC138284
LOCUS
DEFINITION
Mus musculus chromosome 9 clone RP23-356D13 map 9, WORKING DRAFT
SEQUENCE, 5 unordered pieces.
AC138284
AC138284.3 GI:29164640
VERSION
HTG; HTGS PHASE1; HTGS DRAFT.
KEYWORDS
Mus musculus (house mouse)
SOURCE
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 214559)
Birren,B., Nusbaum,C. and Lander,E.
Mus musculus chromosome 9, clone RP23-356D13
Unpublished
2 (bases 1 to 214559)
Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhgalter,B.,
Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,
Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hafez,N.,
Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kellis,C., Landers,T., Levine,R.,
Lindblad-Toh,K., Liu,G., MacLean,C., Macdonald,P., Major,J.,
Mathews,C., McCarthy,M., Meldrim,J., Meneus,L., Mihova,T.,
Miengwa,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C.,
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J.,
Peterson,K., Phunkhang,P., Pierre,N., Raymond,C., Retta,R.,
Rise,C., Rogov,P., Roman,J., Roy,A., Schauer,S., Schuback,R.,
Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Talamas,J., Tesfaye,S., Theodore,J., Topham,K.,
Travers,M., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X.,
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (20-DEC-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 214559)
Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
Boguslavsky,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y.,
Collymore,A., Cooke,P., Cooke,P., Corum,B., DeArellano,K.,
Diaz,J.S., Dodge,S., Doolley,K., Dorris,L., Erickson,J., Faro,S.,
Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,
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Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kellis,C., Landers,T., Levine,R.,
Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., MacLean,C.,
Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,
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Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
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Rachupka,A., Ramasamy,J., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Schauer,S., Schuback,R., Seaman,S., Severy,P., Smith,C.,
Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,
Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (23-MAR-2003) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 23, 2003 this sequence version replaced gi:28460994.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://fcp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR

Roman, J., Schauer, S., Schupbach, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Steange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Vziel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (04-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

On Mar 4, 2003 this sequence version replaced gi:28201704.

All repeats were identified using RepeatMasker:

Smith, A.F.A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

* NOTE: This is a 'working draft' sequence. It currently
* consists of 9 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of 'N', but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

[illegible]

FEATURES

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misc feature

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Query Match:	52.58%	Gaps:	5
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US-10-047-021-86 (1-303) x AC105958 (1-209012)

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[illegible]

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9151 GGTAGGCCCAAGGGGAGCAGAGTTAGCTGTGATGCTTGTGTCTCAGGGAAATACGAGAG 9210

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Db 9211 TCTGTCTGTGAAGGGAGGCAGGAGCTGAGGCTCTTGGGATGGAGAACTAGTTAAACTAG 9270

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Db 9271 AGATAGAGGGGCAAGGAAGTGGTAGAGCAGAAATGGGTAGCATGTTCCGGATAAGCCATC 9330

Qy 133 ----- 133

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Qy	134	-----ValLeuArgGluAspPheGlnIleGlnProArgAspMetValAlaValVal	150
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Best Local Similarity: 62.00% Mismatches: 3
Query Match: 56.72% Indels: 111
DB: 9 Gaps: 1

US-10-047-021-86 (1-303) x AK074163 (1-4694)

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QY 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60
DB 69 ----- 69

QY 61 ProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80
DB 69 ----- 69

QY 81 HisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100
DB 69 ----- 69

QY 101 AspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeu 120
DB 69 ----- 69

QY 121 GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln 140
DB 70 -----GTCCTCCGGGAGGATTTCCAG 90

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DB 151 CCCTGGGGCCACCCAGAGCCACAGTCTCATGGTGGGAAGATGGGAACCCCTGGCCCTC 210

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DB 211 CAGCCCGGAAGGACACAGTCTCCGGGGGTCCTGCTGATGGCAAGAGAGAGAGAGT 270

QY 201 AspGlu***ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAla 220
DB 271 GACGAAGGAGGACCTACATGTGTGTGGCCACCAACAGCGGAGGACATAGGAGGCGCGCA 330

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QY 261 ArgProAlaValTTPLeu***TTPlysValSerGlyPro***ArgLeuProAsnLeuTh 280
DB 451 AGACCGGGGTGTGGCTCAGCTGGAAGGTCACTGGCCCTGTGCGCTGCCCATCTTAC 510
QY 280 rArgProCysSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArg 299
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RESULT 12
AC105958
LOCUS

DEFINITION Mus musculus clone RP24-325P4, WORKING DRAFT SEQUENCE, 9 unordered
pieces.

AC105958 209012 bp DNA linear HTG 04-MAR-2003
AC105958.6 GI:28827995
HTG; HTGS PHASE1; HTGS DRAFT.
Mus musculus (house mouse)
Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 209012)

Birren,B., Nusbaum,C. and Lander,E.

Mus musculus, clone RP24-325P4

Unpublished

2 (bases 1 to 209012)

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

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AUTHORS

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TITLE

JOURNAL

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 3467)
TITLE Strausberg, R.
JOURNAL Direct Submission
 Submitted (01-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
 Email: cgapb-help@mail.nih.gov
 Tissue Procurement: Dr. Mark Watson
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
 Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Len Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saedi, Jacqueline Schein, Duane Smalrus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
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 /tissue_type="Spleen"
 /clone_lib="NIH MGC 113"
 /lab_host="DH10B-R"
 /note="Vector: pOTB7"
BASE COUNT 704 a 1132 c 967 g 664 t
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 Alignment Scores:
 Pred. No.: 1.56e-55 Length: 3467
 Score: 1121.00 Matches: 213
 Percent Similarity: 98.16% Mismatches: 0
 Best Local Similarity: 98.16% Gaps: 0
 Query Match: 69.71% Indels: 1
 DB: 9 Gaps: 0
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 Qy 84 ProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGln 103
 Db 2 CCTGATGGAGCCCTTCTGCTGCTACAGCCCTTCCCGGGGACATGCCACGATGGCCAG 61
 Qy 104 AlalaSerThrAspLeuGlyValThrCysGluAlaSerAsnArgLeuGlyThrAla 123
 Db 62 GCCCTGTCCAGACCTGGGTGTCTACATGTGTGGCCAGACACCGGCTTGGCAGCGCA 121
 Qy 124 ValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnPro 143
 Db 122 GTCAGCAGAGCGCTCGGCTGCTGTGCTGTCTCCCGGAGGATTCACATCCAGCGCT 181
 Qy 144 ArgAspMetValAlaValAlaValGlyGlnGlnPheThrLeuGlyCysGlyProProTrpGly 163
 Db 182 CGGGACATGGTGGCTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 241
 Qy 164 HisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGly 183

242 CACCAGAGCCACAGTCTCATGTTGGAAGATGGGAACCCCTGGCCCTCCAGCCCGGA 301
 Qy 184 ArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu*** 203
 Db 302 AGGCACACAGTGTCCGGGGATCCCTGCTGATGGCAAGACAGAGAGATGACGAAGGG 361
 Qy 204 ThrTyMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgVal 223
 Db 362 ACTACATGTGTGGCCACCAACAGCGCAGGACAGGAGGAGCGCGGACCGCGGTT 421
 Qy 224 SerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGln 243
 Db 422 TCCATCCAGGAGCCCGAGGACTACAGGAGCTGTGGAGCTTCTGGGTGCGAATTCAG 481
 Qy 244 LeuGluAsnValThrLeuLeuAsnProAspProAlaGlyProLysProArgProAla 263
 Db 482 CTGGAAATGTGACACTGCTGAACCCGGATCTCTGCAGAGGGCCCCAAGCCCTAGACCGCG 541
 Qy 264 ValTrpLeu***TrpLysValSerGlyPro***ArgLeuProAsnLeuThrArgProC 283
 Db 542 GTGTGGCTCAGTGGAGGTTCAGTGGCCCTGCTGGCTGCCCAATCTTACAGCGCCTTG 601
 Qy 283 sSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArg 299
 Db 602 TTCAGGACCCAGACTGCCCGGGAGGCGCAGGAGCTCCGTGGGCGAGAGG 650

RESULT 11
AK074163
LOCUS AK074163 4694 bp mRNA linear PRI 15-FEB-2002
DEFINITION Homo sapiens mRNA for FLJ00236 protein.
ACCESSION AK074163
VERSION AK074163.1 GI:18676673
KEYWORDS fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Jikuya, H., Takano, J., Nomura, N., Kikuno, R., Nagase, T. and Ohara, O.
TITLE The nucleotide sequence of a long cDNA clone isolated from human spleen
JOURNAL Published Only in Database (2002)
REFERENCE 2 (bases 1 to 4694)
AUTHORS Jikuya, H., Takano, J., Nomura, N., Kikuno, R., Nagase, T. and Ohara, O.
TITLE Direct Submission
JOURNAL Submitted (21-JAN-2002) Takahiro Nagase, Kazusa DNA Research Institute, Department of Human Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: cdnainfo@kazusa.or.jp, URL: <http://www.kazusa.or.jp/NEDO>, Tel: 81-438-52-3913, Fax: 81-438-52-3914)
COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert and 5'- & 3'-end one pass sequencing; Research Association for Biotechnology; cDNA library construction and clone selection; Kazusa DNA Research Institute.
FEATURES
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 1. 4694
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gene
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Qy 256 GluGlyProLysProArgProAlaValTrrpLeu***TrrpLys----- 269
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Db 30906 GAGGGCCCAAGCTAGACCGCGGTGGCTCAGCTGGAAGGTGAGGACAGGTGCTAA 30847
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Qy 269 ----- 269
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Db 30846 GGGTAAAGCCGATCCAGAGCTCAAGAAAGGCGTTCCTGAGCTCTCTGACCCCGCGCC 30787
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Qy 270 -----ValSerGlyPro***ArgLeuProLeuThrArgPr 282
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Db 30786 TTCTCGAAACTCTCCAGAGTCAGTGGCCCTGCTGGCCCTGCCCAATCTTACAGGCC 30727
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Qy 282 cysSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArg 299
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Db 30726 TTGTTCCAGACCCAGACTGCCCGCGGAGGCCAGGAGCTCGTGGGCAGAGG 30675
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RESULT 8
BD150226 756 bp DNA linear PAT 17-JAN-2003
LOCUS Primer for synthesizing full-length cDNA and use thereof.
DEFINITION
ACCESSION BD150226
VERSION BD150226.1 GI:27855984
KEYWORDS JP 2002191363-A/5069.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 756)
Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
Primer for synthesizing full-length cDNA and use thereof
PATENT: JP 2002191363-A 5069 09-JUL-2002;
HELIX RESEARCH INSTITUTE
COMMENT OS Homo sapiens (human)
PN JP 2002191363-A/5069
PD 09-JUL-2002
PF 28-JUL-2000 JP 2000280990
PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU
PI SAITO,
PI JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
PI KEIICHI NAGAI,TETSUJI OTSUKI
PC
C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
10,
PC C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key
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Location/Qualifiers
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BASE COUNT 147 a 242 c 236 g 128 t 3 others
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Pred. No.: 4e-60 Length: 756
Score: 1190.00 Matches: 232
Percent Similarity: 97.49% Conservative: 1
Best Local Similarity: 97.07% Mismatches: 6
Query Match: 74.00% Indels: 2
DB: 6 Gaps: 0
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Qy 61 ProThrIleArgTrrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80
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Qy 81 HisLeuLeuProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100
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Qy 101 AspGlyGlnAlaLeuSerThrAspLeuGlyValTrrpCysGluAlaSerAsnArgLeu 120
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Qy 121 GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln 140
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Qy 141 IleGlnProArgAspMetValAlaValAlaValGlyGlnGlnPheThrLeuGlyCysGlyPro 160
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Qy 161 ProTrrpGlyHisProGluProThrValSerTrrpLysAspGlyLysProLeuAlaLeu 180
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Qy 181 GlnProGlyArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSer 200
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Db 580 CAGCCCGGAAAGGCACACAGTGTCCGGGGGTCTCCCTGTGTGTCAGTGGCAGCAGAGAGT 639
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Qy 221 AlaArgValSerIleGlnGluProGlnAspTrrpThrGluProValGluLeuAla 239
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RESULT 9
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LOCUS Rattus norvegicus ROBO4 (Robo4) mRNA, complete cds.
DEFINITION
ACCESSION AV277635
VERSION AV277635.1 GI:30575794
KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 2886)
AUTHORS Roberts,K.G. and Stewart,L.M.
TITLE Direct Submission
JOURNAL Submitted (15-APR-2003) CRT Development Laboratory, Cancer Research
Technology, Suite 23, Dominion House, 59 Bartholomew Close, London,
England EC1A 7BE, United Kingdom
FEATURES
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1..2886
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/mol_type='mRNA'
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Db 820 AGACCGGCGGTGTGCTCACTGAGAGTCAAGTGCCTGCTGCGCCCTGCCAATCTTAC 879
Qy 280 rArgProCysSerGlyProArgLeuProArgGluAlaArgGluLeuAArgGlyGlnArg 299
Db 880 ACGGCTTGTTCAGAGCCCAAGACTGCCCGGAGGCGCAGGAGCTCCGTGGCAGAGG 937

RESULT 6
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LOCUS Homo sapiens CDNA FLJ14946 f18, clone PLACE2000034, weakly similar
DEFINITION to IAR PROTEIN PRECURSOR (EC 3.1.3.48).
ACCESSION AK027852
VERSION AK027852.1 GI:14042831
KEYWORDS oligo capping; f18 (full insert sequence).
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Isegai,T., Oca,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
Nishikawa,T., Nagai,K., Sugano,S., Takahashi-Fujii,A., Hara,H.,
Tanase,T., Nomura,Y., Togiya,S., Kawai,F., Hara,R., Takeuchi,K.,
Arita,M., Nakamura,T., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J.,
Wakamatsu,A., Nakamura,Y., Nagahara,K., Maehno,Y. and Oshima,A.
TITLE NEBO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 4262)
AUTHORS Isegai,T. and Otsuki,T.
TITLE Direct Submission
JOURNAL Submitted (10-MAY-2001) Takao Isegai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yama, Kisarazu, Chiba 292-0812, Japan
(E-mail:genom@helix.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT NEBO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing;
Research Association for Biotechnology; cDNA library construction,
5'-, 3'- and one pass sequencing and clone selection; Helix
Research Institute (supported by Japan Key Technology Center etc.)
and Department of Virology, Institute of Medical Science,
University of Tokyo.
FEATURES
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Location/Qualifiers
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/clone="PLACE2000034"
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PWGHEPTVSWKDEKPLAQGRHTVSGGSLNMAPAKSDEGTVMCVATVAGHRES
RAARVSIQEPDQYPELLAVRIQLENTLLNPDPAGPKRPRAVMISMTVSGPAAP
AOSYALPRTQYAPGGGAPMAABELLAGMOSAEGLGMGDYEFKVRSSGRARGP
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PPAMTVVGEOTLEIATIMPGSTCVQVAATGAGAPSPVCLLLQANRGAHOEP
SEHGPTLEQRLATLKREVIATCGVALMLLGLTAVCIHRRRARVHLGGLRYTGS
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CSRGISPRSLAPABAWKAKKQOELPHANSSPLRSHSLRLACAGTGGGKNLS
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BASE COUNT 873 a 1333 c 1209 g 847 t
ORIGIN

Alignment Scores:
Pred. No.: 2,01e-80 Length: 4262
Score: 1557.00 Matches: 294
Percent Similarity: 98.33% Conservative: 1
Best Local Similarity: 98.00% Mismatches: 4
Query Match: 96.83% Gaps: 1
DB: 9 Indels: 0

US-10-047-021-86 (1-303) x AK027852 (1-4262)

Qy 1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyValArgGlySerLeuProLeuLeuLeu 20
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Qy 21 LeuLeuMetGlyGlyMetAlaGlnAspSerProProGlnLeuValHisProGlnAsp 40
Db 100 CTCAATCATGGAGGAGGAGGCTCAGAGACTCCCGGCCAGATCTTAGTCACCCCAAGGAC 159
Qy 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60
Db 160 CAGCTGTTCAGAGGCTCTGGCCCTGCAGATGAGCTGCCAAGCTCAGAGCCACCACT 219
Qy 61 ProThrIleArgTrrPleuLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80
Db 220 CCCACATCCGCTGCTGTTGTAATGAGGACAGCCCTGAGCATGTGTGCCCCAGACCAACAC 279
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Db 280 CACCTCTGCTGATGAGGACCTTCTCTGCTGTACAGCCCTGCGGAGCATGCTCCAC 339
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Qy 121 GlyThrAlaValSerArgGlyValArgLeuSerValAlaValLeuArgGluAspPheGln 140
Db 400 GGACAGGACAGTCAACAGAGGCGCTCGGCTGTGCTGTGCTGCTCCCGGAGATTTCAG 459
Qy 141 IleGlnProArgAspMetValAlaValValGlyGlnIlePheThrLeuGluCysGlyPro 160
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Qy 161 ProTrrGlyHisProGluProProThrValSerTrrTrrPlyAspGlyLysProLeuAlaLeu 180
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Qy 181 GlnProGlyArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSer 200
Db 580 CAGCCCGGAGGACACAGTGTCCGGGGGCTCCCTGTGATGGCAGAGCAGAGAGAGT 639
Qy 201 AspGlu**ThrrTrrMetCysValAlaThrAsnSerIleGlyHisArgGluSerArgAla 220
Db 640 GACCAAGGAGCTTCATGT 699
Qy 221 AlaArgValSerIleGlnGluProGlnAspTrrThrGluProValGluLeuLeuAlaVal 240
Db 700 GCCCGGCTTCCATCCAGAGAGCCCAAGACTCACAGAGCTGTGGAGCTTCTGGCTGTG 759
Qy 241 ArgIleGlnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysPro 260
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Qy 261 ArgProAlaValTrrPleu**TrrPlyValSerGlyPro***-ArgLeuProAsnLeuTh 280
Db 820 AGACCGGCGGTGTGCTCACTGAGAGTCAAGTGCCTGCTGCGCCCTGCCAATCTTAC 879
Qy 280 rArgProCysSerGlyProArgLeuProArgGluAlaArgGluLeuAArgGlyGlnArg 299
Db 880 ACGGCTTGTTCAGAGCCCAAGACTGCCCGGAGGCGCAGGAGCTCCGTGGCAGAGG 937

RESULT 7
AP003501/c

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Qy      101 AspGlyGlnAlaLeuSerThrAspLeuGlyValIYrThrCysGlnAlaSerAsnArgLeu 120
Db      340 GATGGCCAGGCGCTGCTGCACAGACCTGGGTGTCTACACATGTAGAGGCCAGCAACGGCTT 399
Qy      121 GYThraAlaValSerArgGlyValAlaArgLeuSerValAlaValLeuArgGlnAspPheGln 140
Db      400 GGCAGGCGAGTACAGAGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 459
Qy      141 IleglnProArgAspMetValAlaValAlaGlyGlnGlnPheThrLeuGlnCysGlyPro 160
Db      460 ATCCAGCCTCGAGACATGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 519
Qy      161 ProTPGlyHisProGlnProThrValSerTPITrPlyAspGlyLysProLeuAlaLeu 180
Db      520 CCTGGGGGCCACCCAGAGCCCAAGTCTCATGTGTGAGAAATGAGAAACCCCTGGGCTTC 579
Qy      181 GlnProGlyArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGlnLysSer 200
Db      580 CAGCCCGGAGGACACACAGTGTCCGGGGGGTCCCTGCTGTATGACAGACAGACAGAGACT 639
Qy      201 AspGlu**ThrTyMetCysValAlaThrAsnSerAlaGlyHisArgGlnSerArgAla 220
Db      640 GACGAAAGGACCTTACATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 699
Qy      221 AlaArgValSerIleglnGlnProGlnAspTYrThrGlnProValGlnLeuAlaVal 240
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Qy      241 ArgIleglnLeuGlnAsnValThrLeuLeuAsnProAspProAlaGlnGlyProLysPro 260
Db      760 CCAATTCACACTGAAATGTGACACTGCTGAACCCGAGATCTGACAGAGGCCCCCAAGCT 819
Qy      261 ArgProAlaValThrLeu**TrpLysValSerGlyPro***ArgLeuProAsnLeuTh 280
Db      820 AGACCGGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 879
Qy      280 rArgProCysSerGlyProArgLeuProArgGlnAlaArgGlnLeuArgGlyGlnArg 299
Db      880 ACGGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 937

RESULT 5
LOCUS   BD160172          4262 bp      DNA      linear      PAT 17-JUN-2003
DEFINITION
Primer for synthesizing full-length cDNA and use thereof.
ACCESSION   BD160172
VERSION     BD160172.1 GI:27865930
KEYWORDS   JP 2002191363-A/15015
SOURCE      Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 4262)
Ota,T., Isegai,T., Nishikawa,T., Hayaishi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002191363-A 15015 09-JUL-2002;
HELIX RESEARCH INSTITUTE
COMMENT
OS Homo sapiens (human)
PN JP 2002191363-A/15015
PD 09-JUL-2002
PF 28-JUL-2000 JP 200280990
PI TOSHIO OTA, TAKAO ISEGA, TETSUO NISHIKAWA, KOJI HAYASHI, KAZUO
PI SAITO,
PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
PI KEIICHI NAGAI, TETSUJI OTSUKI
PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC

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PC      C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key
Location/Qualifiers
(40)...(2415).
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BASE COUNT      873 a      1333 c      1209 g      847 t
ORIGIN
Alignment Scores:
Pred. No.:      2,01e-80      Length:      4262
Score:      1557.00      Matches:      294
Percent Similarity:      98.33%      Conservative:      1
Best Local Similarity:      98.00%      Mismatches:      4
Query Match:      96.83%      Indels:      1
DB:      Gaps:      0
US-10-047-021-86 (1-303) x BD160172 (1-4262)
Qy      1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeu 20
Db      40 ATGGGCTCTGGAGAGACAGACCTCTGGGGGGGAGGGGTTCCCTGCTGCTGCTG 99
Qy      21 LeuIleMetGlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAsp 40
Db      100 CTCATCATAGGAGGATGCTGAGATCTCCCGCCCGCCAGATCTGATCCACCCCAAGAGAC 159
Qy      41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60
Db      160 CAGCTGTTCAGAGGCGCTGCGCTTCCAGAGTGAAGCTCAAGCTCAGGCGGACCACT 219
Qy      61 ProThrIleArgTPITrPlyLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80
Db      220 CCCACATCCGCTGCTGTCTGATGAGGACGCCCTGAGACATGTGTGCTCCCAAGACCACAC 279
Qy      81 HisLeuLeuProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100
Db      280 CACCTCTGCTGCTGATGAGACCTTCTGTCTGTACAGCCCCCTGCCCCGGGAGCATGCCAC 339
Qy      101 AspGlyGlnAlaLeuSerThrAspLeuGlyValIYrThrCysGlnAlaSerAsnArgLeu 120
Db      340 GATGGCCAGGCGCTTCTCAAGACCTGGGTGTCTACATGTAGAGCCAGCAACGGCTT 399
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Qy      181 GlnProGlyArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGlnLysSer 200
Db      580 CAGCCCGGAGGACACACAGTGTCCGGGGGGTCCCTGCTGTATGACAGACAGAGAGAAAGT 639
Qy      201 AspGlu**ThrTyMetCysValAlaThrAsnSerAlaGlyHisArgGlnSerArgAla 220
Db      640 GACGAAAGGACCTTACATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 699
Qy      221 AlaArgValSerIleglnGlnProGlnAspTYrThrGlnProValGlnLeuAlaVal 240
Db      700 GCCCGGGTTTCATCCAGAGAGCCCGAGACTACAGAGACTGTGTGTGTGTGTGTGTGTGTGT 759
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BASE COUNT 850 a 1245 c 1063 g 714 t
 ORIGIN

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Alignment Scores:

Pred. No.: 6.38e-81 Length: 3872
 Score: 1565.00 Matches: 295
 Percent Similarity: 98.67% Conservative: 1
 Best Local Similarity: 98.33% Mismatches: 3
 Query Match: 97.33% Indels: 1
 Gaps: 0

US-10-047-021-86 (1-303) x AF361473 (1-3872)

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 Db 130 CTGATCAGGAGGAG 189
 QY 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60
 Db 190 CAGCTGTTCCAGGGGCTGGGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 249
 QY 61 ProThrIleArgTTPLeuLeuAnGlyGlnProLeuSerMetValProProAspProHis 80
 Db 250 CCCACATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 309
 QY 81 HisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100
 Db 310 CACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 369
 QY 101 AspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGlyAlaSerAspArgLeu 120
 Db 370 GATGGCCAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 429
 QY 121 GlyThrAlaValSerArgGlyValAlaArgLeuSerValAlaValLeuArgGlnAspPheGln 140
 Db 430 GGCAAGGAG 489
 QY 141 IleGlnProArgAspMetValAlaValGlyGlnGlnPheThrLeuGlnCysGlyPro 160
 Db 490 ATCCAGCTCCGAG 549
 QY 161 ProTTPGlyHisAspGlyProThrValSerTTPLeuAspGlyLysProLeuAlaLeu 180
 Db 550 CCTGGGGGCAAG 609
 QY 181 GlnProGlyArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGlyLysSer 200
 Db 610 CAGCCCGGAG 669
 QY 201 AspGlu***ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGlnSerArgAla 220
 Db 670 GACGAG 729
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 Db 730 GCCCGGGTTTCATCCAG 789
 QY 241 ArgIleGlnLeuGlnAsnValThrLeuLeuAsnProAspProAlaGlnGlyProLysPro 260
 Db 790 CGAATTCAGCTGGAG 849
 QY 261 ArgProAlaValTTPLeu***TTPLeuValSerGlyPro***ArgLeuProAsnLeuTh 280
 Db 850 AGACCGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 909
 QY 280 TArgProCysSerGlyProArgLeuProArgGlnAlaArgGlnLeuArgGlyGlnArg 299

Db 910 AGCGCTTGTTCAGAGACCAGACTGCCCGGAGAGCCAGGAGAGCTCCGTGGGAGAGG 967

RESULT 4
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 LOCUS BD012213 4262 bp DNA linear PAT 02-AUG-2002
 DEFINITION Novel genes encoding protein kinase or protein phosphatase.
 ACCESSION BD012213
 VERSION BD012213.1 GI:22092402
 KEYWORDS WO 0109345-A/11.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS
 Iehi,S., Sugiyama,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
 Funahashi,S., Seno,C. and Nezu,J.
 Novel genes encoding protein kinase or protein phosphatase
 Patent: WO 0109345-A 11 08-FEB-2001;
 HELIX RESEARCH INSTITUTE, TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA,
 KOJI HAYASHI, KAORU SAITO, JUNICHI YAMAMOTO, SHIZUKO ISHII, OMOKASU
 SUGIYAMA, AI MAKAMATSU, KEIICHI NAGAI, TETSUO NISHIKAWA, KOJI HAYASHI,
 FUNAHASHI, HIROKI SENO, JUNICHI NEZU
 OS Homo sapiens (human)
 PN WO 0109345-A/11
 PD 08-FEB-2001
 PR 29-JUL-1999 JP 99P 248036,11-JAN-2000 JP 00P 118776 PR
 02-MAY-2000 JP 00P 183767,18-OCT-1999 US 60/159590 PR
 17-FEB-2000 US 60/183322
 PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, PI
 KAORU SAITO,
 JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI MAKAMATSU,
 PI KEIICHI NAGAI, TETSUO OTSUKI, SHINICHI FUNAHASHI, CHIHIKI SENO,
 PI JUNICHI NEZU
 PC C12N1/54, C12N1/55, C12N9/12, C12N9/16, C12N5/10, C12N1/21 PC
 , C12N1/19, C07K16/40,
 CC G01N33/53, G01N33/566
 C12N1/19, C07K16/40,
 CC G01N33/53, G01N33/566

FEATURES

COMMENT

1. .4262
 Location/Qualifiers
 CDS (40)..(2415).
 FH Key
 FT CDS

BASE COUNT 873 a 1333 c 1209 g 847 t
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Alignment Scores:

Pred. No.: 2.01e-80 Length: 4262
 Score: 1557.00 Matches: 294
 Percent Similarity: 98.33% Conservative: 1
 Best Local Similarity: 98.00% Mismatches: 4
 Query Match: 96.83% Indels: 1
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US-10-047-021-86 (1-303) x BD012213 (1-4262)

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 Db 100 CTGATCAGGAGGAG 159
 QY 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60
 Db 160 CAGCTGTTCCAGGGGCTGGGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 219
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BASE COUNT 628 a 1101 c 927 g 611 t

ORIGIN

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Best Local Similarity:	98.33%	Mismatches:	3
Query Match:	97.33%	Indels:	1
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US-10-047-021-86 (1-303) x AX405719 (1-3267)

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QY 21 LeuLeuMetGlyGlyMetAlaGlnAspSerProGlnIleLeuValHisProGlnAsp 40
    |||||
DB 95 CTCATCATGGAGGAGCATGGCTCGAGACTCCGCCCCAGACTTACTAGTCAACCCCAAGAC 154
    |||||
QY 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60
    |||||
DB 155 CAGCTTTCAGAGGCGCCCTGGCCCTGCGAAGATGAGCTGCCAACCCTCAGGCCAGCAACT 214
    |||||
QY 61 ProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80
    |||||
DB 215 CCCACCATCCGCTGTTGCTGGAATGGGCAAGCCCTGAGCATGTGTGCCCAAGACCAACAC 274
    |||||
QY 81 HisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100
    |||||
DB 275 CACCTCTCTGCTGATGGAGCCCTTCTGCTGCTACACCCCTGCTCCGGGAGCAATGCCAC 334
    |||||
QY 101 AspGlyGlnAlaLeuSerThrAspLeuGlyValIleTrpCysGlnAlaSerAsnArgLeu 120
    |||||
DB 335 GATGGCAAGCCCTGCTCCACAGACTGGGTGTCTACACATGTAGGCCACAGAACCGGCTT 394
    |||||
QY 121 GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGlnAspPheGln 140
    |||||
DB 395 GGCACGGCAGTCAGCAGAGCGCTGCTGTCTGTGCTGCTCCCGGAGGATTTCCAG 454
    |||||
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DB 455 ATCCACCTCTGGGACATGTGGCTGTGGGGAGACAGTTTACTGTGAATCTGGCCCG 514
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DB 515 CCTGGGGCCACCAAGCCCAAGCTCATGTGTGAAGATGGGAAACCCCTGGGCTTC 574
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QY 221 AlaArgValSerIleGlnLeuProGlnAspTrpThrGlnProValGlnLeuLeuAlaVal 240
DB 695 GCCCGGTTTTCATCCAGAGAGCCCGCAGACTACAGAGACCTGTGTGAGCTTGTGCTGTG 754
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QY 261 ArgProAlaValTrpLeu**TrpLysValSerGlyPro***ArgLeuProAsnLeuThr 280
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QY 280 rArgProCysSerGlyProArgLeuProArgGlnAlaArgGlnLeuArgGlyGlnArg 299
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LOCUS AF361473
DEFINITION Homo sapiens magic roundabout mRNA, complete cds.
ACCESSION AF361473
VERSION AF361473.1 GI:16930357
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3872)
AUTHORS Huminecki, L. and Bicknell, R.
JOURNAL In silico cloning of novel endothelial-specific genes
MEDLINE Genome Res. 10 (11), 1796-1806 (2000)
PUBMED 20530916
11076864
REFERENCE 2 (bases 1 to 3872)
AUTHORS Huminecki, L. and Bicknell, R.
JOURNAL Direct Submision
TITLES Submitted (15-MAR-2001) ICRF, Institute of Molecular Medicine, John
Raddcliffe Hospital, Oxford OX3 9DS, UK
FEATURES
source Location/Qualifiers
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BD074325
LOCUS BD074325 1346 bp DNA linear PAT 27-AUG-2002
DEFINITION 50 human secreted proteins.
ACCESSION BD074325
VERSION BD074325.1 GI:22619928
KEYWORDS JP 2001514024-A/30.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1346)
Moore, P.A., Ruben, S.M., Lafleur, D.W., Shi, Y., Rosen, C.A.,
Olsen, H.S., Bbner, R. and Brewer, L.A.
50 human secreted proteins
Patent: JP 2001514024-A 30 11-SEP-2001;
HUMAN GENOME SCIENCES INC
COMMENT OS Homo sapiens (human)
PN JP 2001514024-A/30
PD 11-SEP-2001
PR 03-SEP-1998 JP 2000508394
PR 05-SEP-1997 US 60/057626, 05-SEP-1997 US 60/057663 PR
05-SEP-1997 US 60/057669, 12-SEP-1997 US 60/058667 PR
12-SEP-1997 US 60/058974, 12-SEP-1997 US 60/058973 PR
12-SEP-1997 US 60/058666
PI PAUL, A MOORE, STEVEN M RUBEN, DAVID W LAFLEUR, YANGSU SHI, CRAIG A
ROSEN,
PI HENRIK S OLSEN, REINHARD BBNER, LAURIE A BREWER PC
C12N15/09, A61K38/00, A61K48/00, A61P17/02, A61P19/00, PC
A61P19/02,
PC A61P29/00, A61P31/04, A61P31/12, A61P35/00, C07K14/435, C07K16/18,
PC C12N1/15,
PC C12N1/19, C12N1/21, C12N5/10, C12P21/02, C12O1/68, C01N33/53, C12N15/ PC
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ORIGIN
Alignment Scores:
Pred. No.: 1,75e-83 Length: 1346
Score: 1602.00 Matches: 303
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.63% Indels: 0
Gaps: 0
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QY 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60
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QY 61 ProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80

DB 211 CCCACCATCCGCTGGTTGCTGAATGGCAGCCCTCGAGCATGTGTCCCGCCAGACCAC 270
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DB 271 CACCTCTGCTGATGGAGCCCTTCTGCTGTACAGCCCTGCGCGGAGCATGTCCAC 330
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AX405719 3267 bp DNA linear PAT 14-JUN-2002
LOCUS AX405719
DEFINITION Sequence 134 from Patent WO0222660.
ACCESSION AX405719
VERSION AX405719.1 GI:21438877
KEYWORDS
ORGANISM Homo sapiens (human)
SOURCE Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1
Tang, Y.T., Liu, C., Zhou, P., Asundi, V., Zhang, J., Zhao, Q.A., Ren, F.,
Xue, A.J., Yang, Y., Weinman, T. and Dimahe, R.T.
Novel nucleic acids and polypeptides
Patent: WO 0222660-A 134 21-MAR-2002;
HYSEQ, INC. (US)
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GenCore version 5.1.6
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Title: US-10-047-021-86

Perfect score: 1608
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Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

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Total number of hits satisfying chosen parameters: 5777422

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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40: em_hcgo_mus:*
41: em_hcgo_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1602	99.6	1346	6	BD074325
2	1565	97.3	3267	9	AX405719
3	1565	97.3	3872	9	AF361473
4	1557	96.8	4262	6	BD012213
5	1557	96.8	4262	6	BD160172
6	1557	96.8	4262	9	AK027852
7	1262	78.5	186971	9	AP003501
8	1190	74.0	756	6	BD150226
9	1133.5	70.5	2886	10	AY277635
10	1121	69.7	3467	9	BC014995
11	912	56.7	4694	9	AK074163
12	845.5	52.6	209012	2	AC105958
13	845.5	52.6	214559	2	AC138284
14	814.5	50.7	223269	2	AC120636
15	814.5	50.7	250318	2	AC109983
16	453	28.2	6789	9	HSDDT1
17	452.5	28.1	3384	6	AX714308
18	452.5	28.1	3384	9	AK056544
19	450.5	28.0	4956	6	AF041082
20	448	27.9	6922	10	NM017793
21	446.5	27.8	4956	9	BD085989
22	446.5	27.6	4956	9	AF040990
23	444.5	27.6	991	5	AF364047
24	432	26.9	6435	5	AF461119
25	425.5	26.5	4871	5	AF337035
26	414.5	25.8	5259	10	AF060570
27	407	25.3	1565	5	AF364048
28	406	25.2	5067	5	AF304131
29	405	25.2	4188	6	BD085986
30	405	25.2	5384	5	AF337036
31	405	25.2	6440	3	AF040989
32	404.5	25.2	5598	9	AB046788
33	404.5	25.2	6215	6	AX556709
34	400.5	24.9	6860	5	AF304130
35	397.5	24.7	4306	6	AF312580
36	396.5	24.7	6445	6	AX556703
37	360	22.4	3822	3	AF041053
38	358	22.3	5381	3	AF312579
39	356.5	22.2	3894	6	BD085988
40	354	22.0	3650	10	AF182037
41	348.5	21.7	1129	5	AF337034
42	345	21.5	4146	6	BD085987
43	299.5	18.6	186971	9	AP003501
44	297.5	18.5	16652	2	AC014298
45	297.5	16.5	169534	3	AC008350

RESULT 1

ALIGNMENTS

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Best Local Similarity 98.8%; Pred. No. 4.1e-101;
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Db 1 MGNMAQSDPPQILVHPQDLFQGGPARMSCRAGQPPPTIRWLINGQLSNVPPDPHHL 60
Qy 83 LPDGTLLLLQPPARGHADGOALSTDIGVYTCEASNRILGTAVSRGARSUAVLRDFOIQ 142
Db 61 LPDGTLLLLQPPARGHADGOALSTDIGVYTCEASNRILGTAVSRGARSUAVLRDFOIQ 120
Qy 143 PRDMVAVVGEQFTLECGPPWGHPEPTVSWKDGKPLALQPGRHTVSGGSLLMARAEKSDE 202
Db 121 PRDMVAVVGEQFTLECGPPWGHPEPTVSWKDGKPLALQPGRHTVSGGSLLMARAEKSDE 180
Qy 203 XYTCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLLNPDPAEGPKPRP 262
Db 181 GTYTCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLLNPDPAEGPKPRP 240
Qy 263 AVLXKXKVSQP 273
Db 241 AVLXKXKVSQP 251

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Job time : 31.8756 secs

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Query Match 83.1%; Score 1337; DB 11; Length 985;

Best Local Similarity 98.8%; Pred. No. 4.1e-101; Indels 0; Gaps 0; Matches 248; Conservative 1; Mismatches 2;

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 Qy 83 LPDGTLLLLQPPARGHAHDGQALSTDLGVYTCESNRLGTAVSRGARSVAVLREDFOIQ 142
 Db 61 LPDGTLLLLQPPARGHAHDGQALSTDLGVYTCESNRLGTAVSRGARSVAVLREDFOIQ 120
 Qy 143 PRDMVAVVGEFTLECGPWGHPPTVSWKDGKPLALQPGHRTVSGSLMAREKSDE 202
 Db 121 PRDMVAVVGEFTLECGPWGHPPTVSWKDGKPLALQPGHRTVSGSLMAREKSDE 180
 Qy 203 XYTCVATNSAGHRESRAARVSIQEPDYTFEVELLAVRIQLENVTLNPPDPAEGKFRP 262
 Db 181 XYTCVATNSAGHRESRAARVSIQEPDYTFEVELLAVRIQLENVTLNPPDPAEGKFRP 240
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 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
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 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James;
 ; APPLICANT: Paoni, Nicholas P.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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; PRIOR APPLICATION NUMBER: 60/084627
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323

; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 83.1%; Score 1337; DB 11; Length 985;
Best Local Similarity 98.8%; Pred. No. 4.1e-101;
Matches 248; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 23 MGGWAQDSPPQILVHPQDQLFQGGPARMSCRAGQPPPTIRWLLNGQPLSMVPPDPHLL 82
Db 1 MGGWAQDSPPQILVHPQDQLFQGGPARMSCRAGQPPPTIRWLLNGQPLSMVPPDPHLL 60

Qy 83 LPDGTLLLLQPPARGHAHDQALSTDLGVYTCEASNRGLGTAVSRGARLSVAVLREDFQIQ 142
Db 61 LPDGTLLLLQPPARGHAHDQALSTDLGVYTCEASNRGLGTAVSRGARLSVAVLREDFQIQ 120

Qy 143 PRDMVAVVGEQFTLECGPPWGHPEPTVSMWKDGKPLALQPGRHVTVSGSLLMARAEKSDE 202
Db 121 PRDMVAVVGEQFTLECGPPWGHPEPTVSMWKDGKPLALQPGRHVTVSGSLLMARAEKSDE 180

Qy 203 XYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLNPPDPAEGPKPRP 262
Db 181 GTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLNPPDPAEGPKPRP 240

Qy 263 AVMLXWKVSGP 273
Db 241 AVMLXWKVSGP 251

RESULT 14
US-09-999-833A-211
; Sequence 211, Application US/09999833A
; Publication No. US20030054405A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerbet, Hanspeter
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey

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RESULT 13
US-09-978-564A-211
: Sequence 211, Application US/09978564A
: Publication No. US20030050241A1
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Baker, Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleon
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth J
: APPLICANT: Klujavin, Ivar J.
: APPLICANT: Kuo, Sophia S.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Shelton, David L.
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: Secrated and Trans
: TITLE OF INVENTION: Acids Encoding th
: FILE REFERENCE: P2630PLC25
: CURRENT APPLICATION NUMBER: US/09/978
: CURRENT FILING DATE: 2001-10-16
: PRIOR APPLICATION NUMBER: 09/918585
: PRIOR FILING DATE: 2001-07-30
: PRIOR APPLICATION NUMBER: 60/062250

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1	PRIOR FILING DATE: 1998-04-15
2	PRIOR APPLICATION NUMBER: 60/082568
3	PRIOR FILING DATE: 1998-04-21
4	PRIOR APPLICATION NUMBER: 60/082569
5	PRIOR FILING DATE: 1998-04-21
6	PRIOR APPLICATION NUMBER: 60/082704
7	PRIOR FILING DATE: 1998-04-22
8	PRIOR APPLICATION NUMBER: 60/082804
9	PRIOR FILING DATE: 1998-04-22
10	PRIOR APPLICATION NUMBER: 60/082700
11	PRIOR FILING DATE: 1998-04-22
12	PRIOR APPLICATION NUMBER: 60/082797
13	PRIOR FILING DATE: 1998-04-22
14	PRIOR APPLICATION NUMBER: 60/082796
15	PRIOR FILING DATE: 1998-04-23
16	PRIOR APPLICATION NUMBER: 60/083336
17	PRIOR FILING DATE: 1998-04-27
18	PRIOR APPLICATION NUMBER: 60/083322
19	PRIOR FILING DATE: 1998-04-28
20	PRIOR APPLICATION NUMBER: 60/083392
21	PRIOR FILING DATE: 1998-04-29
22	PRIOR APPLICATION NUMBER: 60/083495
23	PRIOR FILING DATE: 1998-04-29
24	PRIOR APPLICATION NUMBER: 60/083496
25	PRIOR FILING DATE: 1998-04-29
26	PRIOR APPLICATION NUMBER: 60/083499
27	PRIOR FILING DATE: 1998-04-29
28	PRIOR APPLICATION NUMBER: 60/083545
29	PRIOR FILING DATE: 1998-04-29
30	PRIOR APPLICATION NUMBER: 60/083554
31	PRIOR FILING DATE: 1998-04-29
32	PRIOR APPLICATION NUMBER: 60/083558
33	PRIOR FILING DATE: 1998-04-29
34	PRIOR APPLICATION NUMBER: 60/083559
35	PRIOR FILING DATE: 1998-04-29
36	PRIOR APPLICATION NUMBER: 60/083500
37	PRIOR FILING DATE: 1998-04-29
38	PRIOR APPLICATION NUMBER: 60/083742
39	PRIOR FILING DATE: 1998-04-30
40	PRIOR APPLICATION NUMBER: 60/084366
41	PRIOR FILING DATE: 1998-05-05
42	PRIOR APPLICATION NUMBER: 60/084414
43	PRIOR FILING DATE: 1998-05-06
44	PRIOR APPLICATION NUMBER: 60/084441
45	PRIOR FILING DATE: 1998-05-06
46	PRIOR APPLICATION NUMBER: 60/084637
47	PRIOR FILING DATE: 1998-05-07
48	PRIOR APPLICATION NUMBER: 60/084639
49	PRIOR FILING DATE: 1998-05-07
50	PRIOR APPLICATION NUMBER: 60/084640
51	PRIOR FILING DATE: 1998-05-07
52	PRIOR APPLICATION NUMBER: 60/084598
53	PRIOR FILING DATE: 1998-05-07
54	PRIOR APPLICATION NUMBER: 60/084600
55	PRIOR FILING DATE: 1998-05-07
56	PRIOR APPLICATION NUMBER: 60/084627
57	PRIOR FILING DATE: 1998-05-07
58	PRIOR APPLICATION NUMBER: 60/084643
59	PRIOR FILING DATE: 1998-05-07
60	PRIOR APPLICATION NUMBER: 60/085339
61	PRIOR FILING DATE: 1998-05-13
62	PRIOR APPLICATION NUMBER: 60/085338
63	PRIOR FILING DATE: 1998-05-13
64	PRIOR APPLICATION NUMBER: 60/085323
65	PRIOR FILING DATE: 1998-05-13
66	PRIOR APPLICATION NUMBER: 60/085582
67	PRIOR FILING DATE: 1998-05-15
68	PRIOR APPLICATION NUMBER: 60/085700
69	PRIOR FILING DATE: 1998-05-15
70	PRIOR APPLICATION NUMBER: 60/085689
71	PRIOR FILING DATE: 1998-05-15
72	PRIOR APPLICATION NUMBER: 60/085579
73	PRIOR FILING DATE: 1998-05-15

;; PRIOR APPLICATION NUMBER: 60/082700
;; PRIOR FILING DATE: 1998-04-22
;; PRIOR APPLICATION NUMBER: 60/082797
;; PRIOR FILING DATE: 1998-04-22
;; PRIOR APPLICATION NUMBER: 60/082796
;; PRIOR FILING DATE: 1998-04-23
;; PRIOR APPLICATION NUMBER: 60/083336
;; PRIOR FILING DATE: 1998-04-27
;; PRIOR APPLICATION NUMBER: 60/083322
;; PRIOR FILING DATE: 1998-04-28
;; PRIOR APPLICATION NUMBER: 60/083392
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083495
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083496
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;; PRIOR APPLICATION NUMBER: 60/083499
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083545
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083554
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083558
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083559
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;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083742
;; PRIOR FILING DATE: 1998-04-30
;; PRIOR APPLICATION NUMBER: 60/084366
;; PRIOR FILING DATE: 1998-05-05
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;; PRIOR APPLICATION NUMBER: 60/084441
;; PRIOR FILING DATE: 1998-05-06
;; PRIOR APPLICATION NUMBER: 60/084637
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084639
;; PRIOR FILING DATE: 1998-05-07
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;; PRIOR FILING DATE: 1998-05-07
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;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084643
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/085339
;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085338
;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085323
;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085582
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085700
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085689
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085579
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085580
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 83.1%; Score 1337; DB 11; Length 985;

Best Local Similarity 98.8%; Pred. No. 4.1e-101;
Matches 248; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 23 MCGMAQDSPPQILVHPDQOLFQGGCPARMSCRASQGPPTIRWLNGQPLSMVPPDPHHL 82
DB 1 MCGMAQDSPPQILVHPDQOLFQGGCPARMSCOASQGPPTIRWLNGQPLSMVPPDPHHL 60
QY 83 LPDGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLRDFOIQ 142
DB 61 LPDGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLRDFOIQ 120
QY 143 PRDMVAVVGEQFTLECGPPWGHPEPTVSWKDGKPLALQPGRHTVSGSLLMARAEKSD 202
DB 121 PRDMVAVVGEQFTLECGPPWGHPEPTVSWKDGKPLALQPGRHTVSGSLLMARAEKSD 180
QY 203 XYTCVATNSAGHRESRAARVSIQEPDQYTFEVELLAVRIQLENTVLNPDPAEGKPRP 262
DB 181 GTYMCVATNSAGHRESRAARVSIQEPDQYTFEVELLAVRIQLENTVLNPDPAEGKPRP 240
QY 263 AVLXKWKVSGP 273
DB 241 AVLXKWKVSGP 251

RESULT 12

US-09-978-403A-211

; Sequence 211, Application US/09978403A

; Publication No. US20030050240A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James;

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C17

; CURRENT APPLICATION NUMBER: US/09/978,403A

; CURRENT FILING DATE: 2002-03-19

; PRIOR APPLICATION NUMBER: 09/918585

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/064249

; PRIOR FILING DATE: 1997-11-03

; PRIOR APPLICATION NUMBER: 60/065311

; PRIOR FILING DATE: 1997-11-13

; PRIOR APPLICATION NUMBER: 60/066364

; PRIOR FILING DATE: 1997-11-21

; PRIOR APPLICATION NUMBER: 60/077450

; PRIOR FILING DATE: 1998-03-10

Db 61 LPDGTLLLOPPARGHAHDGQALSTDLGVYTCASNRLGTAVSRGARLSVAVLREDFQIQ 120
QY 143 PRDVAVGEFTLECGPWGHPPTVSWKDGKPLALQPGRHVTVSGSLIMARAESKDE 202
Db 121 PRDVAVGEFTLECGPWGHPPTVSWKDGKPLALQPGRHVTVSGSLIMARAESKDE 180
QY 203 XYTCVATNSAGHRESRAARVSIQBPQDYTPBVVELLAVRIQLENVTLINPDPAEGPKPRP 262
Db 181 GTYMCVATNSAGHRESRAARVSIQBPQDYTPBVVELLAVRIQLENVTLINPDPAEGPKPRP 240
QY 263 AVLWKKVSGP 273
Db 241 AVLWSKVSGP 251

RESULT 11
US-09-978-191A-211
; Sequence 211, Application US/09978191A
; Publication No. US20030050239A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary B.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavir, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tunes, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC4
; CURRENT APPLICATION NUMBER: US/09/978,191A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
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; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
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; PRIOR APPLICATION NUMBER: 60/078004

; PRIOR FILING DATE: 1998-03-13
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; PRIOR APPLICATION NUMBER: 60/078910
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; PRIOR FILING DATE: 1998-04-15
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; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082569
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22

QY 23 MCGMAQDSPPQILVHPDQLFQGGPARMSCRASQPPPTIRWLLNGQPLSNVPPDPHLL 82
DB 1 MCGMAQDSPPQILVHPDQLFQGGPARMSCRASQPPPTIRWLLNGQPLSNVPPDPHLL 60
QY 83 LPDGTLILLQPPARGHAGDQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLRDFOIQ 142
DB 61 LPDGTLILLQPPARGHAGDQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLRDFOIQ 120
QY 143 PRDMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSD 202
DB 121 PRDMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSD 180
QY 203 XTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENTVLLNPDPAEGPKPRP 262
DB 181 GTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENTVLLNPDPAEGPKPRP 240
QY 263 AVWLXWKVSGP 273
DB 241 AVWLXWKVSGP 251

RESULT 9

US-09-978-608A-211

; Sequence 211, Application US/09978608A

; Publication No. US20030045462A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnovers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Kijavin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James;

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2630PIC22

; CURRENT FILING DATE: 2001-10-16

; NUMBER OF SEQ ID NOS: 624

; Prior Application removed - See File Wrapper or Palm

; SEQ ID NO 211

; LENGTH: 985

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-978-608A-211

Query Match 83.1%; Score 1337; DB 11; Length 985;

Best Local Similarity 98.8%; Pred. No. 4.1e-101;

Matches 248; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 23 MCGMAQDSPPQILVHPDQLFQGGPARMSCRASQPPPTIRWLLNGQPLSNVPPDPHLL 82

DB 1 MCGMAQDSPPQILVHPDQLFQGGPARMSCRASQPPPTIRWLLNGQPLSNVPPDPHLL 60

QY 23 MCGMAQDSPPQILVHPDQLFQGGPARMSCRASQPPPTIRWLLNGQPLSNVPPDPHLL 82
DB 1 MCGMAQDSPPQILVHPDQLFQGGPARMSCRASQPPPTIRWLLNGQPLSNVPPDPHLL 60
QY 83 LPDGTLILLQPPARGHAGDQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLRDFOIQ 142
DB 61 LPDGTLILLQPPARGHAGDQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLRDFOIQ 120
QY 143 PRDMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSD 202
DB 121 PRDMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSD 180
QY 203 XTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENTVLLNPDPAEGPKPRP 262
DB 181 GTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENTVLLNPDPAEGPKPRP 240
QY 263 AVWLXWKVSGP 273
DB 241 AVWLXWKVSGP 251

QY 83 LPDGTLILLQPPARGHAGDQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLRDFOIQ 142
DB 61 LPDGTLILLQPPARGHAGDQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLRDFOIQ 120
QY 143 PRDMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSD 202
DB 121 PRDMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSD 180
QY 203 XTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENTVLLNPDPAEGPKPRP 262
DB 181 GTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENTVLLNPDPAEGPKPRP 240
QY 263 AVWLXWKVSGP 273
DB 241 AVWLXWKVSGP 251

RESULT 10
US-09-978-585A-211
; Sequence 211, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 211
; LENGTH: 985
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-585A-211

Query Match 83.1%; Score 1337; DB 11; Length 985;
Best Local Similarity 98.8%; Pred. No. 4.1e-101;
Matches 248; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 23 MCGMAQDSPPQILVHPDQLFQGGPARMSCRASQPPPTIRWLLNGQPLSNVPPDPHLL 82
DB 1 MCGMAQDSPPQILVHPDQLFQGGPARMSCRASQPPPTIRWLLNGQPLSNVPPDPHLL 60
QY 83 LPDGTLILLQPPARGHAGDQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLRDFOIQ 142

; PRIOR APPLICATION NUMBER: 60/078936
 ; PRIOR FILING DATE: 1998-03-20
 ; PRIOR APPLICATION NUMBER: 60/078910
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 ; PRIOR APPLICATION NUMBER: 60/085704
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 83.1%; Score 1337;; DB 11; Length 985;
 Best Local Similarity 98.8%; Pred. No. 4.1e-101;
 Matches: 248; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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;; PRIOR APPLICATION NUMBER: 60/085573
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;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 83.1%; Score 1337; DB 10; Length 985;
Best Local Similarity 98.8%; Pred. No. 4, 1e-101;
Matches 248; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 23 MCGMAQDSPPQILVHPQDLFGQPGARMSCRASQPPPTIRWLNGQPLNSVPPDPHLL 82
Db 1 MCGMAQDSPPQILVHPQDLFGQPGARMSQASQPPPTIRWLNGQPLNSVPPDPHLL 60
QY 83 LPDGTLLILLOPPARGHNDGQALSTDLGYTCEASNRGLTAVSRGRLSVAVLRDFFQIQ 142
Db 61 LPDGTLLILLOPPARGHNDGQALSTDLGYTCEASNRGLTAVSRGRLSVAVLRDFFQIQ 120
QY 143 PRDMVAVVGEQFTLECGPPWGHPEPTVSWWKGKPLALQPGRHTVSGGSLLMARAEKSD 202

Db 121 PRDMVAVVGEQFTLECGPPWGHPEPTVSWWKGKPLALQPGRHTVSGGSLLMARAEKSD 180
QY 203 XYTNCVATNSAGHRESRAARVSIQEPQDYTPVELLAVRIQLENTVLNPDPAEGKPRP 262
Db 181 GTYNCVATNSAGHRESRAARVSIQEPQDYTPVELLAVRIQLENTVLNPDPAEGKPRP 240
QY 263 AVLWKXKVS GP 273
Db 241 AVLWSKVS GP 251

RESULT 8

US-09-978-189-211
; Sequence 211, Application US/09978189
; Publication No. US20030004102A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deanoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C7
; CURRENT APPLICATION NUMBER: US/09/978,189
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20

Db 241 AVLWSWKVSGP 251

RESULT 7

US-09-999-032A-211

; Sequence 211, Application US/09999832A

; Publication No. US20020192706A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2630P1C63

; CURRENT APPLICATION NUMBER: US/09/999,832A

; CURRENT FILING DATE: 2001-10-24

; PRIOR APPLICATION NUMBER: 09/918585

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/064249

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72	PRIOR FILING DATE: 1998-04-29
73	PRIOR APPLICATION NUMBER: 60/083554

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PRIOR FILING DATE: 1998-05-15	PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15	PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15	PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15	PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15	PRIOR APPLICATION NUMBER: 60/085697

Query Match 83.1%; Score 1337; DB 10; Length 985;

Query Match 93.1%; Score 1337; BB 10;
Best Local Similarity 98.8%; Pred. No. 4.1e-101;

Best local similarity 30.00, Rec. no. 413 101
Matches 248; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Qy	83	LPDGTLLLLQPPARGAHHDGQALSTDLGVVYTCASNRLGTAVSRGARLSVAVLREDFQIQ	14
Db	61	LPDGTLLLLQPPARGAHHDGQALSTDLGVVYTCASNRLGTAVSRGARLSVAVLREDFQIQ	12
Qy	143	PRDMVAVVGEQFTLECGPPWGHBPPTYSWWKDGKPLALQPGRHVTVSGSLLMARAEKSD	20
Db	121	PRDMVAVVGEQFTLECGPPWGHBPPTYSWWKDGKPLALQPGRHVTVSGSLLMARAEKSD	18
Qy	203	XYTMCVATNSAGHRESRAARVSIOEPDYTPVELLAVRIQLENVTVLLNPPDPAEGPKPRP	26
Db	181	GYTMCVATNSAGHRESRAARVSIOEPDYTPVELLAVRIQLENVTVLLNPPDPAEGPKPRP	24
Qy	263	AVWLXWKVSGP	273

; PRIOR APPLICATION NUMBER: 60/084366
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; PRIOR APPLICATION NUMBER: 60/084414
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; PRIOR APPLICATION NUMBER: 60/084627
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; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
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; PRIOR FILING DATE: 1998-05-15
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 83.1%; Score 1337; DB 10; Length 985;

Best Local Similarity 98.8%; Pred. No. 4.1e-101;

Matches 248; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 23 MGGAAQSPPOILVHPQDQLFGGPGPARMSCRAGSQPPPTIRWLLNGOPLSMVPPDPHLL 82
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1 MGGAAQSPPOILVHPQDQLFGGPGPARMSCRAGSQPPPTIRWLLNGOPLSMVPPDPHLL 60

Qy 83 LPDGTLLLLQPPARGHAHDGQALSTDGLGVYTCEASNRGLGTAVSRGARLSVAVLREDFOIQ 142
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
61 LPDGTLLLLQPPARGHAHDGQALSTDGLGVYTCEASNRGLGTAVSRGARLSVAVLREDFOIQ 120

Qy 143 PRDVAVVGEOFTLECGPWGHPBPTVSWKDGKPLALQPGRHTVSGSLMARAESKDE 202
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
121 PRDVAVVGEOFTLECGPWGHPBPTVSWKDGKPLALQPGRHTVSGSLMARAESKDE 180

Qy 203 XYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENNVTLLNPPASGPKPRP 262
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
181 GTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENNVTLLNPPASGPKPRP 240

Qy 263 AVLXKWKVSGP 273
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
241 AVLXKWKVSGP 251

RESULT 6

US-09-978-192A-211
; Sequence 211, Application US/09978192A
; Patent No. US2002017553A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deanoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: KJavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C9
; CURRENT APPLICATION NUMBER: US/09/978,192A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
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; PRIOR FILING DATE: 1998-03-27

APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kluvin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC27
CURRENT APPLICATION NUMBER: US/09/978,697
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
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	/	PRIOR APPLICATION NUMBER:	60/085704		
	/	PRIOR FILING DATE:	1998-05-15		
	/	PRIOR APPLICATION NUMBER:	60/085697		
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	/	Best Local Similarity	98.8%; Pred.		
	/	Matches	248; Conservative	1;	Mi
Qy		23	MGMAQDSPQTILVHPDQLFQGPGI		
Db		1	MGMAQDSPQTILVHPDQLFQGPGI		
Qy		83	LPDGTLLLLQPARGHAHQALSTI		
Db		61	LPDGTLLLLQPARGHAHQALSTI		
Qy		143	PRDMVAVGEOFTLECGPWNHGPPEP		
Db		121	PRDMVAVGEOFTLECGPWNHGPPEP		
Qy		203	XTYMVCATNSAGHRESRAARVSIOE		
Db		181	GTYMVCATNSAGHRESRAARVSIOE		
Qy		263	AVWLXKVVSGP	273	
Db		241	AVWLSKWVSGP	251	

RESULT 5
US-09-978-697-211
Sequence 211, Application US/09978697
Patent No. US20020169284A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Pilvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter

;; TITLE OF INVENTION: KINASE/PROTEIN PHOSPHATASE
;; FILE REFERENCE: 06501-098001
;; CURRENT APPLICATION NUMBER: US/10/059,585
;; CURRENT FILING DATE: 2002-01-29
;; PRIOR APPLICATION NUMBER: PCT/JP00/05060
;; PRIOR FILING DATE: 2000-07-28
;; PRIOR APPLICATION NUMBER: US 60/183,322
;; PRIOR FILING DATE: 2000-02-17
;; PRIOR APPLICATION NUMBER: US 60/159,590
;; PRIOR FILING DATE: 1999-10-18
;; PRIOR APPLICATION NUMBER: JP 2000-118776
;; PRIOR FILING DATE: 2000-01-11
;; PRIOR APPLICATION NUMBER: JP 2000-183767
;; PRIOR FILING DATE: 2000-05-02
;; PRIOR APPLICATION NUMBER: JP 11-248036
;; PRIOR FILING DATE: 1999-07-29
;; NUMBER OF SEQ ID NOS: 64
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 22
;; LENGTH: 792
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-059-585-22

Query Match 89.3%; Score 1436; DB 15; Length 792;
Best Local Similarity 98.5%; Pred. No. 2.4e-109;
Matches 269; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY	1	MSGGDSLLGGGSLPLILLIMGMAQDSPQILVHPQDLFQGGPARMSCRASCQPPP	60
Db	1	MSGGDSLLGGGSLPLILLIMGMAQDSPQILVHPQDLFQGGPARMSCQASGQPP	60
QY	61	PTIRLLNGQPLSMVPPDPHLLPDGTLILLQPPARGHAHDGQALSTDGLVYTCEASNRL	120
Db	61	PTIRLLNGQPLSMVPPDPHLLPDGTLILLQPPARGHAHDGQALSTDGLVYTCEASNRL	120
QY	121	GTAVERGARLSVAVLREDFQIQPRDMVAVGEGFTLEGCPWGHPEPTVSWKDKPLAL	180
Db	121	GTAVERGARLSVAVLREDFQIQPRDMVAVGEGFTLEGCPWGHPEPTVSWKDKPLAL	180
QY	181	QPRHTVSGGSLLMARAEKSEXTVMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAV	240
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QY	241	RIQENVTLNPDPAEGPKPRPAVWLXWKVSGP	273
Db	241	RIQENVTLNPDPAEGPKPRPAVWLXWKVSGP	273

RESULT 4

US-09-978-295A-211
; Sequence 211, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary B.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.

;; APPLICANT: Pan, James;
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Shelton, David L.
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2630PIC11
;; CURRENT APPLICATION NUMBER: US/09/978,295A
;; CURRENT FILING DATE: 2001-10-15
;; PRIOR APPLICATION NUMBER: 09/918585
;; PRIOR FILING DATE: 2001-07-30
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/064249
;; PRIOR FILING DATE: 1997-11-03
;; PRIOR APPLICATION NUMBER: 60/065311
;; PRIOR FILING DATE: 1997-11-13
;; PRIOR APPLICATION NUMBER: 60/066364
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;; PRIOR FILING DATE: 1998-03-31
;; PRIOR APPLICATION NUMBER: 60/080327
;; PRIOR FILING DATE: 1998-04-01
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;; PRIOR FILING DATE: 1998-04-01

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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (203)
; OTHER INFORMATION: Xaa equals any amino acid
; NAME/KEY: SITE
; LOCATION: (267)
; OTHER INFORMATION: Xaa equals any amino acid
; NAME/KEY: SITE
; LOCATION: (274)
; OTHER INFORMATION: Xaa equals any amino acid
US-10-047-021-86

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Best Local Similarity 100.0%; Pred. No. 1.8e-123;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MSGGDSLLGGRGSLPLLLLLIMGMAQDSPPQILVHPDQLFQGGPARMSCRASGQPP 60

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Qy 181 QPGRHTVSGSLLMARAESKDEXTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAV 240
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Qy 241 RIQENVTLNPDPAEGPKPRPAVWLXWKVSGPXLPLNLTTPCSGPRLPREARELGRQR 300
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Qy 301 NTG 303
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RESULT 2
US-10-411-224-86
; Sequence 86, Application US/10411224
; Publication No. US20030166906A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 50 Human Secreted Proteins
; FILE REFERENCE: PZ016P1
; CURRENT APPLICATION NUMBER: US/10/411,224
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: US/09/722,329
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/262,109
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: 60/057,626
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/057,663
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/057,669
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/058,667
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/058,974
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/058,973
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/058,666
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/090,112
; PRIOR FILING DATE: 1998-06-22

; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 86
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (203)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (267)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (274)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (304)
; OTHER INFORMATION: Xaa equals stop translation
US-10-411-224-86

Query Match          99.6%; Score 1602; DB 12; Length 304;
Best Local Similarity 100.0%; Pred. No. 1.8e-123;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSGGDSLLGGRGSLPLLLLLIMGMAQDSPPQILVHPDQLFQGGPARMSCRASGQPP 60
Db 1 MSGGDSLLGGRGSLPLLLLLIMGMAQDSPPQILVHPDQLFQGGPARMSCRASGQPP 60

Qy 61 PTTIRLLNGQPLSMVPPDPHLLPDGTLTLLQPPARGHAHQALSTDLGVYTCEASNRL 120
Db 61 PTTIRLLNGQPLSMVPPDPHLLPDGTLTLLQPPARGHAHQALSTDLGVYTCEASNRL 120

Qy 121 GTAVSRGARLSVAVLREDFOIQRDMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLAL 180
Db 121 GTAVSRGARLSVAVLREDFOIQRDMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLAL 180

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Db 181 QPGRHTVSGSLLMARAESKDEXTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAV 240

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Db 241 RIQENVTLNPDPAEGPKPRPAVWLXWKVSGPXLPLNLTTPCSGPRLPREARELGRQR 300

Qy 301 NTG 303
Db 301 NTG 303

RESULT 3
US-10-059-585-22
; Sequence 22, Application US/10059585
; Publication No. US20030082776A1
; GENERAL INFORMATION:
; APPLICANT: Ota, Toshio
; APPLICANT: Isogai, Takao
; APPLICANT: Nishikawa, Tetsuo
; APPLICANT: Hayaashi, Koji
; APPLICANT: Otsuka, Kaoru
; APPLICANT: Yamamoto, Jun-ichi
; APPLICANT: Ishii, Shizuko
; APPLICANT: Sugiyama, Tomoyasu
; APPLICANT: Wakamatsu, Ai
; APPLICANT: Nagai, Keiichi
; APPLICANT: Otsuki, Tetsuji
; APPLICANT: Funahashi, Shin-Ichi
; APPLICANT: Senoo, Chiaki
; APPLICANT: Nezu, Jun-Ichi
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 30, 2004, 15:54:49 ; Search time 30.8756 Seconds
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Title: US-10-047-021-86
Perfect score: 1608
Sequence: 1 MGSQDLSLLGSGSLPLLLL.....SGPLPREARELQRRNTG 303

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Gapop 10.0 , Gapext 0.5

Searched: 789580 seqs, 207824079 residues

Total number of hits satisfying chosen parameters: 789580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
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- 3: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB.pep.*
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- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1602	99.6	304	12	Sequence 86, Appl
3	1436	89.3	792	15	US-10-411-224-86
4	1337	83.1	985	10	US-10-059-585-22
5	1337	83.1	985	10	US-09-978-295A-211
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8	1337	83.1	985	11	US-09-999-832A-211
9	1337	83.1	985	11	US-09-978-189-211
10	1337	83.1	985	11	US-09-978-608A-211
11	1337	83.1	985	11	US-09-978-585A-211
12	1337	83.1	985	11	US-09-978-403A-211
13	1337	83.1	985	11	US-09-978-564A-211
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16	1337	83.1	985	11	US-09-978-824-211	Sequence 211, App
17	1337	83.1	985	11	US-09-918-585A-211	Sequence 211, App
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19	1337	83.1	985	11	US-09-978-193A-211	Sequence 211, App
20	1337	83.1	985	11	US-09-999-830A-211	Sequence 211, App
21	1337	83.1	985	11	US-09-978-757A-211	Sequence 211, App
22	1337	83.1	985	11	US-09-978-187B-211	Sequence 211, App
23	1337	83.1	985	11	US-09-978-643A-211	Sequence 211, App
24	1337	83.1	985	12	US-09-978-375A-211	Sequence 211, App
25	1337	83.1	985	12	US-09-978-188A-211	Sequence 211, App
26	1337	83.1	985	12	US-09-978-298A-211	Sequence 211, App
27	1337	83.1	985	12	US-10-143-031A-211	Sequence 211, App
28	1337	83.1	985	12	US-10-002-967A-211	Sequence 211, App
29	1337	83.1	985	12	US-10-017-083A-211	Sequence 211, App
30	1337	83.1	985	12	US-10-143-030A-211	Sequence 211, App
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36	1337	83.1	985	12	US-10-013-926A-211	Sequence 211, App
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39	1337	83.1	985	12	US-10-165-067A-211	Sequence 211, App
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44	1337	83.1	985	12	US-09-978-681A-211	Sequence 211, App
45	1337	83.1	985	12	US-09-999-829A-211	Sequence 211, App

ALIGNMENTS

RESULT 1
US-10-047-021-86
; Sequence 86, Application US/10047021
; Publication No. US20040002591A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 50 Human Secreted Proteins
; FILE REFERENCE: P2016P2
; CURRENT APPLICATION NUMBER: US/10/047,021
; CURRENT FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: US 60/262,066
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 09/722,329
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/262,109
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: PCT/US98/18360
; PRIOR FILING DATE: 1998-09-03
; PRIOR APPLICATION NUMBER: US 60/057,626
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/057,663
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/057,669
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/058,667
; PRIOR FILING DATE: 1997-09-12
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; PRIOR APPLICATION NUMBER: US 60/058,973
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: US 60/058,666
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: US 60/090,112
; PRIOR FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 86
; LENGTH: 303

SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-707-802-12

Query Match 14.4%; Score 232; DB 4; Length 607;
Best Local Similarity 28.7%; Pred. No. 1.6e-14;
Matches 84; Conservative 41; Mismatches 108; Indels 60; Gaps 14;

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QY	123	AVSRGARLSVAVLRDFQIQPRDMV-AVVGQFTLECGPPMGHPPTVSWWKGKPLAL-	180
DB	120	VVSREAILRFGFLOE-FSKERDPYKAHEGWGVMPCNPPAHYFGLSYRWLLNEFPNFI	178
QY	181	QPGRHTVS--GGSLIMARAEEKSDEXTVMCVATNSAGHRE-----SRAARVSIQ----	226
DB	179	TDGRHFVSQTTGNLYIARTNASDLGNYSCLATS---HMDFTKSVFSKFAQLNLAEDTR	235
QY	227	-----EPQDYTEPVVELLAVRIQLENVTLLNPDPAEGPKPRPAVWLXW-KVSG	272
DB	236	LPAPSIKARFPAETVALVGQVTLCECFAGFNPVPR-----IKWRKVDG	278

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Job time : 16.1762 secs

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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1501 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-716-679-3

Query Match 14.8%; Score 237.5; DB 2; Length 1501;
Best Local Similarity 30.9%; Pred. No. 1.6e-14;
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DB 74 NSQRFETIDFDE---SSGAVLRIQP-----LRTPRDENVYECVAQNSVG-EIT 117
QY 126 RGRALSUAVLRDFQIQPRDMVAVVGEQF-----TLGCGPPWGHPEPTVSWKDGK 176
DB 118 VHAKLT--VLRED-QLPFCFFNIDGPOLKVVERTRTATMLCAAS-GNPDPEITWFKDFL 173
QY 177 PL--ALQPCR-HTVSGSLLMARAESDXTYMCVATNSAGHRESRAARVSIQ 226
DB 174 VPDPSASNGRIKQLRSGALQIESSETDQGYECVATNSAGVRYSSPANLYVR 226

RESULT 14
US-08-752-307B-12
Sequence 12, Application US/08752307B
Patent No. 5952171
GENERAL INFORMATION:
APPLICANT: McCarthy, Sean A.
APPLICANT: Gearing, David P.
APPLICANT: Levinson, Douglas A.
TITLE OF INVENTION: METHOD FOR IDENTIFYING GENES
ENCODING NOVEL SECRETED OR MEMBRANE-ASSOCIATED PROTEIN
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752.307B
FILING DATE: 19-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 09404/020001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 607 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-752-307B-12
Query Match 14.4%; Score 232; DB 2; Length 607;
Best Local Similarity 28.7%; Pred. No. 1.6e-14;
Matches 84; Conservative 41; Mismatches 108; Indels 60; Gaps 14;
QY 3 SGDSLILGSGSLPLLLLLLMGMAQDPPQILVHPDQLFQPGPARMSCRASQPPPT 62
DB 23 SAMSALGSQTT-----FGPVFEDQPLSVL-FPEESTEE---QVLLACRARASPAT 70
QY 63 IRWLLNGQPLSMVPPDPHLLPDGTLQLLPARGHAHDGQALSTDLGVYTCASNRLGT 122
DB 71 YRWKNGTGMKLEFGSRHQLV-GGNLVIMNF-----TKAQDAGVYQCLASNPVGT 119
QY 123 AVSGARLSUAVLRDFQIQPRDMV-AVVGQFTLECGPPWGHPEPTVSWKDGKPLAL- 180
DB 120 VVSREAILRFGLQE-FSKEERDPVKAHEGVMGLPCNPPAHYPGLSYRWLLNEFPNIP 178
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QY 227 -----BPQDYTEPVELLAVRIQLENTVTLNPDPAEGPKPRPAVWLXW-KVSG 272
DB 236 LFAPSIKARPAETVALVGQQTLECFAGNPVR-----IKWRKVDG 278

RESULT 15
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Sequence 12, Application US/09707802
Patent No. 6391586
GENERAL INFORMATION:
APPLICANT: McCarthy, Sean A.
APPLICANT: Gearing, David P.
APPLICANT: Levinson, Douglas A.
TITLE OF INVENTION: METHOD FOR IDENTIFYING GENES
ENCODING NOVEL SECRETED OR MEMBRANE-ASSOCIATED PROTEIN
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
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FILING DATE: 07-NO. 6391586-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/752.307
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 09404/020001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 607 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

PRIORITY APPLICATION DATA: US 08/122,032
 FILING DATE: 14-SEP-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: WALLEN, JOHN W III
 REGISTRATION NUMBER: 35403
 REFERENCE/DOCKET NUMBER: 18992
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 908-594-3905
 TELEFAX: 908-594-4720
 TELEX: 138825
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1911 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US94-10166-5

Query Match	15.3%	Score	246;	DB 5;	Length	1911;			
Best Local Similarity	30.9%;	Pred.	No. 3.2e-15;						
Matches	75;	Conservative	43;	Mismatches	85;	Indels	40;	Gaps	11;
QY	2	GS	GD	SLLGGRSLPLILLIMGMADSPFQLLVHPDQLFOCGPGPARMSCRASGQPPP	61				
Db	6	GPGMVS	VVGPMG--	--LLVLLVGGCAAEPRFIKEPKDI	IGVSGRVASFVCQTGDKP	62			
QY	62	TIRW----	LLNQPLSMVPDPHLLLPDGTLLLOPPARGHADGQAIST--	DLGVYTTC	114				
Db	63	RVTWNKKGKKVNQR	FETIEBDE-----SAGAVLRIQP-----	LRTPRDENVIYC	107				
QY	115	EASNRLGTAVSRGARLSVA	VLRED-----FQIQPRDMVA	VVGEFTLLECQPGPWGHE	166				
Db	108	VAQNSVG-EITVHA	KLT--VLREDQLPSGFPNIDMG	POLKVETRTRATVLMCAAS-GNPD	163				
QY	167	PTYSWWKDGKPL--ALQPGR-HTVSGS	LMLMARAKSDEXTVMCVATNSAGHRESRAARV	223					
Db	164	PEITWKDFUPVDPSAN	NGRIKQLRSALQIESSEEDTQGKYECVATNSAGVRYSSPANL	223					
QY	224	SIQ	226						
Db	224	YVR	226						

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RECORD 12
US-08-447-464-3
; Sequence 3, Application US/08447464
; Patent No. 5840842
; GENERAL INFORMATION:
; APPLICANT: Schlessinger, Joseph
; APPLICANT: Yan, Hai
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PROTEIN
; TITLE OF INVENTION: PHOSPHOTYROSINE PHOSPHATASE-SIGMA
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,464
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/130,570

```

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; FILING DATE: 01-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Miarock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7683-043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1501 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-447-464-3

Query Match          14.8%; Score 237.5; DB 2; Length 1501;
Best Local Similarity 30.9%; Pred.No.1.6e-14;
Matches 72; Conservative 40; Mismatches 82; Indels 39; Gaps 11;

QY      13  GSPLLLLLLLIMGMAQDSPPIQLVHPQDQLFOCGPGPARMSCRASGQPPTIRW-----LL 67
Db       | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY      68  NGQPLSMVPDPDHHLLPDGTLLLQPPARGHAHDGQALST--DLGVYTCEASNRLTAVS 125
Db       | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY      74  NSORFETIDFE-----SSGAVLRIQP-----LRTPRDENYYECVAQNSVG-EIT 117
Db       | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY     126  RGARLSAVLREDPQIQPRDMVAIVGEQF-----TLECGPPMGHPEPTVSWWKDGK 176
Db       | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY     118  VHAUKL--VLRED-QLPFGFNIDMGPQLKVVERTATMLCAAS-GNPDPPEITWPKDFL 173
Db       | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY     177  PL--ALQPKR-HTVSGCSLLMARAEKSDEXTVMCVATNSAGHRSPAARVSIQ 226
Db       | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY     174  PVDPSASGRIKQLRSGLAQIESSEETDQKECVATNSAGVRYSSPANLYVR 226
Db       | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

RESULT 13
US-08-716-679-3
; Sequence 3, Application US/08716679
; Patent No. 5846800
; GENERAL INFORMATION:
; APPLICANT: Schlössinger, Joseph
; APPLICANT: Yan, Hai
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PROTEIN
; TITLE OF INVENTION: PHOSPHOTYROSINE PHOSPHATASE-SIGMA
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/716,679
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/130,570
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Miarock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7683-043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,825A
FILING DATE: 14-FEB-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HAND, J. MARK
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 18992DA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-3905
TELEFAX: 732-594-4720
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1911 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-800-825A-5

Query Match 15.3%; Score 246; DB 2; Length 1911;
Best Local Similarity 30.9%; Pred. No. 3.2e-15;
Matches 75; Conservative 43; Mismatches 85; Indels 40; Gaps 11;

QY 2 GSGDLSLGGSGSLPLLLLLIMGGMAQDSPQILVHPQDLFQGGPGPARMSCRASGQPPP 61
DB 6 GPGMSVVGPMG---LLVLLVGGCAAEPPRFKEPKDQIGVSGRVASFVQCATGDKPK 62
QY 62 TIRW-----LLNGQPLSMVPPDPHLLPDGTLILLQPPARGHAGDQALST--DLGVVTC 114
DB 63 RVTWKKKKYNSQRFETIEFDE----SAGAVLRQP-----LRTPRDENVYEC 107
QY 115 EASNRLGTAVSRGARLSVAVLRD-----FOIQRDMVAVVGEQFTLEGPPWGHPE 166
DB 108 VAQNSVG-EITVHAKLT--VLREDQLPSGFPNDMGPKLVKVERTRTATMLCAAS-GNPD 163
QY 167 PTVSWKDKGKPL--ALQPR--HTVSGSLLMARAKSDXTYMCVATNSAGHRESRAARV 223
DB 164 PEITWFKDFLPVDPASNGRIKQLRSALQIESSEETDQGYECVATNSAGVRYSSPANL 223
QY 224 SIQ 226
DB 224 YVR 226

RESULT 10
US-09-158-657-5
Sequence 5, Application US/09158657
Patent No. 6214564
GENERAL INFORMATION:
APPLICANT: RODAN, GIDEON A.
APPLICANT: SCHMIDT, AZRIEL
APPLICANT: RUTLEDGE, SU JANE
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: J. MARK HAND - MERCK & CO., INC.
STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/158,657
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/800,825
FILING DATE: 14-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: HAND, J. MARK
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 18992DA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-3905
TELEFAX: 732-594-4720
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1911 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-158-657-5

Query Match 15.3%; Score 246; DB 3; Length 1911;
Best Local Similarity 30.9%; Pred. No. 3.2e-15;
Matches 75; Conservative 43; Mismatches 85; Indels 40; Gaps 11;

QY 2 GSGDLSLGGSGSLPLLLLLIMGGMAQDSPQILVHPQDLFQGGPGPARMSCRASGQPPP 61
DB 6 GPGMSVVGPMG---LLVLLVGGCAAEPPRFKEPKDQIGVSGRVASFVQCATGDKPK 62
QY 62 TIRW-----LLNGQPLSMVPPDPHLLPDGTLILLQPPARGHAGDQALST--DLGVVTC 114
DB 63 RVTWKKKKYNSQRFETIEFDE----SAGAVLRQP-----LRTPRDENVYEC 107
QY 115 EASNRLGTAVSRGARLSVAVLRD-----FOIQRDMVAVVGEQFTLEGPPWGHPE 166
DB 108 VAQNSVG-EITVHAKLT--VLREDQLPSGFPNDMGPKLVKVERTRTATMLCAAS-GNPD 163
QY 167 PTVSWKDKGKPL--ALQPR--HTVSGSLLMARAKSDXTYMCVATNSAGHRESRAARV 223
DB 164 PEITWFKDFLPVDPASNGRIKQLRSALQIESSEETDQGYECVATNSAGVRYSSPANL 223
QY 224 SIQ 226
DB 224 YVR 226

RESULT 11
PCT-US94-10166-5
Sequence 5, Application PC/TUS9410166
GENERAL INFORMATION:
APPLICANT: RODAN, GIDEON A
APPLICANT: SCHMIDT, AZRIEL
APPLICANT: RUTLEDGE, SU JANE
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: JOHN W. WALLEN III
STREET: P.O. BOX 2000, 126 E. LINCOLN AVE.
CITY: RAHWAY
STATE: NJ
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10166
FILING DATE: 09-SEPT-1994
CLASSIFICATION:

5

RESULT 5

US-08-752-307B-14
; Sequence 14, Application US/08752307B
; Patent No. 5952171

; GENERAL INFORMATION:

; APPLICANT: McCarthy, Sean A.
; APPLICANT: Gearing, David P.

; APPLICANT: Levinson, Douglas A.

; TITLE OF INVENTION: METHOD FOR IDENTIFYING GENES

; TITLE OF INVENTION: ENCODING NOVEL SECRETED OR MEMBRANE-ASSOCIATED PROTEIN

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson, P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: US

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows95

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/752,307B

; FILING DATE: 19-NOV-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Meiklejohn, Ph.D., Anita L.

; REGISTRATION NUMBER: 35,283

; REFERENCE/DOCKET NUMBER: 09404/020001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-542-5070

; TELEFAX: 617-542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 630 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-752-307B-14

Query Match 15.6%; Score 251; DB 2; Length 630;

Best Local Similarity 34.5%; Pred. No. 2.2e-16;

Matches 71; Conservative 34; Mismatches 71; Indels 30; Gaps 11;

Qy 32 PQILVHPDQLFQPG-PARMSCRASGPPPTIRWLLNGQPLSMVPPDPHLLPDGTLIL 90

Db 355 PYWLDEPQN-LILAPGDEGRILVCRANGPKPSIQWLVNGEPIEGSPNPSREVAGDTIVF 413

Qy 91 LQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLRDFQIQPR----- 144

Db 414 -----RDTQIGSS--AVYQCNASNEHGVL---ANAFSVL-----DVPPRILAPRN 455

Qy 145 DMVAVVGQFT-LECGPPWGHPEPTVSWKDGKPLALQPGRHV-SGGSLLMARAEKSD 202

Db 456 QLIKVIQYNRLDLC-PFPGSPIPTLRWFKNGQGNMLOGGNYKAHENGSLMSMARKEDQ 514

Qy 203 XYTMCVATNSAGHRSRAARVSIQEP 228

Db 515 GIYTCVATNILGKVEAQ-VRLEVKDP 539

RESULT 6

US-09-707-802-14

; Sequence 14, Application US/09707802

; Patent No. 6391586

; GENERAL INFORMATION:

; APPLICANT: McCarthy, Sean A.

;

; Gearing, David P.

; Levinson, Douglas A.

; TITLE OF INVENTION: METHOD FOR IDENTIFYING GENES

; TITLE OF INVENTION: ENCODING NOVEL SECRETED OR MEMBRANE-ASSOCIATED PROTEIN

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson, P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: US

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows95

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/707,802

; FILING DATE: 07-No. 6391586-2000

; CLASSIFICATION: <unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/752,307

; FILING DATE: <unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Meiklejohn, Ph.D., Anita L.

; REGISTRATION NUMBER: 35,283

; REFERENCE/DOCKET NUMBER: 09404/020001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-542-5070

; TELEFAX: 617-542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 630 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-09-707-802-14

Query Match 15.6%; Score 251; DB 4; Length 630;

Best Local Similarity 34.5%; Pred. No. 2.2e-16;

Matches 71; Conservative 34; Mismatches 71; Indels 30; Gaps 11;

Qy 32 PQILVHPDQLFQPG-PARMSCRASGPPPTIRWLLNGQPLSMVPPDPHLLPDGTLIL 90

Db 355 PYWLDEPQN-LILAPGDEGRILVCRANGPKPSIQWLVNGEPIEGSPNPSREVAGDTIVF 413

Qy 91 LQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLRDFQIQPR----- 144

Db 414 -----RDTQIGSS--AVYQCNASNEHGVL---ANAFSVL-----DVPPRILAPRN 455

Qy 145 DMVAVVGQFT-LECGPPWGHPEPTVSWKDGKPLALQPGRHV-SGGSLLMARAEKSD 202

Db 456 QLIKVIQYNRLDLC-PFPGSPIPTLRWFKNGQGNMLOGGNYKAHENGSLMSMARKEDQ 514

Qy 203 XYTMCVATNSAGHRSRAARVSIQEP 228

Db 515 GIYTCVATNILGKVEAQ-VRLEVKDP 539

RESULT 7

US-09-991-326-14

; Sequence 14, Application US/09991326

; Patent No. 6395872

; GENERAL INFORMATION:

; APPLICANT: McCarthy, Sean A.

; Gearing, David P.

; Levinson, Douglas A.

; TITLE OF INVENTION: METHOD FOR IDENTIFYING GENES

; TITLE OF INVENTION: ENCODING NOVEL SECRETED OR MEMBRANE-ASSOCIATED PROTEIN

; NUMBER OF SEQUENCES: 14

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; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey
; APPLICANT: Kid, Thomas
; APPLICANT: Brose, Katja
; APPLICANT: Tessier-Lavigne, Marc
; TITLE OF INVENTION: Modulating Robo: Ligand Interactions
; FILE REFERENCE: B98-031-3
; CURRENT APPLICATION NUMBER: US/09/540,245A
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 60/065,544
; PRIOR FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: 60/081,057
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 1395
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-540-245A-15

Query Match 25.2%; Score 405; DB 3; Length 1395;
Best Local Similarity 36.6%; Pred. No. 3.8e-31;
Matches 98; Conservative 38; Mismatches 104; Indels 28; Gaps 8;

Qy 15 LPLLLLLIM---GGM---AODSPPOILVHPDQDQFQGGPARMSCRASGQPPPTIRWLL 67
Db 32 LPALLLVIVASGLPAVRGQYQSPRIETHTDILVKKNEPATLNCRVGEPETIIEWFK 91

Qy 68 NQQLSMVPPDPHLL-LPDGTLLLLQPPARGHAHDQALSTDLGVYTCEASNRGLTAVSR 126
Db 92 DGEPVSTNEKSHRVQPKDGALFFVYRTWQKKEQDG-----GEYVCVAKNRVQAVSR 144

Qy 127 CARLSVAVLRDFQIOPDMVAVGEQFTLECGPPWGHPEPTVSWKDGKPL-----ALQP 182
Db 145 HASLQIAVLRRDFRVEPRKTRVAKGETALLCEGPPKGIPEPTLIWIKDGVFLDLKAMSF 204

Qy 183 GRHT-----VSGSLLMARAEKSDEXTYMCVATNSAGHRESRAARVSIQ-EPQDYTEPVEL 237
Db 205 GASSRVRIVDGNLLISNVFIDEGNYKICIAQLNVGTRESSYAKLIVQVYFMKEPKD- 263

Qy 238 LAVRIQLENVTLLNPDPAPGPKPRAVW 265
Db 264 ---QVMLYGTATFHCVGGDPPPKVLW 288

RESULT 3
US-09-540-245A-17
; Sequence 17, Application US/09540245A
; Patent No. 6270984
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey
; APPLICANT: Kid, Thomas
; APPLICANT: Brose, Katja
; APPLICANT: Tessier-Lavigne, Marc
; TITLE OF INVENTION: Modulating Robo: Ligand Interactions
; FILE REFERENCE: B98-031-3
; CURRENT APPLICATION NUMBER: US/09/540,245A
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 60/065,544
; PRIOR FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: 60/081,057
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 1297
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-540-245A-17

Query Match 22.2%; Score 356.5; DB 3; Length 1297;
Best Local Similarity 33.8%; Pred. No. 2.2e-26;

Matches 97; Conservative 45; Mismatches 104; Indels 41; Gaps 11;

Qy 27 AODSPPOILVHPDQDQFQGGPARMSCRASGQPPPT---IRWLLNGQPL---SMVPPDPHLL 82
Db 25 ASNLAPVIIIEHPIDVVVSRGSPATLNC---GAKPSTAKITWYKDGQVITNKEQVNSHRI 81

Qy 83 LPD-GTLLLLQPPARGHAHDQALSTDLGVYTCEASNRGLTAVSRGARLSVAVLRDFQI 141
Db 82 VLDTGSLFLLLKVNKGKNGKD-----SDAGAYCVASNEHGEVKSNEGSLKLAFLRDFRV 136

Qy 142 QPRDMVAVGEQFTLECGPPWGHPEPTVSWKDGKPLALQP-GRHTV-SGSSLMARAEK 199
Db 137 RPRTVQALGEMAVLECSPPRGPEPVVSWRKDKELRIQDMPRYTTLHSDGNLIIDPVDR 196

Qy 200 SDEXTYMCVATNSAGHRESRAARVSI-----QEPQDYTEPVELLAVRIQLENVTLLNP 252
Db 197 SDGTYQCVANNMVGERVSNPARLSVFEKPKFEQEPKDMT-----VDVGAAVLFD 247

Qy 253 DPAEGPKPRPAVLMXKVGXPLPNLTRPCSGPRLPREARELRGQR 299
Db 248 RVTGDPQPOQ---ITWK-----RKNEPMPVTRAYIAKDNRLRIER 284

RESULT 4
US-09-540-245A-16
; Sequence 16, Application US/09540245A
; Patent No. 6270984
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey
; APPLICANT: Kid, Thomas
; APPLICANT: Brose, Katja
; APPLICANT: Tessier-Lavigne, Marc
; TITLE OF INVENTION: Modulating Robo: Ligand Interactions
; FILE REFERENCE: B98-031-3
; CURRENT APPLICATION NUMBER: US/09/540,245A
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 60/065,544
; PRIOR FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: 60/081,057
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 1381
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-540-245A-16

Query Match 21.5%; Score 345; DB 3; Length 1381;
Best Local Similarity 33.7%; Pred. No. 3.2e-25;
Matches 91; Conservative 31; Mismatches 102; Indels 46; Gaps 8;

Qy 32 PQILVHPDQDQFQGGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHLLPDGTLLLL 91
Db 4 PRIIEHPMDTTPKNDPFTFNCOAEGNPTPTIQWFKDGRLEKTDGSHRIMLPAGGLFLL 63

Qy 92 QPPARGHAHDQALSTDLGVYTCEASNRGLTAVSRGARLSVAVLRDFQIOPDMVAVG 151
Db 64 KV-----IHSRR---ESDAGTYWCENKNEFVARSRNATLQVAVLRDFRLEPANTRVAQG 116

Qy 152 EQFTLECGPPWGHPEPTVSWKDGKPLALQPR---HTVSGSLLMARAEKSDEXTYMCVA 209
Db 117 EVALMECGAPRGSPFQISWRKNGQTLNLVGNKRIRIVDGNLAIQEARQSDGGRYQCVV 176

Qy 210 TNSAGHRESRAARVSI-----IQEPQDYTEPVELLAV---RIQLENVTLLNPDPABGPK 259
Db 177 KNVVGTRESATAFELKVHVRPFLIRGPQNTAVGVSSVVFQCRI-----GGD 222

Qy 260 PRPAVLMXKVGXPLPNLTRPCSGPRLP 289
Db 223 PLPDV---LWR-----RTASGNMP 239
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OM protein - protein search, using sw model

Run on: January 30, 2004, 15:53:19 ; Search time 15.1762 Seconds
(without alignments)
844.758 Million cell updates/sec

Title: US-10-047-021-86
Perfect score: 1608
Sequence: 1 MGSQDLSLGGKSLPLLLL.....SGPRLPRELRGQRRTG 303

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pap:*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pap:*
- 5: /cgn2_6/ptodata/1/iaa/6CTUS COMB.pap:*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	446.5	27.8	1651	3	US-09-540-245A-18
2	405	25.2	1395	3	US-09-540-245A-15
3	356.5	22.2	1297	3	US-09-540-245A-17
4	345	21.5	1381	3	US-09-540-245A-16
5	251	15.6	630	2	US-08-752-307B-14
6	251	15.6	630	4	US-09-707-802-14
7	251	15.6	630	4	US-09-991-326-14
8	246	15.3	1911	1	US-08-348-006B-5
9	246	15.3	1911	2	US-08-800-825A-5
10	246	15.3	1911	3	US-09-158-657-5
11	246	15.3	1911	5	PCT-US94-10166-5
12	237.5	14.8	1501	2	US-08-447-464-3
13	237.5	14.8	1501	2	US-08-716-679-3
14	232	14.4	607	2	US-08-752-307B-12
15	232	14.4	607	2	US-09-707-802-12
16	232	14.4	607	4	US-09-991-326-12
17	227.5	14.1	596	2	US-08-752-307B-13
18	227.5	14.1	596	4	US-09-707-802-13
19	227.5	14.1	596	4	US-09-991-326-13
20	206	12.8	1447	3	US-09-041-886-25
21	206	12.8	1447	5	PCT-US94-05277-2
22	203	12.6	615	2	US-08-752-307B-9
23	203	12.6	615	4	US-09-707-802-9
24	203	12.6	615	4	US-09-991-326-9
25	201.5	12.5	946	5	PCT-US95-08493-13
26	194.5	12.1	612	2	US-08-752-307B-11
27	194.5	12.1	612	4	US-09-707-802-11

28	194.5	12.1	612	4	US-09-991-326-11	Sequence 11, Appl
29	194.5	12.1	1268	4	US-08-506-296B-28	Sequence 28, Appl
30	193	12.0	1091	3	US-08-986-485-5	Sequence 5, Appl
31	193	12.0	1266	4	US-08-506-296B-4	Sequence 4, Appl
32	191	11.9	1260	4	US-08-506-296B-21	Sequence 21, Appl
33	188.5	11.7	1101	3	US-08-986-485-2	Sequence 2, Appl
34	186	11.6	416	4	US-09-638-649-1	Sequence 1, Appl
35	186	11.6	611	2	US-08-752-307B-10	Sequence 10, Appl
36	186	11.6	611	4	US-09-707-802-10	Sequence 10, Appl
37	186	11.6	611	4	US-09-991-326-10	Sequence 10, Appl
38	186	11.6	1253	4	US-08-506-296B-14	Sequence 14, Appl
39	180	11.2	1209	4	US-09-130-158A-2	Sequence 2, Appl
40	175.5	10.9	380	4	US-09-877-730-4	Sequence 4, Appl
41	175.5	10.9	904	4	US-09-877-730-6	Sequence 6, Appl
42	175.5	10.9	985	4	US-09-877-730-10	Sequence 10, Appl
43	175.5	10.9	1069	4	US-09-877-730-2	Sequence 2, Appl
44	175.5	10.9	1150	4	US-09-877-730-8	Sequence 8, Appl
45	175	10.9	462	2	US-08-752-307B-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-09-540-245A-18
; Sequence 18, Application US/09540245A
; Patent No. 6270984
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey
; APPLICANT: Kid, Thomas
; APPLICANT: Brose, Katja
; APPLICANT: Tessier-Lavigne, Marc
; TITLE OF INVENTION: Modulating Robo: Ligand Interactions
; FILE REFERENCE: E98-031-3
; CURRENT APPLICATION NUMBER: US/09/540.245A
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 60/065,544
; PRIOR FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: 60/081,057
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 1651
; TYPE: PRT
; ORGANISM: human
; US-09-540-245A-18

Query Match	27.8%	Score 446.5;	DB 3;	Length 1651;
Best Local Similarity	41.7%	Pred. No. 3.7e-35;		
Matches	91;	Conservative	31;	Mismatches 87;
			Indels	9;
			Gaps	2;
Qy	28	QDSPQILVHPDQDLFGQPGPARMSCRASGPPPTIRWLNGQPLSMVPPDPHH---	LLP	84
Db	64	EDFPFRIVEHPDLSLVKSGEPATLCKAEGRPTTIEWYKGERVETDKDDPRGRMLLP		123
Qy	85	DGTLILLQPPARGHAHQALSTDLGYTCEASNRLGTAVSRGARLSVAVLRBDFQIOPR		144
Db	124	SGSLFFLR-----IVHGRKSRPDEGVYCVARNYLGEAVSHNASLEVALLRDDFRQNP		177
Qy	145	DMVAVGGEQFTLECGPPWGHPEPTVSWKDGKPLALQPGHRTVSGGSLLMARAEKSDXT		204
Db	178	DMVAVGEPVMEQPPRGHPPTISWKKDGSPLDDKDDERITIRGGKLMITYTRKSDAGK		237
Qy	205	YMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRI		242
Db	238	YVCVGTNNVGERSEVAELTLVRPSPFKRPSNLAVTV		275

RESULT 2
US-09-540-245A-15
; Sequence 15, Application US/09540245A
; Patent No. 6270984

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Db 139 DMVAVGEPVMEQPPRGHEPTISWKKGSPDLDKDERITIRGGKLMITYTRKSDAGK 198
Qy 205 YMCVATNSAGHRESRAARVSIQEPDYTEPVELLAVRI 242
Db 199 YVCVGTNMVGERSEVAELTVLERPSFVKRPSNLAVTV 236

RESULT 14
ABU04090
ID ABU04090 standard; Protein; 753 AA.
AC ABU04090;
XX
XX
XX 29-JAN-2003 (first entry)
XX
XX Human expressed protein tag (EPT) #756.
XX
XX Translational profiling; expressed protein tag; EPT; kinase;
KW phosphatase; protease; protease inhibitor; transporter;
KW cytoskeletal protein; receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer;
KW gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma;
KW leukaemia.
XX
XX Homo sapiens.
XX
XX OS
XX
XX WO200278524-A2.
XX
XX
XX 10-OCT-2002.
XX
XX 28-MAR-2002; 2002WO-US09671.
XX
XX 28-MAR-2001; 2001US-279495P.
XX
XX 21-MAY-2001; 2001US-292544P.
XX
XX 08-AUG-2001; 2001US-310801P.
XX
XX 01-OCT-2001; 2001US-326370P.
XX
XX 04-DEC-2001; 2001US-336780P.
XX
XX 20-FEB-2002; 2002US-358985P.
XX
XX (ZYCO-) ZYCO INC.
XX
XX Chicx RM, Tomlinson AJ, Urban RG;
XX
XX WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX cytoskeletal proteins, receptors or transcription factors), useful for
XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma
XX or leukemia.
XX
XX Example 2; SEQ ID No 756; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor.
XX
XX The polypeptide is useful as an immunogenic composition for eliciting
XX in a mammal an immunogenic response directed against any of the purified
XX polypeptide. The purified polypeptide, or the antibody that binds to
XX this polypeptide, is useful for treating cancer. The polypeptide is
XX also useful for identifying compounds that binds to a naturally
XX processed class I or class II MHC-binding polypeptide. The polypeptides
XX and polynucleotides are particularly useful for treating or preventing
XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX lymphoma or leukaemia. These are also useful for screening agents for
XX treating the above mentioned diseases. This sequence represents an
XX expressed protein tag (EPT) isolated from human tissue for translational
XX profiling.
XX
XX Note: This sequence does not appear in the printed specification but was
XX obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 753 AA;
```

```
Query Match 27.8%; Score 446.5; DB 24; Length 753;
Best Local Similarity 41.7%; Pred. No. 2.3e-30;
Matches 91; Conservative 31; Mismatches 87; Indels 9; Gaps 2;

Qy 28 QDSPPQLVHPDQLFGPGPARMSCRASQPPPTIRWLNGQPLSMVPPDPHH---LLP 84
Db 25 EDFPPRIVEHPSDLIVSKGEPATLCKAEGRPPTIEWYKGGERVETDKDPPSRHMLLP 84

Qy 85 DGTLLLLQPPARGHNDGQALSTDGLVYTCEASNRGLCTAVSRGARLSVAVLRDFQIQPR 144
Db 85 SGLSFFLR-----IVHGRKSRPDEGVYCVARNYLGEAVSHNASLEVALRDDFRNPS 138

Qy 145 DMVAVGEOFTLECGPPGHPPTVSWKDGKPLALQPGRHTVSGSLLMARAEKSDXT 204
Db 139 DMVAVGEPVMEQPPRGHEPTISWKKGSPDLDKDERITIRGGKLMITYTRKSDAGK 198

Qy 205 YMCVATNSAGHRESRAARVSIQEPDYTEPVELLAVRI 242
Db 199 YVCVGTNMVGERSEVAELTVLERPSFVKRPSNLAVTV 236

RESULT 15
AY08404
ID AY08404 standard; Protein; 1649 AA.
AC AY08404;
XX
XX 24-JUL-1999 (first entry)
XX
XX Human ROBO1 protein.
XX
XX ROBO1; ROBO2; roundabout; nerve guidance; human; murine; cell function;
KW cell morphology; screening assay.
XX
XX Homo sapiens.
XX
XX WO9920764-A1.
XX
XX 29-APR-1999.
XX
XX 20-OCT-1998; 98WO-US22164.
XX
XX 14-NOV-1997; 97US-0971172.
XX
XX 20-OCT-1997; 97US-0062921.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX Goodman CS, Kidd T, Mitchell KJ, Tear G;
XX
XX WPI; 1999-312615/26.
XX
XX N-PSDB; AAX08404.
XX
XX Robo polypeptides, a new immunoglobulin superfamily member
XX
XX Claim 1; Page 65-71; 80pp; English.
XX
XX This invention describes novel Robo (roundabout) polypeptides, involved
XX in nerve guidance which have been isolated from Drosophila sp.,
XX C. elegans, human and murine samples. The products of the invention can
XX be used to raise anti-Robo antibodies, which can be used to modulate cell
XX function or morphology. The Robo polynucleotides and fragments are useful
XX as probes and primers and for production of the Robo polypeptides. The
XX probes and primers are also useful in screening assays.
XX
XX Sequence 1649 AA;

Query Match 27.8%; Score 446.5; DB 20; Length 1649;
Best Local Similarity 41.7%; Pred. No. 6.3e-30;
Matches 91; Conservative 31; Mismatches 87; Indels 9; Gaps 2;

Qy 28 QDSPPQLVHPDQLFGPGPARMSCRASQPPPTIRWLNGQPLSMVPPDPHH---LLP 84
Db 25 EDFPPRIVEHPSDLIVSKGEPATLCKAEGRPPTIEWYKGGERVETDKDPPSRHMLLP 84
```

XX WPI; 2001-235372/24.
DR N-PSDB; AAS01694.
XX Isolated secreted proteins and their encoding nucleic acids are used
PT for diagnosis and treatment of e.g. bacterial and viral infections,
FT autoimmune diseases and inflammatory disorders -
XX Claim 9; Fig 13; 261pp; English.
XX The present sequence representing human TANGO 330 form 1 is
CC isolated from cDNA clone jthA060922 from a human adrenal gland
CC cDNA library. TANGO 330 is 1 of 4 novel human transmembrane proteins
CC which also includes TANGO 315 (AAU00498-AAU00499), TANGO 437 (AAU00502)
CC and TANGO 480 (AAU00503). The nucleic acids encoding these proteins
CC are useful as modulating agents in regulating a variety of cellular
CC processes and can be used to express the proteins in a host cell in
CC gene therapy applications. Antisense nucleic acid molecules and
CC expression vectors containing the TANGO nucleic acids are also described.
CC Diagnostic assays can be used to detect genetic alterations in the TANGO
CC nucleic acids and to identify compounds that bind to or modulate activity
CC of the TANGO proteins. Anti-TANGO antibodies are used diagnostically to
CC monitor protein levels in tissue as a clinical testing procedure.
CC TANGO 330 shows homology to human Roundabout. TANGO 330 nucleic acids
CC and proteins may be used to diagnose, treat and monitor disorders of the
CC adrenal cortex e.g. hypoadrenalism, hyperadrenalism, and neoplasia. They
CC can also be used to treat cell proliferative disorders (e.g. cancer),
CC and neurological disorders e.g. Alzheimer's disease.
XX Sequence 934 AA;
SQ

Query Match 59.4%; Score 955; DB 22; Length 934;
Best Local Similarity 98.9%; Pred. No. 9.4e-75;
Matches 179; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 93 PPARGHAGDQALSTDLGYTTCESNRLGTAVSARGARLSVAVLRDFQIQPRDMVAVVGE 152
DB 20 PPARGHAGDQALSTDLGYTTCESNRLGTAVSARGARLSVAVLRDFQIQPRDMVAVVGE 79
QY 153 QFTLECGPPWGHPEPTVSWKDGKPLALQPGHRTVSGGSLLMARAEKSDXTMCAVNS 212
DB 80 QFTLECGPPWGHPEPTVSWKDGKPLALQPGHRTVSGGSLLMARAEKSDXTMCAVNS 139
QY 213 AGHRSRAARVSIQBPQDYTEPVELLAVRIQLENTVLNPDPAEGPKRPAVWLKWKVSG 272
DB 140 AGHRSRAARVSIQBPQDYTEPVELLAVRIQLENTVLNPDPAEGPKRPAVWLKWKVSG 199
QY 273 P 273
DB 200 P 200

RESULT 13
AAW83927
ID AAW83927 standard; Protein; 753 AA.
XX AAW83927;
AC AAW83927;
DT 01-MAR-1999 (first entry)
XX Human T85 protein.
DE T85; FMHB-6D4; FMHV-SD4; human; neurological disorder; therapy;
KW diagnosis.
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH Peptide 1..220
FT Peptide /label= Sig_peptide
FT Protein 21..753
FT /label= Mat_protein
FT 525..610

FT /note= "has homology to a fibronectin type III
FT 638..727 domain"
FT /note= "has homology to a fibronectin type III
FT domain"
FT 43..101
FT /note= "has homology to a Ig superfamily domain"
FT 145..203
FT /note= "has homology to a Ig superfamily domain"
FT 237..298
FT /note= "has homology to a Ig superfamily domain"
FT 329..394
FT /note= "has homology to a Ig superfamily domain"
FT 433..491
FT /note= "has homology to a Ig superfamily domain"
FT 247..249
FT /note= "RGD motif"
FT 516..600
FT /note= "cytokine receptor homology N-terminal
FT domain"
XX WO9848051-A2.
XX 29-OCT-1998.
XX 17-APR-1998; 98WO-US07714.
XX 10-OCT-1997; 97US-0062017.
XX 18-APR-1997; 97US-0044746.
XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX Holtzman D, McCarthy SA;
PI WPI; 1999-024021/02.
XX N-PSDB; AAV69278.
XX New isolated human FTHMA-070 and T85 proteins - used to develop
PT products for the diagnosis and therapy of disorders involving
FT cellular processes, e.g. neuronal development.
XX Claim 31; Fig 3; 127pp; English.
XX This is the amino acid sequence of a novel human protein designated
CC T85 and also referred to as FMHB-6D4 and FMHB-SD4. T85 cDNA (see
CC AAV69278) was identified in a human fetal brain cDNA library using a
CC screen designed to identify genes encoding proteins having a
CC functional signal sequence. T85 nucleic acids and polypeptides of
CC the invention are useful as modulating agents in regulating a
CC variety of cellular processes. They can be used for identifying
CC compounds which bind to or modulate the activity of the polypeptides
CC (claimed). They can also be used in screening assays, detection
CC assays (e.g. chromosomal mapping, tissue typing, forensic biology),
CC predictive medicine (e.g. diagnostic assays, prognostic assays,
CC monitoring clinical trials, and pharmacogenomics), and methods of
CC treatment (e.g. therapeutic and prophylactic) e.g. for neurological
CC disorders.
XX Sequence 753 AA;
SQ

Query Match 27.8%; Score 446.5; DB 20; Length 753;
Best Local Similarity 41.7%; Pred. No. 2.3e-30;
Matches 91; Conservative 31; Mismatches 8; Indels 9; Gaps 2;
QY 28 QDSPPQLVHPDQLFQGPGRMASCASCRASGPPPTIRWLLNGQLSMVPPDPHH---LLP 84
DB 25 EDFPPRIVEHPSDLIVSKGEPATLNCRAEGRPTTIEWYKGERVETDKDPPSRHMLLP 84
QY 85 DGTLLLLQPPARGHAGDQALSTDLGYTTCESNRLGTAVSARGARLSVAVLRDFQIQPR 144
DB 85 SGSLFFLLR-----IVHGRKSRPDEGVVVCARNYLGEAVSHNASLEVAILLRDFRQNS 138
QY 145 DMVAVVGEQFTLECGPPWGHPEPTVSWKDGKPLALQPGHRTVSGGSLLMARAEKSDXT 204

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AC AAU00500;
XX 18-JUL-2001 (first entry)
XX Human TANGO 330 form 1 protein.
XX
XX Human; TANGO 315; clone jthaa060g22; TANGO 330; TANGO 437; TANGO 480;
KW cellular process regulator; gene therapy; adrenal gland; cancer;
KW Roundabout; adrenal cortex; hypoadrenalism; hyperadrenalism; neoplasia;
KW cell proliferative disorder; neurological disorder; Alzheimer's disease.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
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FT species variation"
FT Misc-difference 2 /note= "Alternatively this residue is Ser due to
FT species variation"
FT Misc-difference 3 /note= "Alternatively this residue is Val due to
FT species variation"
FT Modified-site 29..34 /note= "N-myristylation site"
FT Modified-site 37..42 /note= "N-myristylation site"
FT Modified-site 44..46 /note= "N-myristylation site"
FT Modified-site 48..53 /note= "Protein kinase C phosphorylation site"
FT Modified-site /note= "N-myristylation site"
FT Misc-difference 53 /note= "Alternatively this residue is Lys due to
FT species variation"
FT Modified-site 54..59 /note= "N-myristylation site"
FT Domain 78..136
FT /label= Ig-like_domain
FT Modified-site 126..132 /note= "Tyrosine kinase phosphorylation site"
FT Modified-site 130..135 /note= "N-myristylation site"
FT Modified-site 151..154 /note= "Casein kinase II phosphorylation site"
FT Modified-site 173..176 /note= "Asn is N-glycosylated"
FT Modified-site 194..196 /note= "Protein kinase C phosphorylation site"
FT Modified-site 221..226 /note= "N-myristylation site"
FT Modified-site 239..244 /note= "N-myristylation site"
FT Modified-site 254..256 /note= "N-myristylation site"
FT Modified-site 282..284 /note= "Protein kinase C phosphorylation site"
FT Modified-site 287..290 /note= "Protein kinase C phosphorylation site"
FT Modified-site 304..309 /note= "Asn is N-glycosylated"
FT Modified-site 316..319 /note= "N-myristylation site"
FT Modified-site 323..326 /note= "Asn is N-glycosylated"
FT Modified-site 331..334 /note= "Asn is N-glycosylated"
FT Modified-site 352..357 /note= "Casein kinase II phosphorylation site"
FT Modified-site 391..393 /note= "N-myristylation site"
FT Modified-site /note= "Protein kinase C phosphorylation site"
FT Domain 394..417
FT /label= Transmembrane_domain
FT 411..416 /note= "N-myristylation site"
FT Domain 418..934
FT /label= Cytoplasmic_domain
FT Modified-site 434..437 /note= "Casein kinase II phosphorylation site"
FT Modified-site 455..457 /note= "Protein kinase C phosphorylation site"
FT Modified-site 472..474 /note= "Protein kinase C phosphorylation site"
FT Modified-site 510..515 /note= "Protein kinase C phosphorylation site"
FT Modified-site 546..559 /note= "N-myristylation site"
FT Modified-site 553..555 /note= "Casein kinase II phosphorylation site"
FT Modified-site 559..561 /note= "Protein kinase C phosphorylation site"
FT Modified-site 601..606 /note= "Protein kinase C phosphorylation site"
FT Modified-site 607..610 /note= "N-myristylation site"
FT Modified-site /note= "Asn is N-glycosylated"
FT Modified-site 632..635 /note= "Casein kinase II phosphorylation site"
FT Modified-site 701..703 /note= "Protein kinase C phosphorylation site"
FT Modified-site 711..714 /note= "Casein kinase II phosphorylation site"
FT Modified-site 721..724 /note= "Casein kinase II phosphorylation site"
FT Modified-site 732..735 /note= "Casein kinase II phosphorylation site"
FT Modified-site 737..739 /note= "Casein kinase II phosphorylation site"
FT Modified-site /note= "Protein kinase C phosphorylation site"
FT Modified-site 762..765 /note= "Casein kinase II phosphorylation site"
FT Modified-site 794..797 /note= "Casein kinase II phosphorylation site"
FT Modified-site 798..803 /note= "Casein kinase II phosphorylation site"
FT Modified-site 806..809 /note= "Casein kinase II phosphorylation site"
FT Modified-site 814..816 /note= "Protein kinase C phosphorylation site"
FT Modified-site 821..824 /note= "Casein kinase II phosphorylation site"
FT Modified-site 825..830 /note= "N-myristylation site"
FT Modified-site 865..867 /note= "Protein kinase C phosphorylation site"
FT Modified-site 865..868 /note= "Casein kinase II phosphorylation site"
FT Modified-site 875..878 /note= "Asn is N-glycosylated"
FT Modified-site 896..898 /note= "Protein kinase C phosphorylation site"
FT Modified-site 914..916 /note= "Protein kinase C phosphorylation site"
FT Modified-site 929..932 /note= "Casein kinase II phosphorylation site"
FT
XX WO200123523-A2.
XX
XX 05-APR-2001.
XX
XX 02-OCT-2000; 2000WO-US27202.
XX
XX 30-SEP-1999; 99US-0409634.
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Kirst S, Wrighton N, Fraser CC;
```

XX WPI; 2001-235372/24.
DR N-PSDB; AAS01695.
XX
XX Isolated secreted proteins and their encoding nucleic acids are used
PT for diagnosis and treatment of e.g. bacterial and viral infections,
PT autoimmune diseases and inflammatory disorders -
XX
XX Claim 9; Fig 14; 261pp; English.
XX
XX The present sequence representing human TANGO 330 form 2 is
CC isolated from cDNA clone Jthx181e12 from a human astrocyte cDNA
CC library. TANGO 330 is 1 of 4 novel human transmembrane proteins
CC which also includes TANGO 315 (AAU00498-AAU00499), TANGO 437 (AAU00502)
CC and TANGO 480 (AAU00503). The nucleic acids encoding these proteins
CC are useful as modulating agents in regulating a variety of cellular
CC processes and can be used to express the proteins in a host cell in
CC gene therapy applications. Antisense nucleic acid molecules and
CC expression vectors containing the TANGO nucleic acids are also described.
CC Diagnostic assays can be used to detect genetic alterations in the TANGO
CC nucleic acids and to identify compounds that bind to or modulate activity
CC of the TANGO proteins. Anti-TANGO antibodies are used diagnostically to
CC monitor protein levels in tissue as a clinical testing procedure.
CC TANGO 330 shows homology to human Roundabout. TANGO 330 nucleic acids
CC and proteins may be used to diagnose, treat and monitor disorders of the
CC adrenal cortex e.g. hypoadrenalism, hyperadrenalism, and neoplasia. They
CC can also be used to treat cell proliferative disorders (e.g. cancer),
CC and neurological disorders e.g. Alzheimer's disease.
XX
XX Sequence 480 AA;
SQ
Query Match 82.8%; Score 1332; DB 22; Length 480;
Best Local Similarity 98.8%; Pred. No. 4.1e-108;
Matches 247; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 24 GCGAQQSPQILVHPQDLFQGGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHLL 83
DB 55 GCGAQQSPQILVHPQDLFQGGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHLL 114
QY 84 PDGTLILLOPPARGHNDQALSTDLGYTTCASNRLGTAVSARGARLSVAVLREDFOIQP 143
DB 115 PDGTLILLOPPARGHNDQALSTDLGYTTCASNRLGTAVSARGARLSVAVLREDFOIQP 174
QY 144 RDMVAVGQFTLECGPPMGHPPTVSWKDGKPLALQGRHTVSGSLLMARAEKSDX 203
DB 175 RDMVAVGQFTLECGPPMGHPPTVSWKDGKPLALQGRHTVSGSLLMARAEKSDX 234
QY 204 TYMCVATNSAGHRESRAARVSIQEPQDYTEPVVLLAVRIQLENVTLNPDPAEGPKRPA 263
DB 235 TYMCVATNSAGHRESRAARVSIQEPQDYTEPVVLLAVRIQLENVTLNPDPAEGPKRPA 294
QY 264 VMLXWKVSGP 273
DB 295 VMLXWKVSGP 304
RESULT 11
AAU99420
ID AAU99420 standard; Protein; 1015 AA.
XX
AC AAU99420;
XX
XX 07-OCT-2002 (first entry)
XX
DE Mouse ECSM4 protein #1.
XX
KW Mouse; endothelial cell-specific molecule 4; ECSM4; neovasculature;
KW imaging vascular endothelium; proliferative disease; cancer;
KW psoriasis; diabetic retinopathy; atherosclerosis; menorrhagia;
KW endothelial damage; tumour neovasculature; cardiac disease;
KW endometriosis; hypoxic condition; angiogenesis; cytostatic;
KW cardiant.

OS Mus sp.
XX WO200236771-A2.
XX
XX 10-MAY-2002.
XX
XX 06-NOV-2001; 2001WO-GB04906.
XX
XX 06-NOV-2000; 2000US-245566P.
XX 07-MAR-2001; 2001US-273662P.
XX
XX (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
XX Bicknell R, Huminteki L;
XX WPI; 2002-508120/54.
XX N-PSDB; ABK87138.
XX
XX Novel endothelial cell-specific molecule polypeptide 1 or 4, useful for
PT imaging, diagnosing and treating a condition involving vascular
PT endothelium e.g. cancer, cardiac disease, endometriosis, diabetes -
XX
XX Disclosure; Fig 13; 248pp; English.
XX
XX The present invention relates to endothelial cell-specific molecule 4
CC (ECSM4), and the polynucleotide sequences encoding it. The ECSM4
CC proteins are useful for imaging vascular endothelium in the body of
CC an individual, and for diagnosing and treating a proliferative
CC disease or condition involving the vascular endothelium (preferably,
CC neovasculature) such as cancer, psoriasis, diabetic retinopathy,
CC atherosclerosis or menorrhagia. The ECSM4 proteins are also useful in
CC the manufacture of diagnostic or prognostic agent for such conditions.
CC The proteins are also useful for detecting endothelial damage or
CC activation, detecting a tumour or tumour neovasculature, cardiac
CC disease, or endometriosis by detecting the amount of ECSM4 present in
CC a sample. The polynucleotide sequences encoding ECSM4 are useful in
CC gene therapy for treating a hypoxic condition such as cancer, cardiac
CC disease, endometriosis or atherosclerosis and in the manufacture of
CC medicaments for treating the above disease. The sequences are useful
CC for modulating angiogenesis in an individual. The present sequence
CC represents a mouse ECSM4 protein.
XX
XX Sequence 1015 AA;
SQ
Query Match 69.2%; Score 1112.5; DB 23; Length 1015;
Best Local Similarity 77.4%; Pred. No. 1.7e-88;
Matches 212; Conservative 20; Mismatches 41; Indels 1; Gaps 1;
QY 1 MGSGGDSLLGGRGSLPLLLLLLIMGMAQDSPPQILVHPQDLFQGGPARMSCRASGQPP 60
DB 11 MGSGGTGLGTWPLPLLLLLFIMGGEALDSPQILVHPQDLFQGGPARMSCRASGQPP 70
QY 61 PTIRWLLNGQPLSMVPPDPHLLPDGTLILLOPPARGHNDQALSTDLGYTTCASNRL 119
DB 71 PTIRWLLNGQPLSMVPPDPHLLPDGTLILLOPPARGHNDQALSTDLGYTTCASNRL 130
QY 120 LGTAVSRGARLSVAVLREDFOIQPRDVMVAVGQFTLECGPPMGHPPTVSWKDGKPLA 179
DB 131 LGTAVSRGARLSVAVLREDFOIQPRDVMVAVGQFTLECGPPMGHPPTVSWKDGKPLV 190
QY 180 LQGRHTVSGSLLMARAEKSDXTYMCVATNSAGHRESRAARVSIQEPQDYTEPVVLLA 239
DB 191 LQGRHTVSGSLLMARAEKSDXTYMCVATNSAGHRESRAARVSIQEPQDYTEPVVLLA 250
QY 240 VRIQLENVTLNPDPAEGPKRPAVAVLXWKVSGP 273
DB 251 VRIQLENVTLNPDPAEGPKRPAVAVLXWKVSGP 284
RESULT 12
AAU00500
ID AAU00500 standard; Protein; 934 AA.
XX

PT encoding them useful for treating cancer, kidney diseases, bone,
XX cartilage disorders and immune deficiencies -
PS Claim 12; Fig 77; 459pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The
CC PRO polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for
CC linking bioactive molecules to cells expressing PRO polypeptides,
CC for modulating biological activities of cells expressing PRO
CC polypeptides, and for identifying agonists or antagonists. The
CC bioactive molecule may be a toxin, radiolabel or antibody, and causes
CC apoptosis or death of the cell. The PRO polypeptides are useful for
CC treating immune disorders, diabetes or hyper- or hypo-insulinaemia,
CC cardiac insufficiency, nervous system disorders, kidney disorders,
CC bone and cartilage disorders or arthritis, tumours, and wound healing.
CC The polynucleotide sequences encoding PRO polypeptides are useful as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of antisense RNA and DNA, in the preparation of PRO polypeptides, for
CC generating transgenic animals or knockout animals, for the genetic
CC analysis of individuals with genetic disorders, and in gene therapy.
CC ABU61071-ABU61164 represent the human PRO polypeptides of the
CC invention.
CC Note: The sequence data for this patent was obtained in electronic
CC format directly from the USPTO web site at
CC seqdata.uspto.gov/patseq/entry.html.
XX
SQ Sequence 985 AA;

Query Match 83.1%; Score 1337; DB 24; Length 985;
Best Local Similarity 98.8%; Pred. No. 3.7e-108;
Matches 248; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 23 MGGMAQDSPPQILVHPDQQLFGPGPARMSCASGQPPPTIRWLLNGQPLSMVPPDPHLL 82
Db 1 MGGMAQDSPPQILVHPDQQLFGPGPARMSCASGQPPPTIRWLLNGQPLSMVPPDPHLL 60
QY 83 LPDGTLLLLQPPARGHAGDQALSTDLGVYTCASNRLGTAVSGARLSVAVLREDFOIQ 142
Db 61 LPDGTLLLLQPPARGHAGDQALSTDLGVYTCASNRLGTAVSGARLSVAVLREDFOIQ 120
QY 143 PRDWAVVGEQFTLCGPPWGHPEPTVSWKDGKPLALQGRHTVSGSLLMARAEKSD 202
Db 121 PRDWAVVGEQFTLCGPPWGHPEPTVSWKDGKPLALQGRHTVSGSLLMARAEKSD 180
QY 203 XYTMCVATNSAGHRESRAARVSIQSPDYTPVELLAVRIQLENTVLLNPDPAEGKPRP 262
Db 181 GTYMCVATNSAGHRESRAARVSIQSPDYTPVELLAVRIQLENTVLLNPDPAEGKPRP 240
QY 263 AVWLXWKVSGP 273
Db 241 AVWLXWKVSGP 251

RESULT 10
AAU00501
ID AAU00501 standard; Protein; 480 AA.
XX
AC AAU00501;
XX

DT 18-JUL-2001 (first entry)

DE Human TANGO 330 form 2 protein.

XX Human; TANGO 315; clone Jthx181e12; TANGO 330; TANGO 437; TANGO 480;
KW cellular process regulator; gene therapy; astrocyte; cancer;
KW Roundabout; adrenal cortex; hypoadrenalism; hyperadrenalism; neoplasia;
KW cell proliferative disorder; neurological disorder; Alzheimer's disease.
XX
OS Homo sapiens.

XX Key Location/Qualifiers

PI Kirst S, Wrighton N, Fraser CC;

FT Peptide
FT 1..20 /label= Signal_peptide
FT Modified-site 15..17 /note= "Protein kinase C phosphorylation site"
FT Domain 21..480 /label= Extracellular_domain
FT Protein 21..480 /label= Mature_TANGO_330_form_2_protein
FT Modified-site 30..33 /note= "cAMP and cGMP dependent protein kinase phosphorylation site"
FT Modified-site 44..47 /note= "Casein kinase II phosphorylation site"
FT Domain 77..147 /label= Ig-like_domain
FT Modified-site 93..95 /note= "Protein kinase C phosphorylation site"
FT Modified-site 100..105 /note= "N-myristylation site"
FT Modified-site 133..138 /note= "N-myristylation site"
FT Modified-site 141..146 /note= "N-myristylation site"
FT Modified-site 148..150 /note= "N-myristylation site"
FT Modified-site 152..157 /note= "Protein kinase C phosphorylation site"
FT Modified-site 158..163 /note= "N-myristylation site"
FT Domain 182..240 /label= Ig-like_domain
FT Modified-site 230..236 /note= "Tyrosine kinase phosphorylation site"
FT Modified-site 234..239 /note= "N-myristylation site"
FT Modified-site 255..258 /note= "Casein kinase II phosphorylation site"
FT Modified-site 277..280 /note= "Asn is N-glycosylated"
FT Modified-site 298..300 /note= "Protein kinase C phosphorylation site"
FT Modified-site 325..330 /note= "N-myristylation site"
FT Modified-site 343..348 /note= "N-myristylation site"
FT Modified-site 358..360 /note= "Protein kinase C phosphorylation site"
FT Modified-site 386..388 /note= "Protein kinase C phosphorylation site"
FT Modified-site 391..394 /note= "Asn is N-glycosylated"
FT Modified-site 408..413 /note= "N-myristylation site"
FT Modified-site 420..423 /note= "Asn is N-glycosylated"
FT Modified-site 427..430 /note= "Asn is N-glycosylated"
FT Modified-site 435..438 /note= "Casein kinase II phosphorylation site"
FT Modified-site 456..461 /note= "N-myristylation site"
XX WO200123523-A2.
XX
XX 05-APR-2001.
XX 02-OCT-2000; 2000WO-US27202.
XX
XX 30-SEP-1999; 99US-0409634.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Kirst S, Wrighton N, Fraser CC;

Db 1 MCGMAQDSPPQILVHPQDLQFGPGPARMSCOASQPPETIRWLLNGQPLSMVPPDPHLL 60
QY 83 LPDGTLLILQPPARGHAHQALSTDLGVYTCEASNRLCTAVSARGARLSVAVLREDFOIQ 142
Db 61 LPDGTLLILQPPARGHAHQALSTDLGVYTCEASNRLCTAVSARGARLSVAVLREDFOIQ 120
QY 143 PRDMVAVGEQFTLECGPPWGHPEPTVSWKDGKPLALQPGRHRTVSGGSLLMARAEKSD 202
Db 121 PRDMVAVGEQFTLECGPPWGHPEPTVSWKDGKPLALQPGRHRTVSGGSLLMARAEKSD 180
QY 203 XYTMCVATNSAGHRSRAARVSIQBPQDYTEPVELLAVRIQLENTVTLNPDPAEGPKRPP 262
Db 181 GTYMCVATNSAGHRSRAARVSIQBPQDYTEPVELLAVRIQLENTVTLNPDPAEGPKRPP 240
QY 263 AVLXWKVSGP 273
Db 241 AVLXWKVSGP 251

RESULT 9
ABU61102
ID ABU61102 standard; Protein; 985 AA.
XX AC ABU61102;
XX DT 08-MAY-2003 (first entry)
XX DE Human PRO860 polypeptide.
XX KW Human; PRO polypeptide; secreted and transmembrane protein;
KW immune disorder; diabetes; hyper-insulinaemia; hypo-insulinaemia;
KW cardiac insufficiency; nervous system disorder; kidney disorder;
KW bone disorder; cartilage disorder; arthritis; tumour; wound healing;
KW genetic disorder; cytostatic; antidiabetic; antiinflammatory;
KW antithratic; anti-tumour; vulnary; antianaemic; dermatological;
KW cardiant.
XX OS Homo sapiens.
XX PN US2002169284-A1.
XX PD 14-NOV-2002.
XX PF 16-OCT-2001; 2001US-0978697.
XX PR 07-OCT-1998; 98WO-US21141.
PR 20-NOV-1998; 98WO-US24855.
PR 05-JAN-1999; 99WO-US00106.
PR 08-MAR-1999; 99WO-US05028.
PR 10-MAR-1999; 99WO-US05190.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 30-NOV-1999; 99WO-US28313.
PR 02-DEC-1999; 99WO-US28551.
PR 16-DEC-1999; 99WO-US28565.
PR 30-DEC-1999; 99WO-US30095.
PR 30-DEC-1999; 99WO-US31243.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 24-FEB-2000; 2000WO-US05004.
PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.

PR 24-AUG-2000; 2000WO-US23328.
PR 01-DEC-2000; 2000WO-US32678.
PR 28-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 22-MAR-2001; 2001WO-US09552.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 17-OCT-1997; 97US-062250P.
PR 03-NOV-1997; 97US-064249P.
PR 13-NOV-1997; 97US-065311P.
PR 21-NOV-1997; 97US-066364P.
PR 10-MAR-1998; 98US-077450P.
PR 11-MAR-1998; 98US-077632P.
PR 11-MAR-1998; 98US-077641P.
PR 11-MAR-1998; 98US-077649P.
PR 12-MAR-1998; 98US-077791P.
PR 13-MAR-1998; 98US-078004P.
PR 20-MAR-1998; 98US-078886P.
PR 20-MAR-1998; 98US-078910P.
PR 20-MAR-1998; 98US-078936P.
PR 20-MAR-1998; 98US-078939P.
PR 25-MAR-1998; 98US-079294P.
PR 26-MAR-1998; 98US-079656P.
PR 27-MAR-1998; 98US-079663P.
PR 27-MAR-1998; 98US-079664P.
PR 27-MAR-1998; 98US-079689P.
PR 27-MAR-1998; 98US-079728P.
PR 27-MAR-1998; 98US-079786P.
PR 30-MAR-1998; 98US-079920P.
PR 30-MAR-1998; 98US-079923P.
PR 26-MAY-1981; 81US-0267213.
PR 17-MAR-1998; 98US-0040220.
PR 26-JUN-1998; 98US-0105413.
PR 07-OCT-1998; 98US-0168978.
PR 02-NOV-1998; 98US-0184216.
PR 06-NOV-1998; 98US-0187368.
PR 07-DEC-1998; 98US-0202054.
PR 22-DEC-1998; 98US-0218517.
PR 05-MAR-1999; 99US-0254465.
PR 10-MAR-1999; 99US-0265686.
PR 12-APR-1999; 99US-0284291.
PR 14-MAY-1999; 99US-0311832.
PR 14-MAY-1999; 99US-0380137.
PR 25-AUG-1999; 99US-0380138.
PR 25-AUG-1999; 99US-0380142.
PR 08-NOV-2000; 2000US-0709238.
PR 27-NOV-2000; 2000US-0723749.
PR 20-DEC-2000; 2000US-0747259.
PR 22-MAR-2001; 2001US-0816744.
PR 22-MAR-2001; 2001US-0816920.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 01-JUN-2001; 2001US-0872035.
PR 05-JUN-2001; 2001US-0874503.
PR 14-JUN-2001; 2001US-0882636.
PR 19-JUN-2001; 2001US-0886342.
PR 30-JUL-2001; 2001US-0918585.
XX (GETH) GENENTECH INC.
XX Ashkenazi A, Baker KP, Botstein D, Desnoyers L, Eaton D;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;
PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
XX WPI; 2003-288163/28.
DR N-PSDB; AEX92441.
XX Novel secreted and transmembrane polypeptides and polynucleotides
PT


```
XX (HELI-) HELIX RES INST.
XX PA
XX PI Ota T, Isoqai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
XX PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S;
XX PI Senoo C, Nezu J;
XX XX
XX DR WPI; 2001-564736/63.
XX DR N-PSDB; AAH78073.
XX XX
XX PT New genes encoding protein kinase and protein phosphatase, useful for
XX PT identifying modulators which can be used to treat human or animal
XX PT disorders associated with the expression or function of these enzymes -
XX XX
XX PS Claim 2; Page 175-180; 336pp; Japanese.
XX CC
XX CC The present sequence represents a human protein kinase/protein
XX CC phosphatase. The polypeptides are expected to participate in signal
XX CC transduction in cells. The kinase phosphatases are connected with
XX CC intracellular signalling pathways. Antisense oligonucleotides and
XX CC compounds identified by screening (agonists or antagonists) can be
XX CC used to treat human or animal disorders associated with the expression
XX CC or function of the protein. In addition, the polypeptides may be used
XX CC as target molecules for drug development.
XX SQ Sequence 792 AA;
Query Match 89.3%; Score 1436; DB 22; Length 792;
Best Local Similarity 98.5%; Pred. No. 66-117;
Matches 269; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 MSGGDSLLGGRGSLPLLLLLIMGMAQDSPPQILVHPQDQLFQGGPARMSCRASGQPP 60
Db 1 MSGGDSLLGGRGSLPLLLLLIMGMAQDSPPQILVHPQDQLFQGGPARMSCRASGQPP 60
QY 61 PTIRWLLNGQPLSMVPPDPHLLPDGTLTLLQPPARGHAHDGQALSTDLGVYTCASNRL 120
Db 61 PTIRWLLNGQPLSMVPPDPHLLPDGTLTLLQPPARGHAHDGQALSTDLGVYTCASNRL 120
QY 121 GTAVSRGARLSVAVLRDFOTOPRDMVAVGEOFTLECGPPNGHPPTVSWMKDKPLAL 180
Db 121 GTAVSRGARLSVAVLRDFOTOPRDMVAVGEOFTLECGPPNGHPPTVSWMKDKPLAL 180
QY 181 QPGRHTVSGGSLLMARAEKSDXTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAV 240
Db 181 QPGRHTVSGGSLLMARAEKSDXTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAV 240
QY 241 RIQENVTLLNPDPAEGPKPRPAVWLXWKVSGP 273
Db 241 RIQENVTLLNPDPAEGPKPRPAVWLXWKVSGP 273
RESULT 7
AAAY41716
ID AAAY41716 standard; Protein; 985 AA.
XX
XX AC AAAY41716;
XX XX
XX DT 07-DEC-1999 (first entry)
XX XX
XX DE Human PRO860 protein sequence.
XX KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
XX KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
XX KW secreted protein; transmembrane protein.
XX OS Homo sapiens.
XX XX
XX FN WO9946281-A2.
XX PD 16-SEP-1999.
XX XX
XX PF 08-MAR-1999; 99WO-US05028.
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XX 10-MAR-1998; 98US-0077450.
XX PR 11-MAR-1998; 98US-0077632.
XX PR 11-MAR-1998; 98US-0077641.
XX PR 11-MAR-1998; 98US-0077649.
XX PR 12-MAR-1998; 98US-0077791.
XX PR 13-MAR-1998; 98US-0078004.
XX PR 17-MAR-1998; 98US-0040220.
XX PR 20-MAR-1998; 98US-0078886.
XX PR 20-MAR-1998; 98US-0078910.
XX PR 20-MAR-1998; 98US-0078936.
XX PR 20-MAR-1998; 98US-0078939.
XX PR 25-MAR-1998; 98US-0079294.
XX PR 26-MAR-1998; 98US-0079656.
XX PR 27-MAR-1998; 98US-0079663.
XX PR 27-MAR-1998; 98US-0079664.
XX PR 27-MAR-1998; 98US-0079689.
XX PR 27-MAR-1998; 98US-0079728.
XX PR 27-MAR-1998; 98US-0079786.
XX PR 30-MAR-1998; 98US-0079920.
XX PR 30-MAR-1998; 98US-0079923.
XX PR 31-MAR-1998; 98US-0080105.
XX PR 31-MAR-1998; 98US-0080107.
XX PR 31-MAR-1998; 98US-0080165.
XX PR 31-MAR-1998; 98US-0080194.
XX PR 01-APR-1998; 98US-0080327.
XX PR 01-APR-1998; 98US-0080328.
XX PR 01-APR-1998; 98US-0080333.
XX PR 01-APR-1998; 98US-0080334.
XX PR 08-APR-1998; 98US-0081049.
XX PR 08-APR-1998; 98US-0081070.
XX PR 08-APR-1998; 98US-0081071.
XX PR 09-APR-1998; 98US-0081195.
XX PR 09-APR-1998; 98US-0081203.
XX PR 09-APR-1998; 98US-0081229.
XX PR 15-APR-1998; 98US-0081817.
XX PR 15-APR-1998; 98US-0081838.
XX PR 15-APR-1998; 98US-0081952.
XX PR 15-APR-1998; 98US-0081955.
XX PR 21-APR-1998; 98US-0082568.
XX PR 21-APR-1998; 98US-0082569.
XX PR 22-APR-1998; 98US-0082700.
XX PR 22-APR-1998; 98US-0082704.
XX PR 22-APR-1998; 98US-0082804.
XX PR 23-APR-1998; 98US-0082767.
XX PR 23-APR-1998; 98US-0082796.
XX PR 27-APR-1998; 98US-0083336.
XX PR 28-APR-1998; 98US-0083322.
XX PR 29-APR-1998; 98US-0083392.
XX PR 29-APR-1998; 98US-0083495.
XX PR 29-APR-1998; 98US-0083496.
XX PR 29-APR-1998; 98US-0083499.
XX PR 29-APR-1998; 98US-0083500.
XX PR 29-APR-1998; 98US-0083545.
XX PR 29-APR-1998; 98US-0083554.
XX PR 29-APR-1998; 98US-0083558.
XX PR 30-APR-1998; 98US-0083559.
XX PR 30-APR-1998; 98US-0083742.
XX PR 05-MAY-1998; 98US-0084366.
XX PR 06-MAY-1998; 98US-0084414.
XX PR 07-MAY-1998; 98US-0084441.
XX PR 07-MAY-1998; 98US-0084598.
XX PR 07-MAY-1998; 98US-0084600.
XX PR 07-MAY-1998; 98US-0084627.
XX PR 07-MAY-1998; 98US-0084637.
XX PR 07-MAY-1998; 98US-0084639.
XX PR 07-MAY-1998; 98US-0084640.
XX PR 13-MAY-1998; 98US-0085323.
XX PR 13-MAY-1998; 98US-0085338.
XX PR 13-MAY-1998; 98US-0085339.
XX PR 15-MAY-1998; 98US-0085573.
XX PR 15-MAY-1998; 98US-0085579.
```


QY 181 QPGRHTVSGSLLMARAESDXTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAV 240
DB 181 QPGRHTVSGSLLMARAESDXTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAV 240
QY 241 RIQLENTVLLNPDPAEGPKPRPAVWLXWKVSGPXRLLPNLTRPCSGPRLPREARELGRQR 300
DB 241 RIQLENTVLLNPDPAEGPKPRPAVWLXWKVSGPXRLLPNLTRPCSGPRLPREARELGRQR 300
QY 301 NTG 303
DB 301 NTG 303

RESULT 3

ID ABB97310 standard; Protein; 1007 AA.

XX ABB97310;

DT 27-JUN-2002 (first entry)

DE Novel human protein SEQ ID NO: 578.

XX Human; antianaemic; vulnery; antiinflammatory; immunomodulator;
KW antiinfertility; cerebroprotective; cytostatic; rheumatic; gene therapy;
KW neuroprotective; antiparkinsonian; protein therapy; EST;
KW expressed sequence tag.

OS Homo sapiens.

PN WO200222660-A2.

XX 21-MAR-2002.

XX 10-SEP-2001; 2001WO-US26015.

XX 11-SEP-2000; 2000US-0659671.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;

PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;

XX WPI; 2002-292408/33.

DR N-PSDB; ABN32496.

XX An isolated polynucleotide for treating diseases associated with its
PT encoded polypeptide such as cancer and multiple sclerosis -

XX Example 2; SEQ ID NO 578; 509pp; English.

XX The present invention provides the protein and coding sequences of 444
CC novel human proteins. These were isolated from expressed sequences tags
CC (ESTs). They can be used to stimulate cell growth, to regulate
CC haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth
CC e.g. in burn treatment, to regulate the immune system e.g. to treat
CC multiple sclerosis, to regulate activin or inhibin e.g. to treat
CC infertility, to regulate haemostasis or thrombolysis e.g. to treat
CC stroke and cancer, to screen for drugs, to treat inflammatory conditions
CC e.g. rheumatoid arthritis, and to treat nervous system disorders e.g.
CC Parkinson's disease. The present sequence is a protein of the invention.

XX Sequence 1007 AA;

Query Match 89.8%; Score 1444; DB 23; Length 1007;

Best Local Similarity 98.9%; Pred. No. 1.6e-117;

Matches 270; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGSQDLSLLGGRGSLPLLLLLIMGMAQDSPQILVHPQDLFCGPGPARMSCRAGQPP 60

DB 1 MGSQDLSLLGGRGSLPLLLLLIMGMAQDSPQILVHPQDLFCGPGPARMSCRAGQPP 60

QY 61 PTIRLLNGQFLSMVPPDPHLLPDGTLTLLQPPARGHAHDGQALSTDLGYVTCESNRL 120
DB 61 PTIRLLNGQFLSMVPPDPHLLPDGTLTLLQPPARGHAHDGQALSTDLGYVTCESNRL 120
QY 121 GTAVSRGARI.SVAVLRDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWKDGKPLAL 180
DB 121 GTAVSRGARI.SVAVLRDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWKDGKPLAL 180
QY 181 QPGRHTVSGSLLMARAESDXTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAV 240
DB 181 QPGRHTVSGSLLMARAESDXTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAV 240
QY 241 RIQLENTVLLNPDPAEGPKPRPAVWLXWKVSGP 273
DB 241 RIQLENTVLLNPDPAEGPKPRPAVWLXWKVSGP 273

RESULT 4

AAU99419

ID AAU99419 standard; Protein; 1104 AA.

XX AAU99419;

AC AAU99419;

DT 07-OCT-2002 (first entry)

DE Human ECSM4 protein.

XX Human; endothelial cell-specific molecule 4; ECSM4; neovasculature;
KW imaging vascular endothelium; proliferative disease; cancer;
KW psoriasis; diabetic retinopathy; atherosclerosis; menorrhagia;
KW endothelial damage; tumour neovasculature; cardiac disease;
KW endometriosis; hypoxic condition; angiogenesis; cytostatic;
KW cardiant.

XX Homo sapiens.

OS WO200236771-A2.

PN 10-MAY-2002.

XX 06-NOV-2001; 2001WO-GB04906.

XX 06-NOV-2000; 2000US-245566P.

PR 07-MAR-2001; 2001US-273662P.

XX (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.

XX Bicknell R, Huminiecki L;

PI WPI; 2002-508120/54.

DR N-PSDB; ABK87137.

XX Novel endothelial cell-specific molecule polypeptide 1 or 4, useful for
PT imaging, diagnosing and treating a condition involving vascular
PT endothelium e.g. cancer, cardiac disease, endometriosis, diabetes -

PS Claim 53; Fig 12; 248pp; English.

XX The present invention relates to endothelial cell-specific molecule 4
CC (ECSM4), and the polynucleotide sequences encoding it. The ECSM4
CC proteins are useful for imaging vascular endothelium in the body of
CC an individual, and for diagnosing and treating a proliferative
CC disease or condition involving the vascular endothelium (preferably,
CC neovasculature) such as cancer, psoriasis, diabetic retinopathy,
CC atherosclerosis or menorrhagia. The ECSM4 proteins are also useful in
CC the manufacture of diagnostic or prognostic agent for such conditions.
CC The proteins are also useful for detecting endothelial damage or
CC activation, detecting a tumour or tumour neovasculature, cardiac
CC disease, or endometriosis by detecting the amount of ECSM4 present in
CC a sample. The polynucleotide sequences encoding ECSM4 are useful in
CC gene therapy for treating a hypoxic condition such as cancer, cardiac
CC disease, endometriosis or atherosclerosis and in the manufacture of
CC medicaments for treating the above disease. The sequences are useful

```
XX WPI; 2002-599716/64.
DR N-PSDB; ABQ92573.
XX
XX New polynucleotides and polypeptides useful for diagnosing, prognosing,
PT treating or preventing e.g. neurodegenerative, central nervous system,
PT autoimmune, respiratory, reproductive, or inflammatory diseases or
PT disorders
XX
XX Claim 11; Fig 1; 785pp; English.
XX
XX The invention relates to novel genes (ABQ92553-ABQ92607) and proteins
CC (ABP62013-ABP62153) useful for preventing, treating or ameliorating
CC medical conditions e.g. by human or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
XX
XX Sequence 303 AA;
SQ
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Best Local Similarity 100.0%; Pred. No. 5.3e-132;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MGSGDLSLLGGSGSLPLLLLLIMGMAQDSPQILVHPDQLFQGGPARMSCRASGQPP 60
QY 61 PTIRWLLNGQPLSMVPPDPHLLPDGTLILLQPPARGHAGDQALSTDGLVYTCEASNRL 120
DB 61 PTIRWLLNGQPLSMVPPDPHLLPDGTLILLQPPARGHAGDQALSTDGLVYTCEASNRL 120
QY 121 GTAVSRGARLSVAVLRDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKGKPLAL 180
DB 121 GTAVSRGARLSVAVLRDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKGKPLAL 180
QY 181 QPGRHTVSGSLLMARAEKSDXTVMCVATNSAGHRESRAARVSIQEPDYTEPVELLAV 240
DB 181 QPGRHTVSGSLLMARAEKSDXTVMCVATNSAGHRESRAARVSIQEPDYTEPVELLAV 240
QY 241 RIQENVTLNPDPAEGPKPRPAVWLXWVSGPXRLPNLTRPCSGPRLPREARELRGQR 300
DB 241 RIQENVTLNPDPAEGPKPRPAVWLXWVSGPXRLPNLTRPCSGPRLPREARELRGQR 300
QY 301 NTG 303
DB 301 NTG 303
RESULT 2
AA12934
ID AA12934 standard; Protein; 304 AA.
XX
XX AA12934;
XX
XX 17-JUN-1999 (first entry)
XX
XX Amino acid sequence of a human secreted peptide.
XX
XX Human secreted protein; cancer; immune disorder; infection;
KW inflammatory disorder; skin disorder; tumour; atherosclerosis;
KW restenosis; autoimmune disorder; Alzheimer's disease;
KW peripheral neuropathy; trauma; spinal cord injury; allergy;
KW hematopoietic disorder; skeletal disorder; neurological disorder;
```

```
KW arthritic disorder; asthma; immunodeficiency disease; AIDS;
KW transplant rejection; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
FH 1..27
FT Peptide /note= "signal peptide"
FT Protein 28..303
FT /note= "secreted protein"
XX
XX WO9911293-A1.
XX 11-MAR-1999.
XX 03-SEP-1998; 98WO-US18360.
XX 12-SEP-1997; 97US-0058974.
XX 05-SEP-1997; 97US-0057626.
XX 05-SEP-1997; 97US-0057663.
XX 05-SEP-1997; 97US-0057669.
XX 12-SEP-1997; 97US-0058666.
XX 12-SEP-1997; 97US-0058667.
XX 12-SEP-1997; 97US-0058973.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Brewer LA, Ebner R, Lafleur DW, Moore PA, Olsen HS;
XX Rosen GA, Ruben SM, Shi Y;
XX WPI; 1999-204988/17.
XX N-PSDB; AAX51721.
XX
XX New isolated human genes and the secreted polypeptides they encode
PT - useful for diagnosis and treatment of e.g. neurological disorders,
PT tumours, immune disorders, inflammation or haematological disorders
XX
XX Claim 11; Page 190-191; 215pp; English.
XX
XX AA12914-68 represent human secreted proteins. The polypeptides and
CC their corresponding polynucleotides are useful for preventing,
CC treating or ameliorating medical conditions, e.g. by protein or gene
CC therapy. Pathological conditions can also be diagnosed by determining
CC the amount of the new polypeptides in a sample or by determining the
CC presence of mutations in the new polynucleotides. Specific uses are
CC described for each polynucleotide, based on which tissues they are
CC most highly expressed in, and include developing products for the
CC diagnosis or treatment of cancer, immune disorders, infection,
CC inflammatory disorders, skin disorders, tumours, atherosclerosis,
CC restenosis, autoimmune disorders, Alzheimer's disease, peripheral
CC neuropathies, trauma, spinal cord injuries, allergy, hematopoietic
CC disorders, skeletal disorders, neurological disorders, arthritic
CC disorders, asthma, immunodeficiency diseases, AIDS and transplant
CC rejection. The polypeptides are also useful for identifying their
CC binding partners.
XX
XX Sequence 304 AA;
SQ
Query Match 99.6%; Score 1602; DB 20; Length 304;
Best Local Similarity 100.0%; Pred. No. 5.3e-132;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MGSGDLSLLGGSGSLPLLLLLIMGMAQDSPQILVHPDQLFQGGPARMSCRASGQPP 60
QY 61 PTIRWLLNGQPLSMVPPDPHLLPDGTLILLQPPARGHAGDQALSTDGLVYTCEASNRL 120
DB 61 PTIRWLLNGQPLSMVPPDPHLLPDGTLILLQPPARGHAGDQALSTDGLVYTCEASNRL 120
QY 121 GTAVSRGARLSVAVLRDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKGKPLAL 180
DB 121 GTAVSRGARLSVAVLRDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKGKPLAL 180
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 30, 2004, 15:44:59 ; Search time 39.2487 Seconds
(without alignments)
1225.369 Million cell updates/sec

Title: US-10-047-021-86
Perfect score: 1608
Sequence: 1 MGSGDSDLGGRSLPLLL.....SGPRLPREALRGQRNTG 303

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1602	99.6	303	23	ABP62033 Human secreted pro
2	1602	99.6	304	23	AA12934 Amino acid sequenc
3	1444	89.8	1007	23	ABB97310 Novel human protei
4	1444	89.8	1104	23	AAU99419 Human ECSM4 protei
5	1436	89.3	792	22	AA895515 Human protein sequ
6	1436	89.3	792	22	AA895515 Amino acid sequenc
7	1337	83.1	985	20	AA141716 Human PRO860 prote
8	1337	83.1	985	21	AA44272 Human PRO860 (UNQ4
9	1337	83.1	985	24	ABU61102 Human PRO860 polyp

10	1332	82.8	480	22	AAU00501 Human TANGO 330 fo
11	1112.5	69.2	1015	23	AAU99420 Mouse ECSM4 protei
12	955	59.4	934	22	AAU00500 Human TANGO 330 fo
13	446.5	27.8	753	20	AAW83927 Human T85 protein.
14	446.5	27.8	753	24	ABU04090 Human expressed pr
15	446.5	27.8	1649	20	AAU08404 Human ROBO1 protei
16	446.5	27.8	1649	24	ABU04091 Human expressed pr
17	446.5	27.8	1651	20	AAU13566 Human Robo 1 polyp
18	446.5	27.8	1651	24	ABU04089 Human expressed pr
19	446.5	27.8	1651	24	ABU04092 Human expressed pr
20	446.5	27.8	1651	24	ABU04093 Human expressed pr
21	446.5	27.8	1651	24	ABU04094 Human expressed pr
22	405	25.2	1395	20	AAU13563 Drosophila Robo 1
23	405	25.2	1395	20	AAU08401 Drosophila sp. ROB
24	405	25.2	1395	22	ABB68257 Drosophila melanog
25	404.5	25.2	1515	23	AAO19185 Human neurotransmi
26	396.5	24.7	1422	23	AAO19179 Human neurotransmi
27	356.5	22.2	1297	20	AAU13565 C. elegans Robo po
28	356.5	22.2	1297	20	AAU08403 C. elegans Robo pr
29	345	21.5	1380	20	AAU08402 Drosophila sp. ROB
30	345	21.5	1381	20	AAU13564 Drosophila Robo 2
31	323	20.1	823	22	AAU13562 Drosophila melanog
32	307	19.1	885	22	ABB61502 Drosophila melanog
33	267.5	16.6	1496	20	AAW81030 Melanoma associate
34	267.5	16.6	1496	21	AAU70469 Human p53 target m
35	267.5	16.6	1496	24	ABU03498 Angiogenesis-assoc
36	267.5	16.6	1498	22	ABB11587 Human peroxidasin
37	285.5	16.5	1463	23	AAO21660 Human secreted pro
38	260.5	16.2	937	22	AAU78714 Human protein SEQ
39	260.5	16.2	952	22	AAU78715 Human protein SEQ
40	260.5	16.2	1267	24	AAE32108 Human cytoskeleton
41	260.5	16.2	1359	24	AAE32109 Human cytoskeleton
42	260.5	16.2	1370	24	ABU19347 NOVX related prote
43	259	16.1	1527	22	ABB57771 Drosophila melanog
44	254.5	15.8	3931	24	ABU07377 Human protein NOV9
45	253.5	15.8	793	23	AAE14781 Human immunoglobul

ALIGNMENTS

RESULT 1
ABP62033
ID ABP62033 standard; Protein; 303 AA.
AC ABP62033;
XX
XX
DT 12-NOV-2002 (first entry)
XX
XX
DE Human secreted protein SEQ ID NO 86.
XX
KW Human; neutropic; neuroprotective; cytostatic; dermatological; virucide;
KW immunosuppressive; antinflammatory; anti-HIV; antibacterial; vulnery;
KW antiparkinsonian; antisickling; antianemic; antithratic; cancer;
KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine.
XX
OS Homo sapiens.
XX
XX
PN WO200257420-A2.
XX
XX
PD 25-JUL-2002.
XX
XX
PF 17-JAN-2002; 2002WO-US01109.
XX
XX
PR 18-JAN-2001; 2001US-262066P.
XX
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX
PI Moore PA, Ruben SM, LaFleur DW, Shi Y, Rosen CA, Olsen H;
PI Ebner R, Brewer LA;

FT CONFLICT 168 168 /FTID=VSP 002593.
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 Best Local Similarity 22.7%; Pred. No. 3.6e-09;
 Matches 79; Conservative 39; Mismatches 117; Indels 113; Gaps 9;
 QY 3 SPPQILVHPDQLFQGPARGMCRSCQPPPTIRWLLNGOPLSMVPPDHPHLLPDGTL 62
 DB 51 TPFVLEVPDVLTVRSGSSVILNLSAYSEPKLEWKDGTFLNVLVSDRRQLPDGSLF 110
 QY 63 LLOPPARGHARDGOALSTDLGVYTCAS-NRLGTAVSRGARGLSVA----- 106
 DB 111 ISNVVHSHKN-----KPDGYYOCVATVESLGTIIISRTAKLVAGLPRTSOPESPSSVY 164
 QY 107 -----VLRED----- 111
 DB 165 AGGAILNCEVNADLVFVRWEQNRQPLDLDRLVILKPSGMLVLSNATEDGGGLYRCVVE 224
 QY 112 -----PQIOPRDVAVVGEQFTLECGPPWGHPEPTVSWM 145
 DB 225 SGPPKYSDEVELKULDPDEVISDLVFLKQPSPLVRVIGQDVVLPCVAS-GLPTPTIKWM 283
 QY 146 KDGKPLALQPRHTV--SGSLLMARAEKSDXTYMCVATNSAGHRESRAARVSIQEPD 203
 DB 284 KNEALDTESSERLVLLAGSLEISDVTEDDAGTYFCIADNGNETIEAQALTVQAPPEF 343
 QY 204 YTEPVELLAVRIQLENTVLNPDPAEGPKPRPAVWLKVKVSGPXRLPN 251
 DB 344 LKOPTIYA-----HESMDIVFECEVTG-KPTPTV--KWKNGMDWIPS 384
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 AC P28685;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Contactin 2 precursor (Axonin-1).
 GN CNTN2.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=92174898; PubMed=1311675;
 RC Zuellig R.A., Rader C., Schroeder A., Kalousek M.B.,
 RA von Bohlen Und Halbach F., Osterwalder T., Inan C., Stoeckli E.T.,
 RA Affolter H.-U., Fritz A., Hafen E., Sonderegger P.;
 RT "The axonally secreted cell adhesion molecule, axonin-1. Primary
 RT structure, immunoglobulin-like and fibronectin-type-III-like domains
 RT and glycosyl-phosphatidylinositol anchorage.";
 RL Eur. J. Biochem. 204:453-463 (1992).
 CC -!- FUNCTION: AXON-ASSOCIATED CELL ADHESION MOLECULE (AXCAM) WHICH
 CC PROMOTES NEURITE OUTGROWTH BY INTERACTION WITH THE AXCAM L1 (G4)
 CC OF NEURITIC MEMBRANE.
 CC -!- SUBCELLULAR LOCATION: ATTACHED TO THE NEURONAL MEMBRANE BY A
 CC GPI-ANCHOR.
 CC -!- PTM: The N-terminus is blocked
 CC -!- SIMILARITY: Contains 6 immunoglobulin-like C2-type domains.
 CC -!- SIMILARITY: Contains 4 fibronectin type III domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC or send an email to license@isb-sib.ch).
 CC EMBL; X63101; CAA44815.1; -
 DR PIR; S22383; S22383.
 DR PDB; 1CS6; 19-MAY-00.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG_C2.
 DR Pfam; PF00041; fn3; 3.
 DR Pfam; PF00047; ig; 6.
 DR SMART; SM00060; FN3; 4.
 DR SMART; SM00408; IGC2; 5.
 DR PROSITE; PS00835; IG_LIKE; 6.
 KW Immunoglobulin domain; Glycoprotein; Signal; GPI-anchor;
 KW Cell adhesion; Repeat; 3D-structure.
 FT SIGNAL 1 23 OR 25 (POTENTIAL)..
 FT CHAIN 24 ?
 FT PROPEP ? 1036
 FT DOMAIN 32 123
 FT DOMAIN 128 223
 FT DOMAIN 234 317
 FT DOMAIN 322 406
 FT DOMAIN 412 499
 FT DOMAIN 504 598
 FT DOMAIN 599 608
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 FT DOMAIN 608 709
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 FT DOMAIN 812 912
 FT DOMAIN 913 1009
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 DB 54 LTRCARANPPATYRWKNGTGLKM-GPDSRYRLVAGDLVISNP-----VKAKDAG 102
 QY 84 VYTCASNRLGTAVSRGARGLSVAVLREDFOIOPRDVAVV--GEQFTLECGPPWGHPEP 140
 DB 103 SYQCVAATNAGTVVSREASLRFGLQF-PSAERDPPKITEGKGVHFT--CSPPPHYAL 159
 QY 141 TVSWKDGKPLAL-QPGRHTVS--GSLLMARAEKSDXTYMCVATNSAGHRE----- 190
 DB 160 SYRWLLNEFFNPADGRFRVSTGNTGLYIAKTEASDLGNYSFCFATS---HIDFTKSVF 216
 QY 191 SRAARVSI--QEPQDYTEPVE-----LLAVRIQLENTVLNPD 227
 DB 217 SKFSQLSAAEDARQYAPSIKAFKPADTVALTGQWVTLCECFAGFNVPV 264

RESULT 11
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 ID PTK7 HUMAN STANDARD; PRT; 1070 AA.
 AC Q13308; Q13417;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tyrosine-protein kinase-like 7 precursor (Colon carcinoma kinase-4)
 DE (CKK-4).
 GN PTK7 OR CKK4.

Appendix A

10/047024

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